Biological Self-Organization

Guenther Witzany, Telos-Philosophische Praxis, Buermoos, Austria

ABSTRACT

Biological organisation was long assumed to represent mechanical cause and effect reactions on a quantum theoretical basis following the laws of thermodynamics. Current empirical data show an abundance of signaling molecules that serve as information carriers in the exchange of information between biological agents. More recently an abundance of articles demonstrate successful research on communication processes inherent in the interactions of cells, tissues, organs and organisms in biological processes in all domains of life. Without such biological communication processes no coordination of organizational goals is possible. If biocommunication is disturbed, deformed or damaged organization will happen inappropriately or even incomplete. In contrast to former opinions about the essential features of natural communication recent empirical knowledge indicate a non-mechanistic explanation.

Keywords: Communication, Language, RNA Agents, Semiotic Rules, Sign-Mediated Interactions, Viruses

INTRODUCTION

The most coherent definition of communication is sign-mediated and rule-governed interactions, i.e., social interactions that depend on a commonly shared repertoire of signs and rules of sign-use (Habermas 1994). During the last decades interest in communication within and between organisms overtook that of the pure physiological understanding of organisms. Cell-to-cell communication now dominates contemporary cell biology, including an enormous knowledge about a great variety of signaling pathways serving for both organization and coordination of production, release, uptake, and processing of "information" within and between cells.

The use of "language" as a metaphor increased also from the middle of the twentieth century with growing knowledge about the genetic code. Most of the processes that evolve, constitute, conserve, and arrange the genetic storage medium DNA are terms that were originally used in linguistics, such as nucleic acid language, genetic code, coding, copying, translation, transcription, etc. Meanwhile, the linguistic approach also lost its metaphorical character and the similarity between natural languages/codes, and the genetic storage medium DNA is not only accepted but adapted in bioinformatics, biolinguistics, protein linguistics, systems biology, synthetic biology and biosemiotics (Eigen 1971, Popov et al. 1996, Ji 1999, Searls 2002, Chomsky 2006, Zhang 2006, Favareau 2010, Venter 2013)

COMMUNICATIVE INTERACTIONS

In contrast to former opinions, communicative acts are not restricted only to information exchange between a sender and a receiver, but designate a variety of social interactions mediated by signals according to syntactic (combinatorial), pragmatic (context dependent) and semantic (content-specific) rules (Witzany 2000). On one side, development and growth of organisms such as plants, fungi and animals depends upon successful biocommunication within, and between cells of organisms (Witzany & Baluska 2012c, Witzany 2012c, 2014). However, on the other side, sign mediated interactions are necessary to coordinate behavior in e.g., prokaryote life with the same, or related species and with non-related organisms (Witzany 2011b). In order to generate an appropriate response behavior, organisms must be able to sense, interpret and memorize important indices from the abiotic environment and adapt to them appropriately. However, these communication and interpretation processes can also fail. In such cases the overall consequences could be disease-causing, or even lethal (Witzany 2010a).

COMMUNICATIVE INTERACTIONS NEED SEMIOTIC RULES

Biocommunication between cells, cellular parts, tissues, organs, and organisms is far from being a procedure, which can be reduced to mechanistic input/output or cause/ reaction descriptions. It is evident today that communication processes between living organisms include a variety of circumstances and competences that must be fulfilled in parallel if communicative acts are to have successful consequences, such as common coordination (Witzany 2010b):

- No single organism is able to communicate as an emerging property. It must be a community, a society, or a swarm of organisms that each share an group identity and a competence to sense others as being part of this identity or not, even if this competence is shared genetically solely. This indicates the competence to differentiate between self and non-self.

- To communicate, it is necessary that an organism can manipulate chemical molecules either produced directly by itself or as secondary metabolites or even molecules in the surroundings that are not produced by the organism but can still be used according to the organismic needs.

- Organisms must share a competence to use these signs in a coherent manner, which means using these signs in a strict temporal and spatial context. In most cases, it is not just one signaling molecule but several that are combined in a certain manner. This represents a common feature of sign-use in communication processes, which is called syntax.

- Organisms are part of a habitat in which they live together with similar organisms of the same or related species, and in general, with an abundance of nonrelated organisms of other kingdoms. This context exactly represents the natural habitat with its history of organismic communities in which they evolved and developed certain abilities. Sensing, memory and learning are the preconditions for faster adaptations.

