

# **S.E.E.D. Journal (Semiotics, Evolution, Energy, and Development)**

The past 50 years have seen the introduction of information as a physical entity with a mathematical theory. In the last ten years, connections have been developed to energy, evolution and development, as well as to signs, representation, interpretation and the mind. Many of these developments are controversial, such as whether information is intrinsically related to meaning, whether there is a general semiotics that extends beyond human signs, and whether, indeed, there is anything well-defined outside of human theories. This journal deals with these and related issues. More information on topics and debates can be found elsewhere on this site, especially in the program and book from the 1997 SEE meeting, and on the main SEE page.

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**The Immune Self, the Sign, and the Testes**

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## SEED - EDITOR' S INTRODUCTION

The following articles are by authors who presented papers either at the 4<sup>th</sup> Gatherings in Biosemiotics Conference in Prague, July 2004 or at the 5<sup>th</sup> Gatherings in Biosemiotics in Urbino, Italy in July 2005. Each of the papers in question handles issues connected with the extension of Biosemiotic ideas, against received doctrines. In the first paper, for example, Dario Martinelli, is concerned with the extension of biosemiotic ideas from the field of ethno-musicology. The latter concerns itself with the structure of human created and performed music in many cultures of the world; he argues that this field should be extended to non-human music. Both human music and non-human music show structural similarities; this leads him to the provocative proposition that, since all cases of human music-making exhibit a considerable range of aesthetic ideas in relation to sound, so the demonstrated array of variation among each species of sound-making non-human animals also reveals the existence of an aesthetic.

The next three papers deal with alternatives to received thinking in biology and medicine. Guenther Witzany discusses how the radical revisions to evolutionary theory by Lynn Margulis Serial Endosymbiotic Theory (SET) leads him to the conclusion that there is an enormous world of communicative interactions ignored in conventional biology, and that following on from Margulis ideas, that symbiogenesis exhibits a wide range of rule-governed sign mediated interactions (or **rsi**) These communicative interactions are not only evident and open to descriptive evaluation but have pragmatic aspects as well. Witzany examines these pragmatic dimensions. The article by Queiroz, Emmeche and El Hani is part of a series of articles in which they are exploring how the ideas of C. S. Peirce can better explain communicative activities at the molecular dimension than can current examples of information theory. Though the latter is used throughout biology, it is a theory in which the relation of the gene to the cell is entirely absent of meaning. Their article is a ground-breaking approach which demonstrates in detail an alternative explanatory schema in molecular biology.

Finally, Neuman takes issue with current explanations of autoimmunity, in which the process of autoimmunity is described in various terms of “self” in relation to an “other” (pathogens, virus, etc). Using various semiotic ideas, drawn from such authors as Volosinov, Neuman discusses why the processes of the immune system might better be analysed in terms of “context.” The ability to act in context implies an ability to distinguish meanings. Neuman argues that because the immune system is meaningful, contextual understanding is one of its major features.

# Natural history of life: History of communication logics and dynamics

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## ABSTRACT

“A full understanding of the dynamics of semiosis may in the last analysis turn out to be no less than the definition of life” (Th. Sebeok)

If rules governing evolution are equivalent to communication rules which lie behind the history of interaction, then we could refer to the natural history of life as a history of communication logics and dynamics. Communication processes are rule governed sign mediated interactions (**rsi**) which may be described in the evolution of eukaryotic cells as well as - for example - in microbial and plant interactions. The first part of this article supports Margulis theory of symbiogenesis (Serial Endosymbiotic Theory) but questions the use of classical mechanistic language of natural science in describing highly complex interactions of symbiosis and, subsequently, of symbiogenesis. The alternative is to describe these as communication processes which are multi-leveled, regulative, constitutive and generative and whose success depends on sign processes which proceed in a rule-based manner. In my illustrations of **rsi**, I propose the existence of an innovation code (text-generating code, evolution code), a genome editing (*ge*) *MetaCode* hidden in the non-coding DNA. The second part argues that the community of investigators doesn't consist of 'pure observers' but of performative participants of the communicating scientific community which are (a) parts of the investigation itself, (b) parts of the planetary symbiotic interdependence of communicating living nature. I summarize *pragmatic turn* results which lead to an adequate description of communicative rationality by investigating which formal preconditions must be fulfilled so that rule-governed sign-mediated interactions in and between communicating communities can function. This approach of a pragmatic philosophy of biology enables a three-levelled biosemiotics avoid reductionistic fallacies.

## 1 A NATURAL HISTORY OF LIFE: INTRODUCTION

The natural history of life in the 19<sup>th</sup> and 20<sup>th</sup> century was recounted in the framework of Neodarwinism, with its core paradigms (a) “chance mutations” in the genetic text

lead to the origin of new species, genera and organismic kingdoms, and (b) “natural selection” in the struggle for life which leads to “survival of the fittest” of the newly created organisms. Although “natural selection” agrees well with the empirical data of adaptation, the core paradigm of “chance mutations” explains the evolution of new organisms only dogmatically. More recently, the Serial Endosymbiotic Theory of Lynn Margulis contradicts this paradigm. Serial Endosymbiotic Theory (SET) proves that the evolution of eukaryotic cells is the result of merging processes of different bacterial ancestors. Accordingly, the natural history of life becomes a story involving the merger of different organisms with different abilities and capabilities into more complex organisms. Building on Margulis schema, I will propose that the study of interactions between microorganisms clearly shows that the underlying processes are not primarily mechanistic, but rather are complex communication processes in which chemical molecules serve as signs in rule-governed sign-mediated interactions (**rsi's**). These signs have a relation to (a) each other, (b) the sign user/interpreter, (c) designated something (i.e. have a meaning function), so that we may identify them in obeying semiotic rules. I will argue that interorganismic communication processes between members of a species are almost always embedded in parallel intraorganismic (intracellular) and metaorganismic (transpecific) communication processes.

I will also propose that the correct approach to these communication processes is to begin with human processes of understanding, because a language and communication concept coherent with our self-understanding cannot be founded through a pure observer perspective. To be coherent with our self-understanding the approach has to incorporate the basics of a pragmatic turn, i.e. the results of analyzing human rule governed sign mediated interactions or “how to do things with words”. Ultimately, however, we have no choice but to achieve understanding among ourselves using language and communication.

