

## A NOVEL CATEGORICAL AND ONTOLOGY FRAMEWORK FOR COMPLEX SYSTEMS BIOLOGY

ION C. BAIANU, JAMES F. GLAZEBROOK AND RONALD BROWN

ABSTRACT. A novel conceptual framework is developed for the Complexity Levels Theory in a Categorical Ontology of Space, Time and Complex System Dynamics. This conceptual and formal construction supports also computer-based ontological studies of emergent biosystems, supercomplex dynamics, evolution and human consciousness. A claim is defended concerning the universal representation of complexity levels in categorical terms in terms of non-commutative diagrams of complex biological relations. As an essential example, the relational-organizational structures of living organisms are represented by applying the important categorical concept of natural transformations to biomolecular reactions and relational structures that emerge from such relational structures in living systems. Thus, several relational theories of living systems can be represented by natural transformations of organismic, relational structures. We also consider a complete model of the process of Evolution of both organisms and species beginning with the simplest possible algebraic and topological structure for the primordial— the first organism to evolve above the molecular level of proto-enzymes and proto-RNA. Then, the evolution of other super-complex organisms through adaptation, as well as the ascent of man is viewed in novel categorical terms, such as *variable biogroupoid* representations and *varying biotopology* in speciation and the evolution of species.

KEYWORDS: *Complex systems biology (CSB), category framework for CSB, categorical dynamics, emergence and evolution of complex and ultra-complex biosystems*

2000 *Mathematics Subject Classification*: 16B50, 68Q15.

## 1. A CATEGORICAL FRAMEWORK FOR THE ONTOLOGICAL THEORY OF LEVELS

### **Dynamic Complexity and the Emergence of Relational Super-structures**

A novel conceptual framework is here developed for the Complexity Levels Theory in a Categorical Ontology of Space, Time and Dynamic Systems [1]. This conceptual and formal construction supports also computer-based [2] ontological studies of emergent biosystems, supercomplex dynamics [3], evolution and human consciousness [4]. The claim is here defended concerning the universal representation of complexity levels in categorical terms in terms of non-commutative diagrams of highly complex relations occurring in biological, ecological and societal systems. As a key example, let us consider at first the relational-organizational structures (ROS) of living organisms as being represented, or modeled, by applying the important categorical concept of natural transformations between categories of functors to biomolecular reactions and relational structures that emerge through such reactions and other multiple interactions in living systems. Then, we can represent by means of such natural transformations several relational theories of living systems –that may appear to be quite different– in terms of certain underlying organismic relational structures that are common to all relational biology and autopoiesis theories. The ascent of man, and also of other living (or *super-complex*) organisms through flexible adaptation schemes, is viewed in novel categorical terms, such as the variable biogroupoid representations of varying genomic and interactomic biotopology considered here as an important tool for studying dynamic processes that lead to speciation and the evolution of species.

## 2. WHAT IS LIFE ?

### **The Emergence of Super-Complex Systems and Life**

Although the distinction between living organisms and simple physical systems, machines, robots and computer simulations might appear obvious to everyone at first sight, the profound differences that exist both in terms of

dynamics, construction and structure require a great deal of thought, conceptual analysis, development and integration or synthesis. This fundamental, ontological question about Life occurs in various forms, possibly with quite different attempts at answers, in several books (e.g., Schrödinger in 1945 [24], and Rosen in 1995 [25] and in 2000 [26]).

In the following sections we shall discuss from a categorical viewpoint several key, systemic differences in terms of dynamics and modelling between living and inanimate systems. The ontology of super-complex biological systems, or biosystems (BIS), has perhaps begun with a paper by Elsasser (published in 1969 in “*Theoretical Biology*”, ref. [16]) who recognized that organisms are *extremely complex* systems, that they exhibit wide variability in behaviour and dynamics, and also— from a logical viewpoint, that they form unlike physical systems— *logically heterogeneous classes*. (We shall use the ‘shorthand’ term ‘*biosystems*’ or BIS to stand for super-complex biological systems, thus implicitly specifying the attribute super-complex within biosystems). This intrinsic BIS variability was previously recognized as *fuzziness* by Baianu and Marinescu in 1968 in their first paper on *organismic supercategories* published in the *Bulletin of Mathematical Biophysics* [5], and further developed in a series of reports on multi-stability and super-complexity of organisms [6]–[12] with dynamics represented by *natural transformations of algebraic-topological structures* [13]; some of the possible origins of BIS fuzziness were later suggested to be found in the *partial structural disorder* of biopolymers and biomembranes, as reported by Baianu in 1980 [14]. Yet other basic reasons for the presence of both dynamic and structural ‘*bio-fuzziness*’ is the ‘immanent’ LM-logic in biosystems, such as functional genetic networks, and possibly also the Q-logic of signalling pathways in living cells [12]. There are, however, significant differences between Quantum Logic, which is also non-commutative, and the LM-Logics of Life processes. Whereas certain reductionists would attempt to reduce Life’s logics, or even human consciousness, to Quantum Logic (QL), the former are at least logically and algebraically *not reducible to QL*. Nonetheless, it may be possible to formulate QL through certain modifications of *non-commutative LM-logics* [15]. Neurophysiological processes and underlying structures were also approached in higher dimensional algebra (HDA) in a similar formalization, that was however restricted to the human central nervous system (CNS) [16].