- She signaling molecules, which serve as signs, transport messages with meanings (semantics). The content, which is

transported, triggers certain response behaviors by the same or related, or even unrelated, organisms. Interestingly, the signal sequence or signal content does not necessarily depict a single meaning, i.e., function but can vary according to different situational contexts. This means that identical signs can transport a variety of different messages according to different contextual needs. The different uses of identical signs (sequences) enable the generation of dialects within same species that can transport messages, which are microecosphere-specific.

Syntactic (combinatorial), pragmatic (context specific), semantic (content coherent) rules are different to natural laws. Rules do not function mechanistically but may be varied, deleted, or, in certain circumstances, generated de novo. Additionally, semiotic rules do not function by themselves but need semiotic subjects, i.e., living organisms that use such rules. If no living organism is present, semiotic rules, signs, and biocommunication are absent. Although highly conserved semiotic rules are modifiable, environmental circumstances, such as stress, trigger adaptational responses. In such cases, signals may transport new messages, which previously did not exist, broadening the communicative competences of organisms, i.e., broadening evolutionary capabilities. This is different in the case of abiotic processes, where semiotic rules of sign-use are unnecessary as natural laws are sufficient alone. No semiotic rules are used or necessary for water molecules to freeze into ice (Witzany 2000, 2010).

THE GENETIC CODE IS A NATURAL CODE: CODED BY COMPETENT AGENTS

If we go deeper now we have to look at the genetics of communicative cells, organs and organism. In the first decades of molecular biology it was a common thought that DNA mainly stored the information from which protein-coded sequences are translated (Brenner 2012). Today we know that the largest parts of the genome do not code for proteins but serve as regulatory elements (Brosius 1999, Mattick 2009, Mattick et al. 2010, Qureshi & Mehler 2012, Mercer & Mattick 2013). Since Barbara McClintock it became obvious that there are DNA sequences that can move within the genomic content: Mobile genetic elements, transposable elements, genetic parasites and selfish DNA are some of the attempts to find a correct molecular biological term for nucleotide sequences that move, insert, delete and change the genetic identity of host organisms. These "elements", in most cases non-coding RNAs, now take center stage in discussions regarding regulatory elements in epigenetics and genetics, evolutionary novelties and the coordination of growth and development (Slotkin & Martienssen 2007, Witzany 2010a,b, Shapiro 2011).

Although the abundance of different terms for these molecular structures and functions is increasing, no unifying perspective is available. Their origins are still in the dark, although some of them, a variety of ribozymatic structures, seem to date back to the early RNA world, and even RNA viruses and their defectives may be older than cellular life (Forterre 2005, Atkins et al. 2011, Villarreal & Witzany 2010).

Viruses represent the most abundant source of nucleic acids on earth and each cellular organism is infected by multiple viruses and

RNA agents of viral origin (Ryan 2009). The genome ecosphere for competing viral settlers is a rather limited resource. It is most likely that there is no nucleic acid sequence space to be free or unsettled (Villarreal 2005, 2011).

Three novel core concepts suggest a fundamental change in our view on life: Viruses and ribozymatic interactions predate the evolution of cellular life (Atkins et al. 2011, Koonin et al. 2006, Koonin 2009; Villarreal and Witzany 2010). Viruses and virus-derived subviral groups of RNAs are the agents of genetic/epigenetic invention, recombination, repair and regulation in cellular life. These agents are able to coherently combine the molecular syntax of nucleic acid language according to contextual needs (Villarreal 2009a,b, Witzany 2006, 2012a). This means the explanation of evolutionary novelty by means of random changes in the genetic text, via replication errors that are precondition for variation is outdated. Yes, certainly, mutations are an empirical fact, but they don't contribute very much for evolutionary novelty.

The change from a mechanistic view of molecular biology on nucleic acid sequences as random assemblies of physical entities to an agent-based perspective on genetic texts as the result of complex viral-driven natural genetic engineering seems to be coherent with recent empirical data (Witzany 2009, 2011b). Investigations can now focus on action and interaction motifs of persistent viral consortia with their hosts rather than solely on physical and chemical properties (Villarreal and Witzany 2013a,b). Agent-driven natural genome editing of genetic text sequences is completely absent in inanimate nature. Therefore, the borderline between life and non-life is not only metabolism but the emergence of natural genome editing (Witzany 2010a,b).

DNA HABITATS WITH RNA INHABITANTS

Endogenous viruses and defectives, transposons, retrotransposons, long terminal repeats, non-long terminal repeats, long interspersed nuclear elements, short interspersed nuclear elements, group I introns, group II introns, phages and plasmids are currently investigated examples that use genomic DNA as their preferred live habitat (Villarreal & Witzany 2013a,b). This means that DNA is not solely a genetic storage medium that serves as an evolutionary protocol, but it is also an ecological niche. A great variety of such mobile genetic elements have been identified during the last 40 years as obligate inhabitants of all genomes, either prokaryotic or eukaryotic.