## **2 AN EXCLUSIVE BACTERIAL WORLD UNTIL HALF TIME**

Lynn Margulis theory is well supported by numerous genetic analyses: the higher development of species, genera and organismic kingdoms on our planet developed beyond the bacteria stage through the merging of different bacteria with different capabilities (Margulis 1996, 1999, 2004; Margulis et al., 2000; Margulis and Sagan, 2002; Cavalier-Smith, 2002; Stechmann and Cavalier-Smith, 2003). The SET proposes that the differentiation of bacteria groups with very different capabilities during the first two billion years of our planet’s natural history of life gave rise to a global bacterial gene pool of astounding diversity. Today we know that the first half of biological natural history was not characterized by biological monads, but rather by

highly complex social life-worlds of the bacteria groups, which entered into symbiotic and parasitic relationships with one another.

Later I will argue that even on the level of bacteria, symbiotic associations require numerous rule-governed sign-mediated interactions (**rsi's**); without them coordinated behaviour cannot function. The bacterial world is a social and communicative one (Kaiser and Losick 1993, Fuqua et al., 1996; Losick and Kaiser, 1997; Zook, 1998; Bassler, 1999; Crespi, 2001; Schauder and Bassler, 2001; Schauder et al., 2001; Federle and Bassler, 2003). The production and the exchange of messenger molecules enable unicellular organisms to coordinate their behaviour *like a multicellular organism* (Shapiro, 1998; Schauder and Bassler, 2001; Ben Jacob, 2004). The **rsi's** in bacteria communities are not restricted to species-specific levels but represent a clear metaorganismic, multilevel communication that enables hundreds of different bacteria groups to co-occupy one and the same ecological niche (Walker, 2003; Bais, 2004). It has been proven that bacteria groups use quorum sensing (QS) to determine their strength and to react by coordinating their behaviour (Montana State University 1999; Sharma et al., 2003). “Studies of quorum sensing systems demonstrate that bacteria have evolved multiple languages for communicating within and between species. Intra- and interspecies cell-cell communication allows bacteria to coordinate various biological activities in order to behave like multicellular organisms” (Schauder and Bassler, 2001: 1476). Bacteria use a form of “bacterial esperanto” to communicate with other bacteria groups (Schauder and Bassler, 2001).

### **3 SYMBIOGENESIS: FROM RAMIFICATION TO UNIFICATION**

Natural scientists have described ten thousand different species of bacteria. The capabilities of the individual subgroups often differ considerably, i.e. anaerobic and aerobic, photo- and chemosynthetically active, acido-, thermoacidophilic, halophilic, methane- and oxygen-producing, osmotic and lipophilic. Natural scientists have recently become aware that in early evolution bacteria exchanged gene components, even entire gene blocks, with one another. Such gene blocks suddenly enriched the genome of another bacterium that had previously not had the respective competence, i.e. the genome enrichment often had a direct phenotypic effect. Horizontal Gene Transfer (HGT) enables the bacteria kingdom to merge different basic competences (Wagner et al., 1999; Wolf, 1999, 2000; Jain et al., 1999, 2003; Xie et al., 2004; Timmis et al., 2004).

What were these mergings like? They represent nothing less than the substantial change of protein individuals with particular, immutable basic

characteristics into protein individuals that differ substantially from their predecessors. It involves a true creation from simple to more complex organisms. If symbiogenesis, via symbiosis, creates a new species and therefore extinguishes the formerly independent individuals, then this involves generative DNA text processing in which genetically different gene pools are combined into one DNA text. Rather than involving a physical change in aggregate status, this is one of the most revolutionary phenomena in biology. It requires a recombination that makes the foreign data set into one's own, the "non-self" to a "self", an object of external perception to a subject of internal proprioception.

The eukaryotic revolution marked the beginning of a development in which bacteria groups conquered space and time: organisms in the eukaryotic kingdoms such as animals, fungi and plants are themselves inhabited up to 90 % by bacteria groups (Bleich, 2000), which thereby vanquish limitations of space (vertical, horizontal) and time (movement, mobility). The symbiotic (metaorganismic) communication with this bacterial world is vital for all eukaryotic organisms.

The SET underlines that the origin of new tissues, organs, organisms and species lie in the long-term and continuous symbioses that they enter into. Symbiogenesis, in the next step, enables life-forms to incorporate entire organisms along with their genetic makeup. Thus bacteria became permanently incorporated into plant and animal cells as plastids and mitochondria. The novel aspect of symbiogenesis is that the natural history of life is no longer one of chance mutations and their selection: symbiogenesis unites individuals into larger individuals composed of many separate elements.

The fact that genetic subunits (e.g. organelles) in eukaryotic cells are present within the cell structures, but outside the nucleus, is remarkable. Margulis draws attention to the fact that some genetic factors in plants and animals are distributed throughout the cell and therefore, whatever the role of 'genetic determination', are not only determined by the genes in the nucleus. She points to experiments that prove without doubt that plastids and mitochondria clearly influence heredity. These extra-nuclear parts of the cell, with their peculiar hereditary history, are remnants of formerly free-living bacteria. Margulis proposes that a double-tracked hereditary system – with (formerly independent) cells inside other cells – is involved (Margulis 1999).

The SET also proposes serial evolution, which indicates that the sequence of merging is important. The initial merger involved (1) a thermoacidophilic bacterium (sulphur reduction/fermentation) with (2) one that could swim (Spirochaeta) in the nucleocytoplasm. These were still anaerobes. This was followed by a merger with (3)

an aerobic form,  $\alpha$ -proteobacteria (aerobic respiration). The resulting organism was able to survive the increasing oxygen concentrations. The final step was the merger with (4) a photosynthetic bacterium (*Synechococcus cyanobacteria*).

With this approach, Margulis contradicts traditional theories of evolution, all of which firmly held that evolutionary directions lay in *ramification* rather than merging. SET, on the other hand, states *one* integrated genome was sufficient in the initial merger of the archae- and eubacterium; in the Proctista, *two integrated genomes* were necessary; in the fungi *three*; in animals at least *four*; and in the plant kingdom (400 million years ago) at least *five*, perhaps even *seven* (Margulis 1996, 1999). Thus, one of the symbiogenetically most complex merging processes, which gave rise to the plant kingdom, is the youngest symbiogenesis of a new organismic kingdom in the natural history of life. The enormous group comprising the flowering plants is only half as old (150 million years) as the chronological origin of the plant kingdom. The corresponding development of seeds and fruits ultimately created an environment that was crucial for the survival of higher animals (Margulis and Schwartz, 1988).