Perhaps the most important attributes of Life are those related to the logics ‘immanent’ in those processes that are essential to Life. As an example,

the logics and logic-algebras associated with functioning neuronal networks in the human brain—which are different from the many-valued (Łukasiewicz–Moisil) logics [17] associated with functional genetic networks [2], [12], [15], self-reproduction of living cells, or reproduction of multi-cellular organisms [6], [7], [9] were shown to be different from the simple Boolean-chryssippian logic upon which machines and computers are built by humans [2].

The former n-valued (LM) logics of functional neuronal or genetic networks [12] are *non-commutative* ones, leading to *non-linear, super-complex* dynamics, whereas the simple logics of ‘physical’ dynamic systems and machines/automata are *commutative* (in the sense of involving a commutative lattice structure). Here, we find a fundamental, logical reason why living organisms are *non-commutative*, super-complex systems, whereas simple dynamical systems have *commutative modelling diagrams* that are based on *commutative Boolean* logic [15]. We also have here the reason why a *commutative* Categorical Ontology of neural networks and CNS would lead to advanced robotics and AI, but has indeed very little to do with the ‘*immanent logics*’ or the actual functioning of the living human brain, contrary to the proposition made by McCulloch and Pitts as early as 1943 in their widely cited report in the *Bulletin of Mathematical Biophysics* founded by *Nicolas Rashevsky* in 1939.

There have been several attempts at defining life in reductionistic terms and a few non-reductionist ones. Rashevsky attempted in 1968 to define life in terms of the essential functional relations arising between organismic sets of various orders, i.e. ontological levels, beginning with genetic sets, their activities and products as the lowest possible order, zero, of on ‘organismic set’ (OS). Then, in 1969, he pursued the idea in terms of logical Boolean predicates, thus attempting to provide the simplest model possible he proposed the organismic set, or OS, as a basic representation of living systems; however, Rashevsky did not attempt himself to endow his OS with either a topological or a categorical structure, in spite of the fact that he previously reported in 1959 on the fundamental connection between Topology and Life. He did attempt, however, a logical analysis in terms of formal symbolic logics and Hilbert’s predicates. Furthermore, his PhD student, Robert Rosen did take up the challenge of representing organisms in terms of simple categorical models—his Metabolic-Repair, **(M,R)**-systems, or **MRs**, in two seminal papers [20], [21].

These first **MR** reports were then followed by a series of follow up reports with many interesting, biologically relevant results and consequences in spite of the simplicity of the **MR**, categorical set ‘structure’. Further extensions and

generalizations of MRs were subsequently explored by considering abstract categories with both algebraic and topological structures (refs. [2],[8], [10],[11], [13], [23], [26]).

Whereas simple dynamic systems, or general automata, have *canonically decomposable semigroup* state spaces (the Krone-Rhodes Decomposition Theorem), super-complex systems do not have state spaces that are known to be canonically decomposable, or partitioned into functionally independent subcomponent spaces, that is within a living organism all organs are interdependent and integrated; one cannot generally find a subsystem or organ which retains organismic life—the full functionality of the whole organism. However, in some of the simpler organisms, for example in *Planaria*, regeneration of the whole organism is possible from several of its major parts [7]. Pictorially, and typically, living organisms are not ‘Frankensteins’/chimeras that can be functionally subdivided into independent smaller subsystems (even though cells form the key developmental and ontological levels of any multi-cellular organism that cannot survive independently unless transformed.) By contrast, automata do have in general such *canonical sub-automata/machine decompositions* of their state-space; it is in this sense also that recursively computable systems are ‘simple’, whereas organisms are *not* [2]. We note here that an interesting, incomplete but computable, model of multi-cellular organisms was formulated in terms of ‘cellular’ or ‘tessellation’ automata simulating cellular growth in planar arrays (cited in ref. [23]). This incomplete model is often imitated in one form or another by seekers of computer-generated/algorithmic, artificial ‘life’.

