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# Review:
# Marcello Barbieri (Ed) (2007) Introduction to Biosemiotics. The new biological synthesis. Dordrecht: Springer

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## 1 Thematic background

Maybe it is no chance that the discovery of the genetic code occurred during the hot phase of philosophy of science discourse about the role of language in generating models of scientific explanation. The code-metaphor was introduced parallel to other linguistic terms to denote language like features of the nucleic acid sequence molecules such as “code without commas” (Francis Crick). At the same time the 30 years of trying to establish an exact scientific language to delimit objective sentences from non-objective ones derived one of his peaks in the linguistic turn.

### 1.1 Changing subjects of knowledge

The crucial steps of early Wittgenstein and scholars of logical empiricism to delimitate scientific sentences from non-scientific ones, the following failure of all trials to establish a scientific language of theory which would be coherent with the language of observations, or to define a scientific language which could be able to depict objective reality in a one to one fashion, lead to the unescapeable effort to get clear how we can define human language according to its main principles; i.e., all three semiotic levels of rules not only from the (objective) observer perspective but even more from the (subjective) perspective of participants. This would be coherent to the evidence, that without utterances we can not integrate our position into any discourse. Even without utterances we act as non-uttering individuals being dependent on the discourse derived meaning processes of a linguistic (e.g. scientific) community.

This position marks the primary difference to the subject of knowledge of Kantian knowledge theories wherein one subject alone in principle could be able to generate sentences in which it generates knowledge. This abstractive fallacy was ruled out in the early 50s of the last century being replaced by the “community of investigators” (Peirce) represented by the scientific community in which every single scientist is able the place his utterance looking for being integrated in the discourse community in which his utterances will be proven whether they are good arguments or not. Definitively the *solus ipse* subject of knowledge was replaced by the “indefinite community of investigators” which doesn’t not produce ever lasting knowledge principles about scientific areas, but try to get forward in discursive truthfulness “in the long run” (Peirce) principally ending with human species in an “ultimate opinion” (Peirce) of the things which are discussed.

### 1.2 Anthropomorphistic use of language metapher in early molecular biology

The code-metaphor introduced on modern biology therefore was an escape of pure physics and chemistry because it introduced certain features of languages into the description of chemical structures. What seemed to be an obvious anthropomorphism was the introduction of linguistic terms on biological sciences and medicine when they used phrases like “communication within cells”, “communication between cells”, “genetic code”, “genetic text sequence”, “chemical messengers”, “neuronal communication”, “hormonal communication”, “transcription of the nucleic acid language”, “amino acid language”, “translation of RNA in DNA”, “Letter pairs of DNA”, and so on.

The investigations of biological disciplines and subdisciplines according the knowledge of the genetic code are legendary. It led to the most developing field of science we know today.

It started the first 3 decades that main investigation focused on the “molecular syntax” (Manfred Eigen), i.e. the combinatorial patterns of nucleic acids and its corresponding protein acid sequences which determined protein structures being the constituents of both of any unicellular until most complex multicellular organism and its developmental substeps. This lead to the complete deciphering of the human genome in late 1990ies. But immediately it became clear that the knowledge of a complete sequence order of an organism doesn’t mean to know the complete meaning function which is really inherent in the genome storage medium.

### 1.3 Genetic expression is no one way

This marks a development which arose in early 1980ies where it became clear more and more, that behind the superficial grammar of molecular syntax there is something like a deep grammar of regulation networks which determines the meaning function of a nucleic sequence order. According to the general features of any real language – a real language is a sign system which functions according to the complementary syntactic, pragmatic and semantic rules – there are several levels of higher order regulatory functions which are decisive for the expression and replication patterns of nucleic acid sequences: it means that different environmental influences, i.e. the situational context an organismic individual is interwoven, determines the higher order regulation of replication patterns. This means that of the defined nucleic acid order sequence it is possible to express a great variety of different expression patterns which may be even contradictory: from the same nucleic acid order it is possible to produce different protein meanings. And these different protein meanings may even derive without altering the genetic code or being inheritable. Under certain circumstances these alterations may even be heritable at all.

This knowledge marked the importance of epigenetics, i.e. of environmental influences on protein level which can influence via second messengers the amino acid level, even in coding functions (which would be a neo-lamarckian perspective). For long this view has been ignored or in the realm of Neo-Darwinism dogmatically tabooed, it now becomes more and more important. Now we know that in the human genome only 3 % of the complete genetic data-set are protein coding sequences. The formerly termed “junk DNA”, the noncoding DNA sequences, is now being recognized as higher order regulatory functions which are crucial for an appropriate determination of the protein coding sequences. The difference in the protein coding sequence between human and mouse is only 12 %, so the differences depend on the higher order regulatory functions.