Another example is that of cilia, the rods in the retina, the tail of sperm cells, sensory hairs and many similar appendages of nucleated cells which arose during the original merger of archaeobacteria and a swimming bacterium. The bodies they contain (so-called “centriole-kinetosomes”) arose through this archaic merger. There is also a genetic relationship between cilia and the mitotic spindles responsible for chromosome movement during cell division. According to Margulis, the Spirochaeta are the modern, free-living relatives of these symbiogenetically merged centriole-kinetosomes (Margulis, 1999: 65).

The SET supports this assumption with the fact that most of the DNA found in the cytoplasm of protoctists, animals, fungi and plants stems from the genes of bacteria that became organelles, and does not occur via genetic drift or mutations. Hereditary factors that control metabolic processes are similar to those of archaeobacteria. Eukaryotic genes that participate in information-processing (e.g. translation, transcription), on the other hand, show a close relationship to eubacteria. This higher development after the eukaryotic revolution was also promoted by the ability of bacteria to exchange genes and DNA components very simply and quickly, even between different species, through conjugation or via plasmids. The genetic material of bacteria is much better suited for these processes than eukaryotic material. Evolution therefore progressed, in its most dynamic phases, at a speed reflecting the ability of bacteria for gene-flux.

This demonstrates that complex genomic make-ups could be passed on directly and that the step-by-step development via chance mutations is an outdated conception. Whereas Darwin's natural selection has been documented in numerous studies, the higher development of species or even the origin of new organismic kingdoms could never be satisfactorily explained by chance mutations. In fact, most observed mutations are lethal rather than promoting higher or further development.

Margulis does not explain how the simplest archaebacteria or the RNA-world originated. Early RNA-world is plausible because RNA can reproduce itself autocatalytically, which DNA cannot. Moreover, RNA controls the assemblage of amino acids into protein sequences. Some RNAs are as competent as proteins: it can splice itself, i.e. rearrange its own molecular shape anew – it rearranges and reorganizes genetic material. Something like these capabilities of *ribozymes* had to have been components of the first cells. The metabolism of the first cells functioned without feeding. Photoautotrophic and chemoautotrophic organisms do not need to feed: they obtain their energy from sunlight or from hydrogen-rich compounds.

The first eukaryotic microorganisms developed an incredible diversity, but even today remain poorly studied and insufficiently described. Their role in the natural history of life was deemed too insignificant, even though they were positioned at the base of the eukaryotic superkingdom. Only few of the 250 000 protoctist species (eukaryotic microorganisms) have actually been named (Margulis, 1999: 84).

There is a standard assumption in the history of natural science, namely, plants and animals were the outstanding products of evolution. This now appears in an entirely different light. In fact, animals and plants are more similar to one another than to all other organismic kingdoms, both plants and animals go through an embryonic stage and thereby document their particularly close kinship, compared with other life-forms. The major differences lie elsewhere: the greatest divide lies between the pro- and eukaryotes.

A natural history of the development of a global symbiotic interdependence of all life-forms prompts the "holistic reflex": "Gaia", in the form of a global superorganism coating the earth, the sum of all parts, the whole created by the many separate individuals and its metabolism. Such a holism proposed by James Lovelock (Margulis, 1999: 141) is a classical metaphysical construction. It dissolves each organism's factual individuality into a hypothetical whole, reflecting the cognitive simulation of a quasi-extraterrestrial observer. Margulis therefore rejects this "holistic Gaia," that is to say, a concept of Gaia as superorganism, but accepts Gaia as a useful *model* to represent the sum of interacting ecosystems. In other words, Gaia models the

sum of growing, interacting and dying populations, a sheath of many species covering our planet, consisting of countless, highly different individual organisms.

## **4 SYMBIOGENESIS BY RULE GOVERNED SIGN MEDIATED INTERACTIONS**

### **4.1 “MERGING”, “FUSION”, “INCORPORATION”**

The major defect of SET from my perspective is that it describes the highly complex interactions of a symbiosis and, subsequently, of symbiogenesis, in the classical mechanistic language of natural science: “merging”, “fusion”, and “incorporation”. I will argue that we are dealing less with a “merging” than with communication processes which are multi-leveled, regulative, constitutive and generative and whose success depends on whether the required sign processes proceed in a rule-based manner, or fail. Communication processes between cells and cell components, do not “incorporate”, rather they integrate genetic data sets into available genomes and therefore lead to the development of a new individual.

Biosemitotics has taught us that life functions are always connected to sign processes, or, more precisely, that sign processes regulate and constitute life functions (Noeth, 2000: 254; Kull, 2005). Defective sign processes restrict or terminate life processes. These sign processes regulate life processes on several levels simultaneously: intracellularly, within the cell (DNA, RNA activities, messenger substances, etc.), and intercellularly in the form of cell-cell communication.

### **4.2 MICROBIAL AND PLANT MULTILEVEL COMMUNICATION**

“Communication is the key element in successful organization” (Kolenbrander et al., 2002: 486). The coordinated community, for example of oral bacteria in humans, relies on intra- and interspecies communication. This community encompasses ca. 500 different species, some of which cooperate, others which compete (Kolenbrander et al., 2002). The complexity of potential interactions in the oral cavity and the number of possibilities reach unimaginable proportions if we assume that each of the 500 bacteria species can regulate its genes in response to host-produced molecules and interacts with all the other bacteria species (Kolenbrander et al., 2002).

Highly complex interspecies communication enables bacteria species to communicate even in special sites of hosts such as the gastrointestinal tract, where they can gauge their population sizes by exchanging molecules despite the incredible number of similar molecules surrounding them. Even in such critical situations, the

species can reliably differentiate between population-specific (interorganismic) signals, foreign signals and “noise” (Federle and Bassler, 2003).

The microbiological community is exposed to a broad range of chemical substances in which an incredible variety of chemical messenger substances is embedded, from which they must be able to take up and interpret the correct ones in order to survive. It is very difficult to imagine how bacteria can differentiate between sense and nonsense in their chemical environment, in which they are constantly bombarded from all sides by small molecules (Dunn and Handelsman, 2002).

The discovery of species-specific and trans-specific signal molecules reveals an unexpectedly highly developed communication. In nature, where bacteria typically live together with numerous other species, signal molecules allow them to determine how large their populations are, how many other communities are present and their sizes, and to respond appropriately to this information by adapting their gene expression (Federle and Bassler, 2003).

This discovery has led to the suggestion that under real-life conditions, microorganisms must *simultaneously* be able to conduct many molecular conversations with different types of organisms and even organismic kingdoms (Dunn and Handelsman, 2002). “Using these advanced linguistic capabilities, bacteria can lead rich social lives for the group benefit. They can develop collective memory, use and generate common knowledge, develop group identity, recognize the identity of other colonies, learn from experience to improve themselves, and engage in group decision-making, an additional surprising social conduct that amounts to what should most appropriately be dubbed as social intelligence” (Ben Jacob et al., 2004).