On the one hand, simple dynamical (physical) systems are often represented through groups of dynamic transformations. In GR, for example, these would be Lorentz–Poincaré groups of spacetime transformations/reference frames. On the other hand, super-complex systems, or biosystems, emerging through self-organization and complex aggregation of simple dynamical ones, are therefore expected to be represented mathematically—at least on the next level of complexity—through an extension, or generalization of mathematical groups, such as *groupoids*, for example. Whereas simple physical systems with linear causality have high symmetry, a single energy minimum, and thus they possess only *degenerate* dynamics, the super-complex (living) systems emerge with lower symmetries but higher dynamic and functional/relational complexity. As symmetries get ‘broken’ the complexity degree increases sharply. From groups that can be considered as very simple categories that have just one object and

reversible/invertible endomorphisms, one moves through symmetry breaking to the structurally more complex groupoids, that are categories with many objects but still with all morphisms invertible. Dynamically, this reflects the transition from degenerate dynamics with one, or a few stable, isolated states ('degenerate' ones) to dynamic state regions of many generic states that are metastable; this multi-stability of biodynamics is nicely captured by the many objects of the groupoid and is the key to the 'flow of life' occurring as multiple transitions between the multiple metastable states of the homeostatic, living system. More details of how the latter emerge through biomolecular reactions, such as catabolic/anabolic reactions, will be presented in the next subsections, and also in the next section, especially under natural transformations of functors of biomolecular categories. As we shall see later in Sections 8 through 10 the emergence of human consciousness as an ultra-complex process became possible through the development of the *bilaterally asymmetric* human brain, not just through a mere increase in size, but a basic change in brain architecture as well. Relationally, this is reflected in the transition to a higher dimensional structure, for example a double biogroupoid representing the bilaterally asymmetric human brain architecture. Therefore, we shall consider throughout the following sections various groupoids as some of the 'simplest' illustrations of the mathematical structures present in super-complex biological systems and classes thereof, such as *biogroupoids* (i.e., those groupoids present in biosystems) and variable biogroupoids to represent evolving biological species. Relevant are here also *crossed complexes* of variable groupoids and/or *multi-groupoids* as more complex representations of biosystems that follow the emergence of ultra-complex systems (the mind and human societies, for example) from super-complex dynamic systems (organisms).

Although Darwin's Natural Selection theory has provided for more than 150 years a coherent framework for mapping the Evolution of species, it could not attempt to explain how Life itself has emerged in the first place, or predict the rates at which evolution occurs, or even predict to any degree of detail what the intermediate 'missing links', or intervening species, looked like, especially during their ascent to man. On the other hand, Huxley, the major proponent of Darwin's Natural Selection theory of Evolution, correctly proposed that the great, anthropoid apes were in man's ancestral line going back more than 10 million years. The other two major pieces specified here—as well as the Relational and Molecular Biologies—that are missing from Darwin's and neo-Darwinist theories, are still the subject of intense investigation. We intend

to explore in the next sections some possible, and plausible, answers to these remaining questions.

We note here that part of the answer to the question how did life first emerge on earth is suggested by the modeling diagram of the simplest possible organism, i.e., one that defined the minimum conditions for the emergence of life on earth.

### 3. THE ‘PRIMORDIAL’ AS THE SIMPLEST (M,R)-SYSTEM

#### 3.1. Autopoietic Systems

Additional specifications of the path taken by the emergence of the first super-complex living organism on earth, the ‘primordial’, come from an extension of (M,R)–systems theory and the consideration of its possible molecular realizations and molecular evolution (Baianu, 1984). The question still remains open: why primordial life–forms or super-complex systems no longer emerge on earth, again and again. The usual answer is that the conditions existing for the formation of the ‘primordial’ no longer exist on earth at this point in time. Whereas, this could be part of the answer, one could then further enquire if such conditions may not be generated artificially in the laboratory. The answer to the latter question, however, shows that we do not yet have sufficient knowledge to generate the primordial in the laboratory, and also that unlike natural evolution which had billions of years available to pseudo-randomly explore numerous possibilities, man does not have that luxury in the laboratory.

#### 3.2. Primordial(s), (M,R)-Systems and Enzyme Catalysis. Auto-catalysis, Organismic Self-Repair and Autopoiesis.

Organisms are thought of having all evolved from a simpler, ‘primordial’, proto-system or cell formed (how ?) three, or perhaps four, billion years ago. Such a system, if considered to be the simplest, must have been similar to a bacterium, though perhaps without a cell wall, and also perhaps with a much smaller, single chromosome containing very few RNA ‘genes’ (two or, most likely, four). We shall consider next a simple ‘metaphor’ of metabolic, self-repairing and self-reproducing models called (M,R)-systems, introduced by Robert Rosen (1958 a,b). Such models can represent some of the organismic functions that are essential to life; these models have been extensively studied and they can be further extended or generalized in several interesting ways. Rosen’s simplest MR predicts one RNA ‘gene’ and just one proto-enzyme for

the primordial ‘organism’. An extended MR (Baianu, 1969; 1984) predicts however the primordial, **PMR**, equipped with a *ribozyme* (a telomerase-like, proto-enzyme), and this PMR is then also capable of ribozyme- catalized DNA synthesis, and would have been perhaps surrounded by a ‘simple’ lipid-bilayer membrane some three billion years ago. Mathematically, this can be represented as:

$$A \xrightarrow{f} B \xrightarrow{\Phi} \mathfrak{R}[A, B] \xrightarrow{\beta} \mathfrak{R}[B, \mathfrak{R}[A, B]] \xrightarrow{\gamma} \dots \longrightarrow \infty \dots, \quad (0.1)$$