### 1.4 Superficial and deep grammar of genome storage medium

This different development in the awareness of different levels of nucleic acid storage medium DNA is important because it marks the difference of nucleic acid language to a one to one depiction of meaning functions in the genetic code. Obviously there is a superficial grammar (which in the case of the human genome is deciphered since the human genome project) and *a hierarchical network of higher order regulatory functions which could be termed as a genome-editing MetaCode* (Witzany 2006) characterized by the *strong hierarchical interdependency* of all higher order regulatory modules which we are far away to know in all details.

Interestingly this structure of language features was detected in the early 60s also in human language according to the change of linguistic turn to pragmatic turn in the theory of science discussion when reflecting on the validity claims being held with any utterance in speech acts which showed both:

a) that speech acts are apriori social actions i.e. intersubjective actions which avoid the omnipresent problem of philosophies of consciousness how to make the move from a state of private (*solus ipse)* consciousness (sender/coding-receiver/decoding narrative) to a state of mutual agreement and mutual cooperation;
b) that pure analyses of language and language like structures based on syntactic or syntactic/semantic investigations are not able to extract illocutionary meanings hidden in the pragmatic (situational) contexts which determines different mean-

ings of identical syntactic data-sets (Witzany 2000).

It is obvious that the language games which are played in recent research are not fully compatible. On the one side biological sciences (which define themselves as natural sciences investigating observations according to the universal natural laws of physics and chemistry) which now have to deal with linguistic rules with features which cannot be deduced of natural laws. On the other side a coherent language and communication theory which is limited to the human self-understanding.

## 2 The new player in this universal discourse: Biosemiotics

At this point a new discipline holds validity claims in this universal discourse: Biosemiotics.

Biosemiotics investigates rule-governed sign-mediated interactions within and between cells, tissues, organs and organisms. As Howard Pattee (2005, pp.299) stated: “Life is distinguished from the nonliving world by its dependence on signs”. Biosemiotics also investigates processes and interdependences in the realm of genetics/genomics/proteomics which have features of icons, indices or symbols. The first “Introduction to Biosemiotics” has now been published.

”Introduction to Biosemiotics” combines approaches from semiotics, linguistics, semantics, biology, philosophy, systems theory, theory of science, physics and information theory. All contributions share the conviction that the main processes of coordination and information exchange within and between living organisms, from single cell to most complex multicellular life, are mediated by the use of signs. Every sign process (=semiosis) is coherent with the laws of physics and chemistry. But in difference to physico-chemical interactions in the non-living world semioses are inherently connected with semiotic rules. According to Charles Morris and Charles Sanders Peirce, every sign use is characterized by rules of combination (syntax), context (pragmatics) and content (semantics). The complementarity of these 3 levels of rules in every sign-process enables de novo generation of signs, combinatorial changes, and alternative use of the same sequences to transport different messages with different meanings. Biosemiotics, as introduced by this book, strives to do more than merely promote the biological disciplines from the perspective of rule-governed sign-mediated interactions between living organisms; its validity claim is also to better understand the linguistic features of nucleic acid sequences and their regulations. Biosemiotics therefore proclaims both a communicative approach to sign-mediated interactions among living organisms and a linguistic/semiotic approach to nucleic acid language and protein language. Biosemiotics integrates these approaches by investigating a variety of organic codes, which means that the decisive difference between life and non-life is the generation and use of codes.

## 3 The contributions

The book is divided into three parts.

Part 1 – “Historical Background” with contributions by Donald Favareau (The Evolutionary History of Biosemiotics), Tuomo Jämsä (Semiosis in Evolution), Marcello Barbieri (Has Biosemiotics Come of Age? and Postscript).

Part 2 – “Theoretical Issues” with contributions by Howard Pattee (The Necessity of Biosemiotics: Matter-Symbol Complementarity), Stanley Salthe (What is the Scope of Biosemiotics? Information in Living Systems), Jesper Hoffmeyer (Semiotic Scaffolding of Living Systems), Kalevi Kull (Biosemiotics and Biophysics – The Fundamental Approaches to the Study of Life), Marcello Barbieri (Is the Cell a Semiotic System?), Stefan Artmann (Computing Codes versus Interpreting Life), Anton Markos and coworkers (Towards a Darwinian Biosemiotics. Life as Mutual Understanding), Tommi Vehkavaara (From the Logic of Science to the Logic of the Living. The Relevance of Charles Peirce to Biosemiotics), Marcel Danesi (Towards a Standard Terminology for (Bio)semiotics), Gérard Battail (Information Theory and Error-Correcting Codes in Genetics and Biological Evolution).