The communicative abilities of bacteria are also present in symbiogenetically derived higher eukaryotes such as plants. The rhizosphere of plants is a realm of overlapping communicative interactions (Yoder, 1999; Walker et al., 2003; Bais et al., 2004; Baluska et al., 2005). The rhizosphere is a dynamic environment featuring dense microbiological life, high growth rates and metabolic activities, as well as rapidly changing physical conditions (Dessaux, 2004). Most of the decisions that plants make regarding their growth and development involve communication processes between all parts of the plant and works as neuronal communication (Dustin et al., 2001; Roshchina, 2001; Trewavas, 2003; Davies, 2004; Baluska et al., 2005). Learning and memory are two characteristic features for neuronal networks that require a large number of nerve cells to communicate with one another. Interestingly, nerve cells and plant cells use very similar sequences of signal molecules so that we speak today of neuronal communication in plant neurobiology,

not any longer of the dominant role of action potentials in plant physiology (Trewavas, 2003; Baluska, 2004; Davies. 2004; Baluska et al., 2005).

The communication processes between tissues and cells in plants is incredibly complex and encompasses nucleic acids, oligonucleotides, proteins and peptides, minerals, oxidative signals, gases, mechanical signals, electrical signals, fatty acids, and oligosaccharides, growth factors, several amino acids, various secondary products and simple sugars (Trewavas, 2003).

Communication, i.e. rule governed sign mediated interactions, is indispensable for the normal development of cells, tissues, organs and bodies (Witzany, 2005). They (**rsi**) control movement and coordinated behaviour, developmental stages in time, symbiotic interactions as well as defence strategies. Associated cells require a precise coordination in sending and receiving signals. Disturbance of rule-governed sign-mediated interactions lead to pathological situations ranging from abnormal cell proliferation to cell death (Perbal, 2003).

As in every biosemiotic process of real lifeworld (pragmatic) situations, context determines semantic meaning of signals. Auxin, for example, is an ancient signalling molecule in plants. Since it functions in different hormonal, morphogen and transmitter signalling pathways, it is very difficult to decipher the actual semantics of Auxin which depends on whether it is used as hormonal or morphogen or transmitter signal (Baluska et al., 2005: 108). Because the same signal can take on different meanings and trigger different effects, depending on whether it reaches the whole plant, a tissue or a cell, the respective developmental status of the organism serves as a memory for each individual plant. The individual plant is a complex multicellular and multi-tissue organism in which development is a *permanent* process and in which communication is the driving force (Trewavas, 2003):

“Biologists suggest that intelligence encompasses the characteristics of detailed sensory perception, information processing, learning, memory, choice, efficient optimisation of resource sequestration with minimal outlay, self-recognition, and foresight by predictive modelling. There is good evidence that individual plant species exhibit all of these intelligent behavioural capabilities” (Trewavas, 2005).

I will now give further illustrations of how sign processes regulate and constitute life functions.

## 5 THE GEMETACODE: CODINGS OF “NON-CODING” DNA

If symbiogenesis, via symbiosis, creates a new species and therefore extinguishes the formerly independent individuals, then this involves generative DNA text processing in which genetically different gene pools are combined into one DNA text. This is one of the most revolutionary phenomena in biology. Recombination makes a foreign data set into one's own, the “non-self” to a “self”, an object of external perception to a subject of internal proprioception.

Over the past 20 years, the field of molecular biology has yielded tens of thousands of articles describing in great detail the processes of recombinant DNA, splicing, RNA editing, coding, copying, major and minor repairs, transcription, translation, RNA processing, insertion, the importance of introns and exons for the reading processes, the complementary role of DNAs and RNAs. In the last decade even the significance and indispensable structural function of non-coding RNA becomes more and more interesting (Cavalier-Smith and Beaton, 1999; Sternberg, 2002; Baluska et al., 2004; Shapiro and Sternberg, 2005; Schmitt and Paro, 2004).

In every case, enzyme proteins competent in text processing carry out these highly differentiated tasks on protein-coding DNA regions with great precision.

“No technical production system, regardless how perfect, even approaches the low error rate achieved in the DNA reproduction process in living organisms. This degree of precision is vital for humans as well: even a single mistake in the transmission of hereditary information can have lethal consequences, as for example in sickle cell anaemia or cancer. In the course of developing from a fertilized egg to an adult human being, the three billion letter pairs of the human genome are reproduced nearly a quadrillion times. These orders of magnitude underscore the monumental scale of the task involved in correct transmission. An error rate as low as one in a million would still mean ca. 3000 mistakes per transmission: normal development would be impossible. Three enzymatically controlled processes are responsible for suppressing errors during the reproduction of the genetic text. Polymerases are responsible for selecting the correct letters, i.e., the nucleotide building blocks for the new DNA strands, while exonucleases are responsible for rejecting damaged letters. After these two steps, the error rate is reduced to one in ten million. The third and decisive step – correcting mistakes in the overall manuscript – is far more complex. Several proteins work hand in hand in this process. They recognize and excise sites in which the letters of one strand do not fit with those of the complementary strand. The missing piece is completed by polymerases. After this final quality control step, the error rate is reduced to a mere one in ten billion” (*Spektrum der Wissenschaft*, 1988: 119).

But this text processing on protein-coding DNA is overruled by the genome processing abilities of repetitive DNA of introns coding not for proteins but a lot of

RNAs among them active micro-RNAs. Typically, any mistakes in protein-coding and non-protein coding text processing have grave if not lethal consequences for the organism.

Until recently, only the protein-coding regions of DNA was thought to be crucial to coding. While this may well be the case in the prokaryotes, in higher eukaryotes this region is marginal (3%), for 97% of the eukaryotic genome consists of non-coding DNA. Long termed “junk” DNA because no important functions could be attributed, it was thought to represent ancient remnants of evolutionary history. Accordingly, research concentrated on the 3% that coded. Such one-sided approach, however, left many questions unanswered: Why are the protein-coding genes of humans and mice 99% identical? What actually happens with the 97% RNA remnants during post-transcriptional processing? Why is there no correlation between the complexity of organisms and the number of protein-coding genes, yet a correlation between complexity and the proportion of non-coding DNA?