where the symbol  $\mathfrak{R}$  is the **MR** category representing the ‘primordial’ organism, PMR, and  $\mathfrak{R}[A,B]$  is the class of morphisms (proto-enz and the metabolic output class B (metabolic products of proto-enzymes). The ribozyme  $\gamma$  is capable of both catalizing and ‘reverse’ encoding its RNA template into the more stable DNA duplex,  $\infty$ . One can reasonably expect that such primordial genes were conserved throughout evolution and may therefore be found through comparative, functional genomic studies. The first ribozymes may have evolved under high temperature conditions near cooling volcanoes in hot water springs and their auto-catalytic capabilities may have been crucial for rapidly producing a large population of self-reproducing primordials and their descendant, *Archea*-like organisms.

Note that the primordial **MR** , or  $PMR = \mathfrak{R}$ , is an auto-catalytic, self-reproducing and autopoietic system. However, its ‘evolution’ is not entailed or enabled as yet. For this, one needs define first a variable biogroupoid or variable category, as we shall see in the next sections.

#### 4. GENERALIZED (M,R)-SYSTEMS AS VARIABLE BIOGROUPOIDS

One has here the important example of **MR**-Systems with *metabolic groupoid* structures (that is, *reversible enzyme reactions/metabolic functions–repair replication* groupoid structures), for the purpose of studying RNA, DNA, epigenomic and genomic functions. For instance, the relationship of:

$$\text{METABOLISM} = \text{ANABOLISM} \implies \longleftarrow \text{CATABOLISM}$$

can be represented by a metabolic groupoid of ‘*reversible*’, *anabolic/catabolic processes*. In this respect the simplest MR-system can be represented as a



*topological groupoid* with the open neighbourhood topology defined for the entire dynamical state space of the MR-system, that is an open/generic- and thus, a structurally stable- system, as defined by the dynamic realizations of **MR**-systems [21]. This necessitates a descriptive formalism in terms of *variable groupoids* following which the human MR-system would then arise as the *colimit* of its complete biological family tree expressible in terms of a family of many linked/connected groupoids; this variable biogroupoid formalism is briefly outlined in the next section.

## 5. THE EMERGENCE OF ORGANISMS AND LIFE

### Defining Essential Organismic Functions

Whereas it would be desirable to have a well-defined definition of living organisms, the list of attributes needed for such a definition would be quite lengthy. In addition to super-complex, recursively non-computable and open, attributes such as: auto-catalytic, self-organizing, structurally stable, endowed with dynamic genericity ('generic'), self-repair, self-reproducing, highly interconnected internally, multi-level, and also possessing multi-valued logic and anticipatory capabilities would be recognized as important. One needs to add to this list at least the following: diffusion processes, inter-cellular flows, essential thermodynamically-linked, irreversible processes coupled to bioenergetic processes and (bio)chemical concentration gradients, and fluxes selectively mediated by semi-permeable biomembranes. This list is far from being complete. Some of these important attributes of organisms are inter-dependent and serve to define life categorically as a super-complex dynamic process that can have several alternate, or complementary descriptions/representations; these can be formulated, for example, in terms of variable categories, variable groupoids, generalized Metabolic-Repair systems, organismic sets, hypergraphs, memory evolutive systems (MES), organismic toposes, interactomes, organismic super-categories and higher dimensional algebra.

## 6. BIOLOGICAL SPECIES, SPECIATION AND VARIABLE BIOGROUPOIDS

After a century-long debate about what constitutes a biological species, taxonomists and general biologists seem to have now adopted the operational

concept proposed by Mayr: “*a species is a group of animals that share a common gene pool and that are reproductively isolated from other groups.*” Unfortunately, this concept is not readily applicable to extinct species and their fossils, the subject of great interest to paleoanthropologists, for example. From an ontology viewpoint, the biological species can be defined as a class of equivalent organisms from the point of view of sexual reproduction and or/functional genome, or as a *biogroupoid* (Baianu, Brown, Georgescu and Glazebrook, 2006).

Whereas satisfactory as taxonomic tools these two definitions are not directly useful for understanding evolution. The biogroupoid concept, however, can be readily extended to a more flexible concept, the *variable groupoid*, which can be then utilized in theoretical evolutionary studies, and through predictions, impact on empirical evolutionary studies, and perhaps organismic taxonomy also.

#### 7. SUPER-COMPLEX NETWORK BIODYNAMICS IN VARIABLE BIOGROUPOID CATEGORIES: VARIABLE BIONETWORKS AND THEIR SUPER-CATEGORIES

This section is an extension of the previous one in which we introduced variable biogroupoids in relation to speciation and the evolution of species. The variable category concept generalizes the concept of variable groupoid which can be thought as a variable category whose morphisms are invertible. The latter is thus a more ‘symmetric’ structure than the general variable category.