Part 3 – “Biosemiotic Research” with contributions by Marcella Faria (RNA as Code Makers: A Biosemiotic View of RNAi and Cell Immunity), Luis Emilio Bruni (Cellular Semiotics and Signal Transduction), Stephen Philip Pain (Inner Representations and Signs in Animals), Johannes Huber and Ingolf Schmid-Tannwald (A Biosemiotic Approach to Epigenetics: Constructivist aspects of Oocyte-to-Embryo transition), Dario Martinelli (Language and Interspecific Communication Experiments: a Case to Re-open?).

## 4 The editorial

In an Editorial, Marcello Barbieri gives a short introduction on biosemiotics. He distinguishes 4 major approaches or schools in biosemiotics.

The first is based on the model of Peirce, proposing that interpretation is a crucial element of semiosis and that every semiotic system is characterized by a triad (sign, object and interpretant).

In 1974, Marcel Florkin proposed a second model for biosemiotics, namely the dualistic system of Saussure, i.e. that a “signifier and signified" are equivalent to "genotype and phenotype". Thomas Sebeok adopted the Peircian narrative for zoosemiotics. The Peirce-Sebeok school was the first to be fully accepted by most biosemioticians, especially the Copenhagen-Tartu School (Claus Emmeche, Jesper Hoffmeyer, Kalevi Kull). That the Prague school of Anton Markos also derived from this model as suggested in this editorial seems to be risky because the biohermeneutic approach (first developed by Sergej Chebanov: Chebanov 1999) derives from hermeneutic science founded by Hans-Georg Gadamer, whose methodological aim differs fundamentaly from that of the Peirce-Sebeok school.

As a third model, Barbieri introduces his semantic theory. It states that the cell is a triad of genotype, phenotype and ribotype, wherein the ribotype is the "codemaker", i.e. the generator of the molecular syntax of the nucleic acid language. He furthermore suggests that, in his concept, the rules of the genetic code do not depend on interpretational processes.

As a further (fourth) approach, Barbieri names the model of Howard Pattee and his concept of epistemic threshold. It differentiates between (i) physical preconditions for the organic codes and symbolic regulations and (ii) some kind of emergentism.

## 5 Two examples of the main chapters

Here, I briefly review two examples within the main chapters: Certainly, one of the key contributions is Barbieri's chapter "Is the cell a semiotic system?", in which he attempts to give reasons for his concept of organic codes. He defines a semiotic system as a system "made of two independent worlds that are connected by the conventional rules of a code." (181) These are two distinct entities for Barbieri, and he replaces the Peircean semiosis triad (sign, object, interpretant) by his own triad (sign, meaning, convention). Important in Barbieri's concept are the "copying" and "coding"-processes that represent crucial differences to the non-living world. Here, the codemaker is the ribosomal RNA, which generates chromosomal sequences according to the molecular syntax of the nucleic acid language. This initially involved simple copy functions. "The first protein-maker had to bring together three different types of molecules (messenger, ribosomal and transfer RNAs) and was therefore much more complex than copymakers." (184) Accordingly, gene sequences differ from randomly assembled molecules in the non-animated world because they are a real artefact produced by "molecular machines based on RNAs." (185) This makes the cell a trinity of genotype, phenotype and ribotype. And the early RNA world appeared spontaneously. "Eventually, evolution replaced the ribogenes with genes and the riboproteins with proteins but the synthesizing ribosoids of the ribotype have never been replaced. They are the oldest phylogenetic molecules that exist on earth and they firmly remain at the heart of every living cell." (186)

In this thesis, Barbieri is a forerunner not only in biosemiotics: his approach gives a coherent explanation of fundamental processes of life with its connection to early stages of evolution. This yields a quasi-subject of linguistic competence: the ribotype, which throughout the history of life is able to produce codes by code-making. "The codemaker is the agent, whereas signs and meanings are the instruments of semiosis." (187) Signs come into life in the coding process of this code-maker. Thus, signs/meaning and code-maker/coding are true organic entities.

But the organic code of the ribotype is not the only conventional organic code – other natural conventions share the three basic characteristics of all codes "(1): a correspondence between two independent worlds, (2) the presence of molecular adaptors and (3) a set of rules that guarantee biological specificity."(190) Barbieri identifies the splicing codes, the signal transduction codes, the compartment codes (which are crucial for the "geographical" destination of a cell), the cytoskeletal codes responsible for the necessary dynamic instability because the number of "different structures that cytoskeleton can create is potentially unlimited."(193) Also important are the sequence codes (such as transcription codes, gene splicing codes, translation pausing codes, the DNA structure code, the chromatin code, the translation framing code, the modulation code and the genome segmentation code).