My thesis here is the existence of an innovation code (text-generating code, evolution code) hidden in the non-coding DNA (Witzany, 1993 b; 1997; 2000: 200), a thesis which I developed in the early 90s and which I further developed (Witzany, 2000: 200-212) in the discussion of the contributions to *The Concept of the Gene in Development and Evolution* (Beurton et al., 2000). My assumption that this innovation code codes for enzyme proteins competent in text-processing, proteins that generate the new genetic texts for new organisms may prove to be present in the *early DNA-world of simple organisms*. But it is not proteins that create the genome ratio of *new eukaryotic* texts, but rather a *MetaCode*<sup>1</sup> (Witzany, 2000: 202) which encodes numerous RNAs, among them active micro-RNAs, and is able to generate new genetic datasets. It enables the conduction of structural changes as basic prerequisite of the evolution of diversity in the eukaryotic superkingdom.

## 5.1 “NON-CODING” DNA IS CODING FOR MICRO-RNAS

What was formerly described as “junk” DNA has genetic functions that are not controlled by enzyme proteins, but rather by repetitive elements in the introns of DNA which encode for the manifold forms of micro-RNAs. They originate during the transcriptional process, when the actual text building blocks are put together for a protein and when most of the non-protein-coding RNA is cut out and appears to be left over. This involves an incredible 97% of the genome’s transcriptional output. Comparative genetics has demonstrated that introns are strongly conserved over long evolutionary distances, often in large blocks, i.e. they are functionally related. This

conservation is much more conservative than that of the protein-coding DNA (Shapiro and Sternberg, 2005).

## **5.2 MULTI-TASKS OF MICRO-RNAS:**

Active micro-RNAs control and integrate large-scale structures of the chromosome. The number of different micro-RNAs is estimated to exceed several 10,000 (Mattick and Gagen, 2001). Some of the discovered tasks of these micro-RNAs are co-suppression, suppression of transposition, position effect variegation, start-stop signals, RNA interference, imprinting, chromosomal methylation, transvection, transcriptional and post-transcriptional gene silencing along with numerous other RNA-DNA, RNA-RNA (trans-acting RNAs), RNA-protein interactions. These active RNAs are as competent as proteins in catalysing, signalling and switching (*riboswitch*) (Mattick and Gagen, 2001).

## **5.3 PHENOTYPIC VARIATION**

“Cellular differentiation and phenotypic variation result primarily from variations in this high order regulation, not in the proteins themselves” (Mattick and Gagen, 2001: 1612). The phenotypic variation in complex organisms is the result of a different use of a set of protein-coding core components (Mattick and Gagen, 2001). The higher order regulation in non-protein-coding genome architecture is able to manage a larger genetic data set in its phenotypic range. As far as evolutionary processes are concerned, it is naturally much simpler to change or expand a number of very small control sequences than to duplicate an entire network of protein-coding genes (Mattick and Gagen, 2001: 1623). Variations of this higher order regulation can create an enormous spectrum of different protein expression profiles and we can understand at last why one and the same gene can be used for “multiple protein meanings” (Ast, 2005).

## **5.4 TERMINOLOGY: SYSTEMS BIOLOGICAL/COMPUTATIONAL VS. BIOSEMIOTIC**

Currently, the abilities of the non-protein- yet micro-RNAs-coding regions still receive different scientific designations. The terms are “endogenous network control molecules” or “higher-order regulatory system”, “controlled multitasked Gene Networks”, “major architectonic role of repetitive components” (Mattick, 2001; Mattick and Gagen, 2001; Mattick, 2003; Mattick, 2005; Shapiro and Sternberg, 2005).

In the perspective of biosemiotics undoubtedly a semiotic code is involved. I recommend that we refer to a genome editing (*ge*) *MetaCode*, because this obeys different semiotic rules than does the protein code.<sup>2</sup> There are good reasons for assuming that the semiotic rules of the *geMetaCode* determine the pragmatic rules and therefore the semantics of the protein code.

## 5.5 EVOLUTION BY VARIATIONS IN THE *GEMETACODE*

When the protein-coding regions in the genome of higher eukaryotes do not differ significantly from one another and represent a *set of core components*, then phenotypic differences are understandably determined by the different *geMetaCode*. It organizes, i.e. *variously structures*, the largely uniform protein-coding dataset of higher eukaryotes, thereby generating different organisms. Biosemiotically we can speak of a rule constituting and rule changing competence (“rule changing creativity” Witzany, 2000: 193) hidden in the *geMetaCode*.

In the light of the SET these non-protein-coding sequences (for example, the repetition elements of introns) arose *after* the innovation of eukaryotic cells, although also archaeobacteria genomes may have some introns. The innovation of eukaryotic cells could be an effect of new symbolic functions,<sup>3</sup> constituted by more complex intracellular communication *after* the separation of transcription and translation conferring “(...) an advantage by facilitating the modular shuffling of eukaryotic protein domains in evolutionary time and in real time via alternative splicing (...)” (Mattick, 2001: 987). The absence of these regulation functions of the *geMetaCode* in the eubacterial genome (with rare exceptions of viral introns) shows that a pure protein code had only very limited evolutionary possibilities. Simple organisms are using proteins both for functions and control systems that had reached the limit of analog communicative possibilities. These possibilities became dramatically expanded by the innovative intronic functions, forming the basis for the evolution of the eukaryotic superkingdom (Mattick, 2001).

## 5.6 PROTEIN CODE OBEYS SEMIOTIC RULES OF THE *GEMETACODE*

The unification of several bacteria species into the early form of the eukaryotic cell represented highly complex text processing rather than a merger. The biosemiotic complexity increases many-fold through the *overlying regulative and constitutive role of the geMetaCode* and its grammatical, semantic and pragmatic rules. “Major evolutionary events can initiate within the repetitive sector of the genome and do not have to follow changes in the coding sector” (Shapiro and Sternberg, 2005:16). This enables abrupt evolutionary developments as proposed in Gould’s theory of a “punctuated equilibrium” or as *revolutionary-evolutive* phases such as in the

Cambrian explosion (Witzany, 1993 b: 226). Namely, the *geMetaCode* can integrate larger genetic data sets into the phenotypic range:

“Different genome system architecture can have distinct transmission and expression properties even with the same coding sequences. Meaningful evolutionary change can take place in the repetitive component of the genome without altering coding sequences” (Shapiro and Sternberg, 2005:17).