We have seen that variable biogroupoid representations of biological species, as well as their categorical limits and colimits, may provide powerful tools for tracking evolution at the level of species. On the other hand, the representation of organisms, with the exception of unicellular ones, is likely to require more general structures, and super-structures of structures (Baianu, 1970). In other words, this leads towards higher-dimensional algebras (HDA) representing the super-complex hierarchies present in a complex-functional, multi-cellular organism, or in a highly-evolved functional organ such as the human brain. The latter (HDA) approach will be discussed in a later section in relation to neurosciences and consciousness, whereas we shall address here the question of representing biosystems in terms of variable categories that are lower in complexity than the ultra-complex human mind. A variable category approach is, on the other hand, a simpler alternative to the organismic LM-topos that will be employed in Section 8 and another forthcoming report to represent

the emergence and evolution of genetic network biodynamics, comparative genomics and phylogeny. In terms of representation capabilities, the range of applications for variable categories may also extend to the neurosciences, neurodynamics and brain development, in addition to the evolution of the simpler genomes and/or interactomes. Last-but-not-least, it does lead directly to the super-complex, ‘hierarchical’ structures of higher dimensional algebra.

## 8. EVOLVING SPECIES AS VARIABLE BIOGROUPOIDS

### Molecular Evolution and Speciation

For a collection of *variable groupoids* we can firstly envisage a parametrized family of groupoids  $\{G_\lambda\}$  with parameter  $\lambda$  (which may be a time parameter, although in general we do not insist on this). This is one basic and obvious way of seeing a variable groupoid structure. If  $\lambda$  belongs to a set  $M$ , then we may consider simply a projection  $G \times M \rightarrow M$ , which is an example of a trivial fibration. More generally, we could consider a *fibration of groupoids*  $G \hookrightarrow Z \rightarrow M$  (Higgins and Mackenzie, 1990). However, we expect in several of the situations discussed in this paper (such as, for example, the metabolic groupoid introduced in the previous subsection) that the systems represented by the groupoid are interacting. Thus, besides systems modelled in terms of a *fibration of groupoids*, we may consider a multiple groupoid as defined as a set with a number of groupoid structures any distinct pair of which satisfy an *interchange law* which can be expressed as: each is a morphism for the other, or alternatively: there is a unique expression of the following composition:

$$\begin{bmatrix} x & y \\ z & w \end{bmatrix} \begin{array}{c} \xrightarrow{j} \\ \downarrow i \end{array}, \quad (0.2)$$

where  $i$  and  $j$  must be distinct for this concept to be well defined. This uniqueness can also be represented by the equation

$$(x \circ_j y) \circ_i (z \circ_j w) = (x \circ_i z) \circ_j (y \circ_i w). \quad (0.3)$$

This illustrates the principle that a 2-dimensional formula may be more comprehensible than a linear one. Brown and Higgins (1981a) showed that certain multiple groupoids equipped with an extra structure called *connections*

were equivalent to another structure called a *crossed complex* which had already occurred in homotopy theory. We shall say more on these later.

In general, we are interested in the investigation of the applications of the inclusions

$$(\text{groups}) \subset (\text{groupoids}) \subset (\text{multiple groupoids}).$$

The applications of groups, and Lie groups, in mathematics and physics are well known. Groupoids and Lie groupoids are beginning to be applied (see Landsmann, 2002). Indeed it is well known that groupoids allow for a more flexible approach to symmetry than do groups alone. There is probably a vast field open to study.

One of the difficulties is that multiple groupoids can be very complex algebraic objects. It is known for example that they model weak homotopy  $n$ -types. This allows the possibility of a revolution in algebraic topology.

Another important notion is the *classifying space*  $BC$  of a crossed complex  $C$ . This, and the monoidal closed structure on crossed complexes, have been applied by Porter and Turaev to questions on Homotopy Quantum Field Theories (these are TQFT's with a 'background space' which can be helpfully taken to be of the form  $BC$  as above), and by Martins and Porter (2006), as *invariants* of interest in physics.

The *patching mechanism of a groupoid atlas* connects the iterates of local procedures (Bak et al., 2006). One might also consider in general a *stack in groupoids* (Borceux, 1994), and indeed there are other options for constructing relational structures of higher complexity, such as *double, or multiple* groupoids (Brown, 2004; 2005). As far as we can see, these are different ways of dealing with gluing or patching procedures, a method which goes back to Mercator!