They infect, insert, delete, some cut and paste, others copy and paste and spread within the genome. They change host genetic identities either by insertion, recombination or the epigenetic (re)regulation of genetic content, and co-evolve with the host and interact in a module-like manner. In this respect they play vital roles in evolutionary and developmental processes. In contrast to accidental point mutations, integration at various preferred sites is not a randomly occurring process but is coherent with the genetic content of the host; otherwise, important protein coding regions would be damaged, causing disease or even lethal consequences for the host organism. In contrast to "elements", "entities" and "systems", biological agents are capable of identifying sequence-specific loci of genetic text. They are masters of the shared technique of coherently identifying and combining nucleotides according contextual needs (Witzany 2009, Witzany 2013). This natural genetic engineering competence is absent in inanimate nature, and therefore represents a core capability of life.

EPIGENETICS: IDENTICAL CODE SEQUENCES WITH MULTIPLE MEANINGS

The interrelation between nucleic acid language and linguistics is predominant in the field of bioinformatics, which is a successful tool in genetic comparison techniques such as phylogenetic analyses and comparative genomics. For several decades, it was assumed that the molecular syntax of genetic sequences determined the meaning (semantics) of these sequences according to Manfred Eigen (Eigen 1971, Eigen et al. 1988, Eigen 1993, Eigen & Winkler 1983).

With the rise of epigenetics, it became clear that different marking patterns such as methylation, histone modification and microRNAs of an identical genetic sequence can lead to different reading patterns and, consequently, to the production of different products from this genetic data set (Slotkin & Martienssen 2007, Barlow 2011). Changing environmental circumstances such as stress may alter these markings, which may lead (not necessarily) to inheritable features (Jirtle 2009, Barlow 2011). The evolution of epigenetic marking remained a mystery for a long time. According to the virus-first hypothesis, epigenetic marking is a viral competence. All viruses mark their genome in order to be able to differentiate self from nonself agents. If we assume that viruses are evolutionarily older than cellular life, epigenetic marking is a viral competence transferred to cellular life to broaden host informational content and evolutionary as well as developmental capabilities (Villarreal 2005, 2009a,b).

The integration of viral features to cellular hosts is not a rare event. Considering that viruses are ten times more abundant in sea water and 100-200 times in deep sea sediments (Engelhardt et al. 2014) than cellular microorganisms, which all are infected by phages and plasmids, it seems rather doubtful that this rare habitat of cellular genomes contains free sequence space that is not subjected to competing viral settlers. Therefore future investigations will show a much higher level of these persistent viral agents.

THE GENETIC CODE IN THE LIGHT OF MATHEMATICAL THEORIES OF LANGUAGE

Human languages are also the object of investigation within the realm of formal language theories (Shannon & Weaver 1949, Turing 1950, von Neumann 1966, Eigen 2013). They focus on the common rules of a universal grammar that serves as structure for all languages. This universal grammar is a depiction of material reality, i.e. the hidden logical order of things and its relations determined by natural laws. Mathematics and computer science-based formal language theory function as appropriate mathematical machinery to deal with these phenomena to investigate and analyse language-specific rules that generate meaningful linguistic structures (Nowak & Krakauer 1999, Nowak et al. 2000, Nowak et al. 2001, Nowak et al. 2002). In this respect, languages, grammar and machines have some correspondence: Context-free languages are generated by context-free grammars, which can be implemented by push-down automata. Context sensitive languages are generated by context sensitive grammars. For each of these languages there exists a Turing machine, which can decide whether it is a regular language or not. Therefore mathematics is viewed not only as an appropriate tool to investigate human language and genetic code structures through computer science-based formal language theory but is

itself a depiction of material reality (Brenner 2012, Eigen 2013, Witzany & Baluska 2012a,b).

Similarly to this model of language, systems theory and information theory investigate the empirical significance of scientific sentences by means of a quantifiable set of signs and, additionally, the information transfer of formalised references between a sender and a receiver. Information processing systems are therefore quantifiable themselves (von Neumann 1966, Eigen & Winkler 1983, Eigen 2013). Understanding information is possible because of the logical structure of the universal syntax, i.e. by a process which reverses the construction of meaning (Eigen and Winkler 1983, Witzany 1995). Therefore information theory is also a mathematical theory of language. Manfred Eigen took this formal language theory to describe the genetic code as a regular language.