The *geMetaCode* has also regulatory functions in chromosomal methylation which decide about different signalling pathways of the same genetic setups through different rules of gene silencing and special starts and stops via alternative splicing. With this chromosomal methylation, organisms are able to handle *multiple protein meanings* of the same genetic dataset. As shown through some authors of epigenetics these (*geMetaCode*-) functions are influenced and altered through environmental and other reasons which are (reversibly) heritable but do not involve or depend on mutations of the DNA itself. (Turner, 2000; Jenuwein and Allis, 2001; Turner, 2002; Spotswood and Turner, 2002; Jaenisch and Bird, 2003; True et al., 2004; Wang et al., 2004; Waterland and Jirtle, 2004).<sup>4</sup>

The *geMetaCode* contains the regulating-, constituting- and innovating rules with which existing protein codes are structured. This is possible because, I maintain, the genome is linguistically structured and communicatively organized. It also confirms a thesis of the pragmatic philosophy of biology about central features of language and communication in principle, that “using a finite number of signs and finite number of grammatic, semantic and pragmatic rules, existing rules of sign use can be indefinitely expanded, altered and/or newly combined to yield a new genetic text, new species, genera, organismic kingdoms, new forms of behavior, and new norms of (human) actions” (Witzany, 1993 b: 229).

## **6 HISTORY OF INTERACTION - HISTORY OF EVOLUTION**

If we deal with linguistically structured (analog/symbolic) genome ratio and communicative organization (rule governed sign mediated) of living organisms we have to ask whether we should use traditional terms and concepts for a description of "Life": autopoiesis, emergence, information system or constructivism, game theory, statistic-quantifying models, etc. After mainstream philosophy gave up explanations of Life and transferred these to natural science we find only partially holistic or sometimes hermeneutic approaches to "Life". Most natural science approaches are founded through three common argumentations: (a) We speak about the world of objects in a language of the exact natural sciences, which draws its claim to validity from the laws governing the physical world. Or (b) we assume that the observed

objects have a direct empirical significance that need not be further questioned because the laws of physics are reflected 1:1 in the material foundations of the brains of humans which construct utterances (universal syntax). Or (c) some simulate the radical monological perspective of a quasi-extraterrestrial observer and assume that there is an overriding “system“ in which human populations are a subsystem that communicates about itself and about its co-systems on an information-theoretical basis (Witzany, 2002 a).

To get things straight we have to remind ourselves of the discussion between 1920 and 1980 in the history of theory of science and the transition of metaphysics to “the linguistic turn” and afterwards, to the foundation and justification of scientific languages in “the pragmatic turn”. In various contributions I have reconstructed this discourse in great detail and connected it with the realm of biosemiotics (Witzany, 1993 a, b; 1995; 1998; 2000; 2002; 2003; 2005) which I will briefly summarize here:

a) The *linguistic turn* was the result of an attempt to delimit the *logic of science* from philosophy and other “unscientific“ cognitive methods. With good reasons the linguistic turn states that we do not understand *per se* objects, relations, structures, intelligence, mind, consciousness, cognition, construction, matter, energy, information, system, natural law, etc. but linguistic sentences in utterances. Only protocol propositions of observations that are reproducible in experimental setups are capable of depicting reality on a 1:1 basis. This is also valid for propositions of a language of theory that would have to be brought into agreement with these protocol propositions. What is required is a language that can be formalized, as in logical calculations, algorithms. This language would represent a *universal syntax* that would be universally valid (a) in the things of the external world, (b) in the physicalistic laws and (c) in the material reality of the brain of humans speaking in formalizable propositions (Witzany, 1995; 2005 a). But after several trials Logical Empiricism had to abandon its effort to achieve the ultimate validity claim of a physicalistic universal language. The logical and linguistical 1:1 depiction of physical reality is not possible in principle.

b) The *pragmatic turn* refers to the communicative everyday interactions of historically evolved linguistic communities which are the basis for learning and training linguistic and communicative competences. Historically grown communicative practice of linguistic communities is the prerequisite for organization and coordination of social interactions and later on linguistic abstractions like poetry, fine arts and scientific languages. The pragmatic turn enables the reconstruction of the *a priori of linguistic communities* being decisive for constituting a linguistically mediated and communicatively shared human self-understanding. The pragmatic turn

founded and justified the intersubjective-communicative character of thought, experience and research and was therefore able to avoid the omnipresent subject-object dichotomy and its unavoidable consequences, solipsism and objectivism (Witzany 2005).

As we are speaking together we interact. Everyday language analysis shows the *actional* character of speech acts, or "how to do things with words" (Austin, 1962; Searle, 1974). As we are subjects *and* objects of our utterances we are in a privileged position to take in account, at the same time, our historically evolved everyday language. We need not describe this from outside like the *solus ipse* pure observer who has no alternative possibility to describe communicative actions as classifications of equal behavioral features. To the contrary, we understand utterances as participants of communicative, representative, constitutive and expressive speech acts. This enables us to understand central marks of speech acts as there are, for example:

- The simultaneous understanding of identical meanings in two interacting partners, as expressed in successfully coordinated activity
- The differentiation between deep and superficial grammar of a statement along with differentiation between locutionary, illocutionary and perlocutionary speech acts with which the statements are made
- The differentiation between communication-oriented action and strategic manipulation of the communicating partners
- The critical judgment of the validity being claimed when making a particular statement

An understanding of these marks is not possible for monological *solus ipse* concepts of linguistic turn and its non-participating yet pure observer perspective. Also the monological sender-receiver model together with its "decoding" of meanings by analyzing the cognitive conctructional features of brain functions brings less chances for adequate explanation of understanding than the concept of "empathy", a term long used for a metaphysical-psychological approach to explain "understanding" by trying to feel "mentally" within the receiving person.

The pragmatic turn replaces all *solus ipse* subjects of knowledge by the a priori of linguistic community. This is the end for the former approach, a methodological ideal which lasted nearly 2000 years and which maintained as a principle that *one subject alone* could get knowledge. Its the end of monological Descartes/Kant conceptions of scientific knowledge and its unsolvable metaphysical apparent problems or how Thomas McCarthy said: "The monological approach preordained certain ways of posing the basic problems of thought and action: subject versus object, reason versus sense, reason versus desire, mind versus body, self versus other, and so on" (McCarthy, 1984: ix).

The pragmatic turn emphasizes interactional features of communication. Its decisive aspects are not only its *regulative* but also its *constitutive* features. Not the sign, symbol or word is the elementary unit of communication, but rather the production of signs, symbols or words in the framework of linguistic actions. It is important to stress the *constitutive* character of linguistic rules because linguistic behavior can never be explained by regulative rules alone: there is no a priori activity of speaking a language that could be regulated by rules. The possibility to speak a language *depends* on constitutive rules.