For example, the notion of an *atlas* of structures should, in principle, apply to a lot of interesting, topological and/or algebraic, structures: groupoids, multiple groupoids, Heyting algebras,  $n$ -valued logic algebras and  $C^*$ -convolution algebras. One might incorporate a 3-valued logic here and a 4-valued logic there, and so on. An example from the ultra-complex system of the human mind is *synaesthesia*—the case of extreme communication processes between different types of 'logics' or different levels of 'thoughts'/thought processes. The key point here is *communication*. Hearing has to communicate to sight/vision in some way; this seems to happen in the human brain in the audiovisual (neocortex) and in the Wernicke (W) integrating area in the left-side hemisphere of the brain, that also communicates with the speech centers or the Broca area, also in the left brain hemisphere. Because of this *dual-*

*functional*, quasi-symmetry of the human brain, it may be useful to represent all two-way communication/signalling pathways in the two brain hemispheres by a *double groupoid* as the simplest groupoid structure that may represent such quasi-symmetry of the two sides of the human brain. In this case, the 300 millions or so of neuronal interconnections in the *corpus callosum* that link up neural network pathways between the left and the right hemispheres of the brain would be represented by the geometrical connection in the double groupoid. The brain's overall *asymmetric* distribution of functions and neural network structure between the two brain hemispheres may therefore require a non-commutative, double-groupoid structure for its relational representation. The potentially interesting question then arises how one would mathematically represent the split-brains that have been neurosurgically generated by cutting just the *corpus callosum*— some 300 million interconnections in the human brain (Sperry, 1992). It would seem that either a crossed complex of two, or several, groupoids, or indeed a direct product of two groupoids  $G_1$  and  $G_2$ ,  $G_1 \times G_2$  might provide some of the simplest representations of the human split-brain. The latter, direct product construction has a certain kind of built-in commutativity:  $(a, b)(c, d) = (ac, bd)$ , which is a form of the interchange law. In fact, from any two groupoids  $G_1$  and  $G_2$  one can construct a double groupoid  $G_1 \bowtie G_2$  whose objects are  $Ob(G_1) \times Ob(G_2)$ . The internal groupoid 'connection' present in the double groupoid would then represent the remaining basal/'ancient' brain connections between the two hemispheres, below the *corpus callosum* that has been removed by neurosurgery in the split-brain human patients.

The remarkable variability observed in such human subjects both between different subjects and also at different times after the split-brain (bridge-localized) surgery may very well be accounted for by the different possible groupoid representations. It may also be explained by the existence of other, older neural pathways that remain untouched by the neurosurgeon in the split-brain, and which re-learn gradually, in time, to at least partially re-connect the two sides of the human split-brain. The more common health problem—caused by the senescence of the brain—could be approached as a *local-to-global*, super-complex ageing process represented for example by the *patching* of a *topological double groupoid atlas* connecting up many local faulty dynamics in 'small' un-repairable regions of the brain neural network, caused for example by tangles, locally blocked arterioles and/or capillaries, and also low local oxygen or nutrient concentrations. The result, as correctly surmised by Rosen (1987), is a

*global*, rather than local, senescence, super-complex dynamic process.

On the other hand, for ‘simple’ physical systems it is quite reasonable to suppose that structures associated with symmetry and transitions could well be represented by 1-groupoids, whereas transitions between *quantum* transitions, could be then represented by a special type of quantum symmetry double groupoid that we shall call here simply a *quantum double groupoid* (QDG as defined in [3]), as it refers to *fundamental quantum* dynamic processes (cf. Werner Heisenberg).

## 9. COMPLEX EVOLUTION AS DYNAMICS OF INTERACTING SYSTEMS

### **Super-Complex Networks of Organisms: Evolution through the Emergence of Increasingly Complex Organisms**

*Persistence and Propagation of Organisms through Space and Time: Survival and Extinction of Species.*

The autopoietic model of Maturana (1987) claims to explain the persistence of living systems in time as the consequence of their structural coupling or *adaptation* as structure determined systems, and also because of their existence as *molecular* autopoietic systems with a ‘closed’ network structure. As part of the autopoietic explanation is the ‘structural drift’, presumably facilitating evolutionary changes and speciation. One notes that autopoietic systems may be therefore considered as dynamic realizations of Rosen’s simple MRs. Similar arguments seem to be echoed more recently by Dawkins (2003) who claims to explain the remarkable persistence of biological organisms over geological timescales as the result of their intrinsic, (super-) complex adaptive capabilities.

The point is being often made that it is not the component atoms that are preserved in organisms (and indeed in ‘living fossils’ for geological periods of time), but the *structure-function relational pattern*, or indeed the associated organismic categories or supercategories. This is a very important point: only the functional organismal structure is ‘immortal’ as it is being conserved and transmitted from one generation to the next. Hence the relevance here, and indeed the great importance of the science of abstract structures and relations, i.e., Mathematics. This was the feature that appeared paradoxical or puzzling to Erwin Schrödinger from a quantum theoretical point of view when he wrote his book “*What is Life?*”