In a third chapter, Barbieri explains why these codes are actually physical entities: they are objective, reproducible and defined by operative procedures. So "organic information and organic meaning are both the result of natural processes. Just as it is an act of copying that creates organic information, so it is an act of coding that creates organic meaning. Copying and coding are the processes, copymakers and codemakers are their agents, organic information and organic meaning are their results." (199) (In this context see also the interesting contribution of Marcella Faria in part 3 of this book)

One of the leading positions in biosemiotics is represented by the Prague-school. A contribution by its founder Anton Markos and his co-workers "Towards a Darwinian biosemiotics. Life as mutual understanding" investigates, in a first part, the preconditions of understanding processes. This is the only investigation the book contains in this field. It aims to understand our understanding of sentences, meanings, codes and utterances, which is not definable by formalistic procedures or operationalistic theory of science definitions. This is a crucial contribution for biosemiotics if this new discipline desires to be methodologically coherent. In a second part, the authors demonstrate an actual biosemiotic investigation on "corporeality, life and language", which is indeed one of the outstanding biosemiotic applications. Here, the authors find a definition for a phenomenon observable in all life processes: homoplasy. "From the biosemiotic perspective, homoplasy is not newly derived: rather, it is a result of the persistence of a morphogenetic system which became reawakened or re-invented in an unusual context. Hence, if organisms need to evolve a new adaptive structure, they may activate remote morphogenetic systems and, under the current circumstances, an unexpected shape will appear. From the biosemiotic point of view, such "realization" refers both to understanding (becoming aware of a "knowledge" – of the existence of an engram), recognition of its significance (acknowledgement of a mute sign) and its bodily interpretation (to know the how of the developmental process)." (252)

## 6 Conclusions

Ultimately, I try to evaluate the validity claim held with this "Introduction to Biosemiotics" in the landscape of modern biological sciences.

(1) Is there any advantage which suggests using biosemiotics instead of established disciplines such as biolinguistics or bioinformatics?

Whereas biolinguistics and bioinformatics are established sciences which are applied for informational and bioengineering purposes by several biological disciplines, this is not (yet) the case for biosemiotics. Applied biosemiotic research is less developed, although the research contributions in this book are interesting and useful. Biosemiotics in its present status has a strong focus on theoretical investigations about the role, function and interpretation of signs according to the concepts of Charles Sanders Peirce, Jakob von Uexküll, Stuart Kauffman, Howard Pattee and the more recent publications of Jesper Hoffmeyer, Anton Markos and Marcello Barbieri. Although this broader view is helpful to understand the whole dimension of sign processes in living nature, biolinguistics and bioinformatics are without doubt currently the more practical tools.

(2) Is there a coherent method which serves as a powerful tool for investigations within all domains of biological research?

A unique coherent method of biosemiotics does not yet exist. Biosemiotic investigations rely on ontological, systems theoretical, naturalistic, physicalistic, mechanistic, idealistic, metaphysic, hermeneutic foundation and background knowledge. A theory of science discussion about the status of language and communication in biosemiotics, or about the *scientific foundation and justification of sentences* within biosemiotics according to the linguistic and the pragmatic turn, is missing in this book. The same holds true for the integration of a post-metaphysical (non-solus ipse) subject of knowledge.

(3) Is this discipline merely an additional view on biological phenomenon, or does it have the paradigmatic power to redefine our understanding of living nature?

The recent main deficit of biosemiotics – the lack of a uniform method for applied investigations – may turn out to be its driving force because it needs to integrate very different aims, traditions, paradigms. Especially the approach of Marcello Barbieri (and Marcella Faria) and his differentiation between "copying" and "coding"-functions in the evolution of life gives an outstanding interpretation of recent biological research: In genome rearrangements it is a usual phenomenon, that in a first step parts of the genome are simply duplicated (copying) and in a second step the molecular syntax is recombined (coding) by a set of small RNAs, microRNAs and higher order regulations inherent in the non-protein coding and repetitive elements of the genome (Witzany 2007). This power of a coherent explanation biolinguistics or bioinformatics are lacking.

"Introduction to Biosemiotics" is a key step forward into this dynamic process of creating a new scientific view on a language-like structure of the genome organization and storage medium as well as on rule-governed sign-mediated interactions within and between cells, tissues, organs and organisms. Should this integration prove successful in the long run, then biosemiotics could develop to a major discipline in biology.

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