Languages (human and non human, bee languages) have a finite number of signs (Witzany, 2000: 45-52). They stand in relation to each other in an orderly manner which we term syntactic or grammatic rules. (1) These must be followed in a correct way or they fail. Then (2) there are *rules of interacting* which decide whether communication processes are successful or not, i.e. validity claims which are connected with our utterances, and which may be accepted or refuted by the linguistic community. Thus obeying or failing, pragmatic rules (2) decide about functioning communication – they are the prerequisite for successful social coordination and organization. Concrete interactional context decides about (3) meaning of utterances. One and the same sentence (sequence of signs) may take completely different meanings in different contexts. The meaning of "The shooting of the hunters" in training programs of professional hunters for learning rules about when to shoot in a coordinated action during hunting has a completely different meaning to a criminal inquiry of an unexplored, violent crime, on several hunters.

These analyses of some aspects of communicative rationality show its dependency on everyday language features with which we organize and coordinate interactions in the real lifeworld and therefore the historicity of its genesis and its development. It also shows that we are able to constitute indefinite possibilities of combinations with a finite set of signs and a finite set of rules. These features of linguistic capabilities constitute, in principle, history as *indefinite* process. Human knowledge is according to Peirce always a provisional result and in the end - as result of all possible and real speech acts – would be the "ultimate opinion" of the "indefinite community of investigators".

Modern biological research documents very clearly, that interactions in and between living organisms are sign mediated and rule governed. We can try to describe these interactions as communication processes and the genome ratio as linguistically structured because of its analog/symbolic features. We do not participate in plant-plant communication, but we may accept that we as humans are participants in a global community of interdependent symbiotic lifeworlds. As eukaryotic organisms

we are able to survive because we are involved in irreplaceable interactional levels with, for example, microorganisms. If we would measure the cells of our body, we would find only 10% being originally human, 90% being endo- and ektosymbiotic microorganisms, without them we could not live (Blech, 2000).

If, at the onset, we specifically discuss the terms “language” and “communication” to achieve a linguistically and communicatively fixed understanding of these terms (Witzany 1993 a/b; 1995; 1998; 2000; 2002 b), then we *ourselves* are in the best position to gain an understanding of human language and communication because the theoretical description of these terms must be coherent with, and not in contrast to, our self-understanding, our communicative experience. Moreover, I would argue that the investigator is not the observer in the third person -pure observer-perspective but is a performative participant of the communicating scientific community which is (a) part of the investigation itself, (b) part of the planetary symbiotic interdependence of the communicating living nature.

It therefore makes little sense to refer to sign use in the communication processes of plant or bacterial lifeworlds, all the while presupposing an objectivististic language and communication concepts, and using an empirical methodological ideal to explain the evolution of communicative interactions from the amoeba to humans. This would lead to the dead-end of the solipsistic subject of knowledge and hopeless entanglement in the subject-object dichotomy of objectivism/ physicalism/ naturalism.

The reverse pathway is correct, beginning with humans, and human self-understanding, which must be coherent with the used concept of “language” and “communication”. The alternative is to use pre-pragmatic *solus ipse* conceptions with their entanglement in metaphysical foundations. As I have argued before:

*Referring back to the rules of communicative rationality provides an opportunity to answer questions of evolutionary logic and dynamics as questions of interaction logic and dynamics. Evolutionary history could then be understood as a developmental history of interaction semiosis. If we could further establish that the rules governing evolution are equivalent to the communication rules behind the history of interaction, then we could justify the view that rule-governed sign-mediated behavior is a factor not only in humans, but especially in non-human living nature (Witzany, 1993, 2000: 13).*

So if we use the term of communicative rationality developed in this article for **rsi's** of non human organisms we may use the same **rsi** features as being equally involved in human and non human communication processes. In addition, a three leveled sign relation which does not eliminate all the *various* features of **rsi's** in *different* species, genera, organismic kingdoms is already available.

## 7 THREE-LEVELED SEMIOTICS AND REDUCTION EFFECTS

The semiotics of C. S. Peirce may be helpful here. It can provide immutable conditions for adequately analysing language use, linguistic communication, and even sign use via a three-leveled semiotics. Peirce decisive change - as opposed to Descartes and Kant's solus-ipse subject of knowledge - is his emphasis on the community of interpretation in the "indefinite community of investigators". Scientific knowledge is only possible for members of a *community* of interpreters, not for a solipsistic subject of knowledge. This approach allows Peirce, to underline the intersubjective-communicative character of thought, experience and research - or as the post-Tractatus Wittgenstein meant, no isolated individual can follow one rule.<sup>5</sup> Intersubjective validity of scientific knowledge requires a linguistic communication about sense and consensus-building about statements.

Those who overlook or feel they can negate linguistic communication-a priori (which itself requires a *historically evolved* and reconstructible linguistic community) will commit one of these forms of reductive fallacy. That person will shift the highest point of knowledge (a) in the unity of a self-consciousness like Kant or transfer this point (b) into the reality of a higher system logic that represents a principally unrecognizable yet proximate objective world (objectivism and realism). That person will no longer be in a position to derive the sign-mediated knowledge in the sign-sense interpretation and truth-consensus-building of an indefinite interpretation community of researchers.

According to Peirce, a (1) sign denotes (2) something for an (3) interpreter. Semiotics is an irreducible three-leveled relation of syntactic (1), semantic (2) and pragmatic (3) rules. *Each of the three levels of the sign function already assumes, for its function, the other two.* According to Peirce, those who, in an unreflective manner, fail to consider, incompletely consider or reduce this principally irreducible relation to two levels (syntactic/semantic) or one level (universal grammar), commit an abstractive/reductive fallacy (Apel, 1974). There are quite a number of these:

1. Signs (1) without the signified (some)thing (2) and without sign interpreter (3):  
yields abstraction from the *a priori* of the linguistic community which reflects on the world and produces propositions with validity claims. Examples are linguistic Platonism, model-Platonism of the logic of science in the linguistic turn: in which the linguistic expressions or the explanatory *model* are the real (some)thing.