As individual molecules often interact through multiple quantum interactions, which are most of the time causing *irreversible*, molecular or energetic changes to occur, how can one then explain the hereditary stability over hundreds of years (*or occasionally, a great deal longer, NAs*) within the same genealogy of a family of men? The answer is that the ‘actors change but the play does not!’. The atoms and molecules turn-over, and not infrequently, but the *structure-function patterns/organismic categories remain unchanged*, or are mostly conserved over long periods of time through repeated repairs and replacements of the molecular parts that need repairing, as long as the organism lives. Such stable patterns of relations are, at least in principle, amenable to logical and mathematical representation without tearing apart the living system. In fact, looking at this remarkable persistence of certain gene subnetworks in time and space from the categorical ontology and Darwinian viewpoints, the *existence of live ‘fossils’* (e.g., a coelacanth found alive in 1923 to have remained unchanged at great depths in the ocean as a species for 300 million years!) it is not so difficult to explain; one can attribute the rare examples of ‘live fossils’ to the lack of ‘selection pressure in a very stable niche’. Thus, one sees in such exceptions the lack of any adaptation apart from those which have already occurred some 300 million years ago. This is by no means the only long lived species: several species of marine, giant unicellular green algae with complex morphology from a family called the *Dasycladales* may have persisted as long as 600 million years (Goodwin, 1994), and so on. However, the situation of many other species that emerged through *super-complex adaptations*—such as the species of *Homo sapiens*—is quite the opposite, in the sense of marked, super-complex adaptive changes over much shorter timescales than that of the exceptionally ‘lucky’ coelacanths. Clearly, some species, that were less adaptable, such as the Neanderthals or *Homo erectus*, became extinct even though many of their functional genes may be still conserved in *Homo sapiens*, as for example, through comparison with the more distant chimpanzee relative. When comparing the *Homo erectus* fossils with skeletal remains of modern men one is struck how much closer the former are to modern man than to either the *Australopithecus* or the chimpanzee (the last two species appear to have quite similar skeletons and skulls, and also their ‘reconstructed’ vocal chords/apparatus would not allow them to speak). Therefore, if the functional genomes of man and chimpanzee overlap by about 98%, then the overlap of modern man functional genome would have to be greater than 99% with that of *Homo erectus* of 1 million years ago, if it somehow could be actually found

and measured (but it cannot be, at least not at this point in time). Thus, one would also wonder if another more recent hominin than *H. erectus*, such as *Homo floresiensis*— which is estimated to have existed between 74,000 and 18,000 years ago on the now Indonesian island of Flores— may have been capable of human speech. One may thus consider another indicator of intelligence such as the size of region 10 of the dorsomedial prefrontal cortex, which is thought to be associated with the existence of *self-awareness*; this region 10 is about the same size in *H. floresiensis* as in modern humans, despite the much smaller overall size of the brain in the former (Falk, D. et al., 2005).

Passing the threshold towards human consciousness and awareness of the human self may have occurred—with any degree of certainty—only with the ascent of the *Cro-Magnon* man which is thought to belong to the modern species of *Homo sapiens sapiens*, (chromosomally descended from the Y haplogroup F/mt haplogroup N populations of the Middle East). This important transition seems to have taken place between 60,000 and 10,000 years ago through the formation of Cro-Magnon, human ‘societies’—perhaps consisting of small bands of 25 individuals or so sharing their hunting, stone tools, wooden or stone weapons, a fire, the food, a cave, one large territory, and ultimately reaching human consensus.

## 10. CONCLUSIONS

We outlined a flexible conceptual framework for representing the dynamic complexity of living organisms and organismal evolution in space and time in terms of essential relational—organizational super-structures present in living organisms, ecosystems and human societies. Such emergent super-structures involve *relations among relations* even in the simplest primordial organisms, followed by still *higher-dimensional relations* among such organisms, thus leading to hierarchically super-complex relational structures of increasing adaptability that are also *generic*. Natural transformations, considered as high-level relations among lower, molecular-level relations provide a powerful tool for representing super-complex system dynamics in terms of the biomolecular interactions and transformations underlying physiological processes that are essential to life and developmental processes. This approach opens therefore new possibilities for modeling in higher dimensional algebras the emergence of highly complex systems that have so far resisted all reductionist and linear attempts at modeling complexity.