THE CRUCIAL ERROR IN MATHEMATICAL THEORIES OF LANGUAGE

In 1931 Godel proved in his incompleteness theorem that a machine can principally calculate only those functions for which an algorithm can be provided. But in open systems such as natural languages/codes there are possibilities to generate new sentences and sequences that are not the result of previous ones but are completely new. No algorithm is available in principle to calculate the content of such sentences/sequences. Natural languages prove to be perpetually open 'systems' and cannot guarantee definiteness from within (Godel 1931, Witzany 1995).

The supposition of an 'identical logical structure of language' which constitutes intersubjectivity a priori can only be simulated in computerised models in artificial binary code

languages which are based on formalisable procedures. This, however, has nothing to do with the social praxis and socially shared lifeworld of living agents and their natural languages (Habermas 1994, Tomasello 2008, Witzany 1995, 2000).

Manfred Eigen's concept of natural languages/codes and the current concepts embraced by bioinformatics, biolinguistics, systems biology and synthetic biology are not coherent with current knowledge about key features of natural languages or codes, i.e., the three levels of rules that govern natural code use by competent code-using groups: combinatorial rules (syntax), contextual rules (semantics) and context-dependent rules (pragmatics). In mathematical theories of language the syntax determines semantics (function), but in natural codes pragmatics (context) determines semantics. Pragmatic rules do not exist in Eigen's concept or other mathematical theories of language. Natural code-inherent rules are absent in abiotic matter that is determined strictly by natural laws: no syntax, pragmatic or semantic rules are present if water freezes to ice. Therefore the explanation of the evolution of biological macromolecules in Eigen's concept as well as in other mathematical theories of language cannot explain the evolution of natural codes and its inherent rules (Witzany 2000, 2010a).

The most essential background of natural languages/codes is its concrete use by consortial interacting agents. The real use of a language in its everyday context is always the unity of language embedded in actions. Speaking is a form of social action. Meaning is a social function (Tomasello 2008, Witzany 2011a).

An abundance of theoretical concepts and investigations in the last century suggested to look at organisms like mechanistic automatons, machine like constructions which are

rather input-output determined, and all bodily expressions as mechanistic stimulus-reaction patterns which can be reconstructed and even reprogrammed. Information theory (especially concepts of Turing and von Neumann) and systems biology suggested that in future we can look at self-reproducing automatons which generate information and reproduce via feedback optimized blueprintings. But all of these trials reamined in the conceptual stage. Not even one self-reproducing automaton or machine has been seen until nowadays, no computer has been built from computers, no living cell has been created with all its functions in detail (Witzany & Baluska 2012a,b).

In contrast to mathematical theories of language natural languages and code have features that are not calculable by algorithms and do not fit into the concepts of mathematical theories of language:

- The variety of words combined to sentences that characterize human societies and cultural production in everyday languages and dialects are not the result of copying errors or damage of predating sentences or available sentences based on memory or other data storing techniques. Similarily the natural genetic code and its code using agents do not produce replication errors that underly biological selection to generate fittest types as driving force of genetic novelty.
- According to Gödel there will be really new sequences to be produced in principle that have never been generated before.
- It is inherent feature of natural languages that living agents that use it, can produce new unexpected ones, and such that cannot be deduced out of former ones or available ones. In natural languages/codes there is no universal syntax which transports identical meanings.

CONCLUSION

We now can understand biological self-organisation as well as its temporal and spatial coordination as rather non-mechanistic events. Organisation without communication is not possible, because only communicative interactions can guarantee coordination of a variety of living agents. Biocommunication is sign-mediated, i.e. needs signals, that are combined according syntactic, semantic and pragmatic rules. Biocommunication and its inherent competent sign use by living agents is a kind of social interaction with commonly shared semiotic rules. Natural languages/codes in communicative interactions are social interactions. Meaning is a social function. Communication and signal use is interconnected with living agents that share real life worlds. This indicates the primacy of pragmatic rules because they insure signal use according contextual, i.e. adaptational, environmental needs.

The biocommunication and natural genome editing approach on processual reality of living agents brings some advantages to traditional scholarly conviction: a clear distinction between life and non-life, an empirical non-mechanistic and non-reductionistic description method of biotic interactional patterns throughout all organismic kingdoms. Every coordination within and between organisms can be deciphered by research which identifies signaling molecules and syntactic, pragmatic, semantic rules underlying the mode of signal use. A further advantage is that biological research must not concentrate any longer on theoretical approaches that seek to elucidate language and communication in non-human living nature by algorithm-based modelling.

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