2. The sign interpreter (3) without signs (1) and without the signified (some)thing (2): yields idealism of consciousness: abstraction from the a priori of the linguistic community (Descartes, Kant, Fichte, Hegel, Husserl): that is to say subjective/objective reason is the real (some)thing. Language is only a secondary means of explanation; the external world exists only through reason/rationality.
3. Sign interpreter (3) and sign (1) without the signified (some)thing (2): this yields semiotic idealism: sign and sign interpreters are the signified (some)thing. Everything is a sign: Pansemiotics/metaphysical semioticism.
4. The signified (some)thing (2) without signs (1) and without sign interpreter (3): This yields realism and materialism, pre-Kantian ontology/metaphysics: Being is a physical- chemical law of the material world. We are part of this particular material and can at best recognize approximately, with our sense organs, partial perspectives of this material being. Sign use and sign interpretation are pre-scientific constructions that lack a correspondence in the material world (illusion).
5. The signified (some)thing (2) and the sign interpreter (3) without signs (1): yields psychologism or affection-realism; Leibniz, Locke, Berkeley, Hume, positivism of the sensory data, Popper: the observational language and theoretical language of the logic of science can be brought into agreement. The material function of the sensory organs adheres to a “universal syntax” that is identical to the laws of physics and chemistry.
6. The signified (some)thing (2) and the sign (1) without the sign interpreter (3): yields ontosemantic realism, constructivism, systems theory, information theory. Abstraction from the a priori of the linguistic community yields subjectless, syntactic-semantic phase of a modern science of logic in Carnap, Russell, Frege, (Tractatus-)Wittgenstein, Tarski, Popper; solipsism and realism: each speaker/listener is equipped with the same syntax (depicting material reality), alleviating any need for communication about the structure of language or the structure of the world. Abstraction by the cognizant subject produces scientifically exact statements which depict, in agreement with the laws of physics and chemistry, material real-

ity on a 1:1 basis. Subjects of knowledge only disturb this naturalism and muddy the exact cognitive process.

In contrast, a pragmatic philosophy of biology integrates the irreducible three-leveled semiotics into its justification, just as it does the formal-pragmatic preconditions for the possibility of successful rule-governed sign-mediated interactions in agreement with the post-Tractatus Wittgenstein (*Philosophical Investigations*), Austin, Searle, Apel and Habermas. It therefore avoids the reductive/abstractive fallacy and enables a non-solipsistic and non-objectivistic understanding of the linguistically structured and communicatively organized living nature.

## 8 CONCLUSIONS

Planets *without* living organisms have no unstable mixing conditions of gases and temperatures. The gas composition and the temperatures can be determined solely based on physical factors. A planet *with* living organisms deviates considerably from this scheme. The gas composition and temperature will vary in a manner that cannot be predicted exclusively by the laws of physics and chemistry. Planets with life will have an atmosphere whose temperature and gas-molecular composition is regulated by the totality of biological individuals and not by solar energy and the laws of physics and chemistry alone.

The relation between organisms and matter is one of organisms structuring their non-biological environment according to biological principles. The relationship to other organisms is a communicative one: their *mutual* behavior underlies changeable rules (within the frame of natural laws), more precisely (semiotic) rules of sign use with which the biological individuals interact, i.e. coordinate and organize. The relationship of sign users and sign interpreters to the rules of sign use is not strict and immutable, but rather is changeable, alterable and renewable, although it can ensure relative stability.

The *organization* of life depends on successful intra-, inter- and metaorganismic communication processes. Interestingly, rule governed sign mediated interactions are not only the basis for human communication and coordination but a true principle of life itself. As demonstrated, it is the main principle also in and between microbial as in higher eukaryotic organisms as well as between organisms of different organismic kingdoms.

The *structure* of the genome itself is a linguistic one, more analog in eubacteria, more symbolic in archaeobacteria and (higher) eukaryotes. It obeys syntactic, semantic and pragmatic rules. Interestingly the neodarwinistic paradigm of chance mutations and selection is refuted nowadays through research results which identify a higher order regulation code in the non-protein coding regions of genome architecture. This higher order regulation code is subject/object to environmental influences which become heritable, with the effect that a *different use* of protein coding core components leads to different genetic organization.

A non-solipsistic and non-reductionistic understanding of the linguistically structured and communicatively organized living nature can thus provide the methodological basis for a biology as an understanding social science, one whose descriptions are based not on a third person pure observer perspective but rather on the perspective of performative participants of the planetary communicating community of living nature (Witzany 2005).

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## ENDNOTES

<sup>1</sup> In her excellent articles Lynn Caporale (Caporale, 1998; 2003; 2004) demonstrates that the genome finds ways and means to use blind chance for its own purposes. The hereditary material itself decides at which site mutations occur and where they are blocked. The genome contains information with which *it can describe itself*. This agrees with the research results of Mattick und Shapiro, who were able to document the higher-order regulation functions of active micro-RNAs that are coded in the non-protein-coding DNA, for example in the repetitive elements of introns. In a certain sense, this contradicts an assumption of Hoffmeyer (“Digital codes *do nothing*”, Hoffmeyer 1998: 475).

<sup>2</sup> With regard to the *geMetaCode*, Watson postulated in 1992 that he expected to find “information bearing molecules” in the chromosomes (Watson, 1992:6). Mantegna et al. drew the correct conclusions in 1994 based on statistical-linguistic studies: “These results are consistent with the possible existence of one (or more than one) structured biological language(s) present in non-coding DNA sequences” (Mantegna et al., 1994: 3172).

<sup>3</sup> The growth of complexity from analogous languages to symbolic ones is not limited to genetic codes but a typical characteristic of linguistically structured nature in general. For example, symbolic communication between bees of the northern hemisphere is much more complex than analogous communication between bees of the southern hemisphere. Thus northern hemisphere bees conducted much more complex and indeed new ways of coordinated behaviour. Why the terminology analogous/symbolic should be preferred to analogous/digital in describing this semiotic relation has been explained convincingly by Cvrcková and Markos (Cvrcková and Markos 2005).

<sup>4</sup> This contradicts the conviction, that acquired characters are not inherited: “The rejection of so called ‘lamarckism’, precisely amounts to the claim, that no events in the life of an individual will change the content of the genetic information carried by that individual. Acquired characters are not inherited” (Emmeche and Hoffmeyer, 2005: 48).

<sup>5</sup> “Is what we call “obeying a rule” something that it would be possible for only one man to do, and to do only once in his life? (...) It is not possible that there should have been only one occasion on which someone obeyed a rule. It is not possible that there should have been only one occasion on which a report was made, an order given or understood, and so on – To obey a rule, to make a report, to give an order, to play a game of chess, are customs (uses, institutions)” (Wittgenstein 1968: 80).

*One sign alone is not a sign! A sign is a sign only as part of a context of signs. An interpreter is an interpreter only as a co-subject. In his analysis of the concept “to obey a rule”, Wittgenstein provides proof that the identity of meanings logically depends on the ability to obey intersubjectively valid rules together with at least one further subject.*