REFERENCES

- [1] I. C. Baianu, R. Brown and J. F. Glazebrook. 2007a. Categorical ontology of complex spacetime structures: the emergence of life and human consciousness, *Axiomathes* **17**: 223-352.
- [2] I.C. Baianu. 1987. Computer Models and Automata Theory in Biology and Medicine(A Review). In: *Mathematical Models in Medicine.*,vol.7., M. Witten, Ed., Pergamon Press: New York, pp.1513-1577.
- [3] I. C. Baianu, R. Brown and J. F. Glazebrook. 2007b. A conceptual construction of complexity levels theory in spacetime categorical ontology: non-abelian algebraic topology, many-valued logics and dynamic systems, *Axiomathes* **17**: 409-493.
- [4] I. C. Baianu, R. Brown and J. F. Glazebrook. 2009. Categorical Ontology of Complex Systems, Meta-levels and levels: The Emergence of life, Human Consciousness and Society'. In: "*Theory and Applications of Ontology.*" vol.1, R. Poli, et al., eds., Springer, Berlin (in press).
- [5] Baianu, I.C. and M. Marinescu: 1968, Organismic Supercategories: Towards a Unitary Theory of Systems, *Bulletin of Mathematical Biophysics* **30**, 148-159.
- [6] Baianu, I.C.: 1970, Organismic Supercategories: II. On Multistable Systems, *Bulletin of Mathematical Biophysics* **32**, 539-561.
- [7] Baianu, I.C.: 1971a, Organismic Supercategories and Qualitative Dynamics of Systems, *Bulletin of Mathematical Biophysics*, **33** (3), 339-354.
- [8] Baianu, I.C.: 1971b, Categories, Functors and Quantum Algebraic Computations, in P. Suppes (ed.), *Proceed. Fourth Intl. Congress Logic-Mathematics-Philosophy of Science*, September 1-4, 1971, Bucharest.
- [9] Baianu, I.C. and D. Scripcariu: 1973, On Adjoint Dynamical Systems. *The Bulletin of Mathematical Biophysics*, **35**(4), 475-486.
- [10] Baianu, I.C.: 1973, Some Algebraic Properties of  $(\mathbf{M}, \mathbf{R})$  - Systems. *Bulletin of Mathematical Biophysics* **35**, 213-217.
- [11] Baianu, I.C. and M. Marinescu: 1974, A Functorial Construction of  $(\mathbf{M}, \mathbf{R})$ - Systems. *Revue Roumaine de Mathematiques Pures et Appliquees* **19**: 388-391.
- [12] Baianu, I.C.: 1977, A Logical Model of Genetic Activities in Łukasiewicz Algebras: The Non-linear Theory. *Bulletin of Mathematical Biology*, **39**: 249-258.

- [13] Baianu, I.C.: 1980a, Natural Transformations of Organismic Structures., *Bulletin of Mathematical Biology*,**42**: 431-446.
- [14] Baianu, I.C.: 1980b, On Partial Order and Disorder in Biological Systems. *Letter to the Editor Bulletin of Mathematical Biology*,**42**: 601-605.
- [15] Baianu I. C., Brown R., Georgescu G. and J. F. Glazebrook: 2006b, Complex Nonlinear Biodynamics in Categories, Higher Dimensional Algebra and Łukasiewicz–Moisil Topos: Transformations of Neuronal, Genetic and Neoplastic Networks., *Axiomathes*, **16** Nos. 1–2: 65–122.
- [16] Elsasser, M.W.: 1981, A Form of Logic Suited for Biology., In: Robert, Rosen, ed., *Progress in Theoretical Biology*, Volume 6, Academic Press, New York and London,pp.23-62.
- [17] R. Brown, and T. Porter. 2003. ‘Category theory and higher dimensional algebra: potential descriptive tools in neuroscience’, *Proceedings of the International Conference on Theoretical Neurobiology*, Delhi, February 2003, edited by Nandini Singh, *National Brain Research Centre, Conference Proceedings* vol. **1** 80-92.
- [18] Georgescu, G.: 2006, N-valued Logics and Łukasiewicz–Moisil Algebras, *Axiomathes* **16** (1–2): 123–136.
- [19] R. Brown. 2004. Crossed complexes and homotopy groupoids as non commutative tools for higher dimensional local-to-global problems, *Proceedings of the Fields Institute Workshop on Categorical Structures for Descent and Galois Theory, Hopf Algebras and Semiabelian Categories*, September 23-28, *Fields Institute Communications* **43**: 101-130.
- [20] R. Rosen. 1958. The Representation of Biological Systems from the Standpoint of the Theory of Categories., *Bull. Math. Biophys.*, **20**, 317-341.
- [21] R. Rosen. 1973. On the Dynamical realization of (M,R)-Systems. *Bull. Math. Biology.*, **35**:1-10.
- [22] M. Warner. 1982. Representations of (M,R)-Systems by Categories of Automata., *Bull. Math. Biol.*, **44**: 661-668.
- [23] Arbib, M. A.: 2002, The mirror system, imitation and evolution of language, (in Nehaviv, C. and Dautenhahn, K. eds.) *Imitation in Animals and Artefacts*, MIT Press, Cambridge MA, 229–280.
- [24] Erwin Schrödinger.:1945. *What is Life ?*. Cambridge Univ. Press.: Cambridge.
- [25] Robert Rosen.: 1995. *Essays on Life*.
- [26] Robert Rosen.: 2000. *Life, Itself* , Columbia Univ. Press.

I. C. Baianu, PhD., Professor, ACES College and NPRE Department, University of Illinois at Urbana-Champaign, Urbana IL 61801, USA

email: *ibaianu@illinois.edu*

James. F. Glazebrook, PhD, Professor, Department of Mathematics and Computer Science, Eastern Illinois University, Charleston IL 61920, USA.

email: *jfglazebrook@eiu.edu*

Ronald Brown, PhD., Professor School of Informatics, University of Wales, Dean St. Bangor, Gwynedd LL57 1UT UK.

email: *r.brown@bangor.ac.uk*