

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11

## From Umwelt to Mitwelt: Natural laws versus rule-governed sign-mediated interactions (rsi's)

12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31

GUENTHER WITZANY

32  
33  
34  
35

### *Abstract*

36  
37  
38  
39  
40  
41  
42

*Within the last decade, thousands of studies have described communication processes in and between organisms. Pragmatic philosophy of biology views communication processes as rule-governed sign-mediated interactions (rsi's). As sign-using individuals exhibit a relationship to following or not-following these rules, the rsi's of living individuals differ fundamentally from cause-and-effect reactions with and between non-living matter, which exclusively underlie natural laws. Umwelt thus becomes a term in investigating physiological influences on organisms that are not components of rsi's. Mitwelt is a term for the investigation of all rsi's of organisms. Living organisms are never solus ipse subjects of semioses, but share common sets of rules and signs. Life depends decisively on symbiotic communities. Serial Endosymbiotic Theory proved that the evolution of higher eukaryotic superkingdom was a merger of ancestral bacteria. The integration of bacterial genomes into eukaryotic genomes was also a step from analog to symbolic genetic codes. Now we know, that so-called 'junk DNA' has higher order regulatory functions on genome architecture and protein coding DNA plays only the role of a structural vocabulary.*

*Keywords: Mitwelt; epigenetic apriori; symbiotic interdependence; geMetaCode.*

### **1. The supplement of the *Umwelt*-concept with a *Mitwelt*-concept**

Within the last decade, the tendency to describe interactions in and between organisms as communication processes has continued to grow. Intra- und interorganismic communication is supplemented by meta-organismic communication that is between members of different species, genera and organismic kingdoms. An explosion of research in the field

*Semiotica* ■■■-1/4 (2006), 1-14

0037-1998/06/0■■■-0001  
© Walter de Gruyter

## 2 G. Witzany

1 of symbioses proved that, in fact, life on our planet is entirely dependent  
2 upon functioning symbiotic interaction communities (Zook 1998; Kowal-  
3 lik 1999; Wagner et al. 1999). A pragmatic philosophy of biology as basis  
4 of a three-leveled biosemiotics found and justify communication processes  
5 as rule-governed sign-mediated interactions (Witzany 1993a, 1993b, 1995,  
6 2002a, 2002b, 2005b). Sign use by interaction partners simultaneously  
7 obeys syntactic, semantic, and pragmatic rules in principle (Witzany  
8 2005b, in press).

9 The conditions on the planet's surface *without* living organisms are de-  
10 termined entirely by the sun's energy and the laws of physics and chemis-  
11 try (Margulis 1999). A planet *with* living organisms, i.e., with biosemiotic  
12 processes deviates considerably from this scheme. The gas composition  
13 and temperature will vary in a manner that cannot be predicted exclu-  
14 sively by the laws of physics and chemistry alone. Such a planet contains  
15 incompatible gas mixtures and temperatures whose relatively stable bal-  
16 ance is actively controlled by organisms.

17 The interaction between organisms and matter is one in which organ-  
18 isms interpret and structure their abiotic environment according to bi-  
19 ological principles. The relationship to other organisms is a communicative  
20 one: their mutual behavior underlies changeable rules, within the frame of  
21 natural laws, more precisely (semiotic) rules of sign use with which the bi-  
22 ological individuals interact, i.e., coordinate and organize. The difference  
23 is that organisms cannot develop such a 'to follow or not follow' relation-  
24 ship with natural laws, but underlie them in the strict sense.

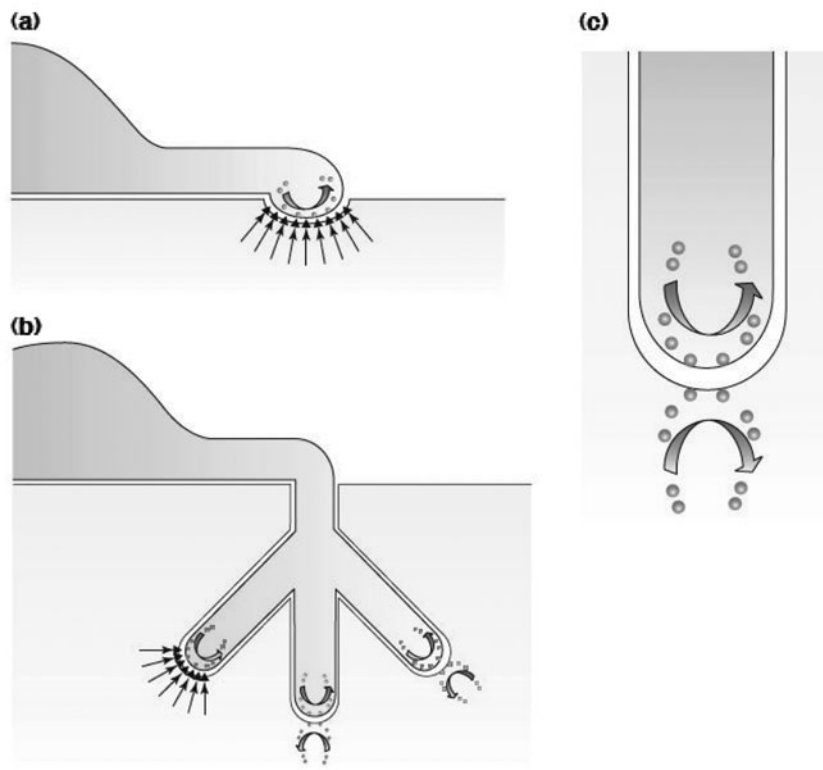
25 The *Umwelt* concept cannot do justice to the fundamental differences  
26 between natural laws and rsi's because this concept reduces rsi's to the  
27 information transmission effect and therefore to a level of coding and  
28 decoding via an individual organism's physiological sensory organ. The  
29 intersubjective-communicative character of the rsi's, and therefore the  
30 relationship to following or not-following commonly shared rules of sign  
31 use, does not manifest itself here.

32 In investigating communication processes in and between organisms, it  
33 is therefore sensible to supplement the *Umwelt* concept with a *Mitwelt*  
34 concept (Witzany in press). The *Mitwelt* concept underlines the difference  
35 between the cause and effect reactions in natural laws and rsi's: *Umwelt*  
36 thus becomes a helpful term in investigating those physiological influ-  
37 ences on organisms that are not components of rsi's. *Mitwelt* is a term  
38 for the integrative investigation of all rsi's of organisms, i.e., all intra-,  
39 inter- and metaorganismic communication processes themselves and their  
40 developmental history.

41 For example, plants maintain two types of membrane domains that re-  
42 semble the neuronal and immunological synapses of animal cells (Baluska

1 et al. 2005). The *first* one transports Auxin and allows the highly plastic  
 2 development of plants. The activity of this developmental plant synapse is  
 3 modulated by two physical factors — light and gravity. The developmen-  
 4 tal plant synapse assembles those molecules of non-living matter which  
 5 are necessary to structure the plants non-biological environment accord-  
 6 ing to biological principles, i.e., molecules become features of signs for  
 7 an interpreting organism. There, the *Umwelt* term is useful in describing  
 8 how organisms develop themselves by metabolizing within natural laws.

9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34



35 Figure 1. 'Immunological plant synapses for cell-to-cell communication between plant host  
 36 cells and their pathogens, parasites and symbionts. (a) Closely apposed plasma membranes  
 37 of intruder and host cell during a penetration attempt. If the host cell succeeds in effectively  
 38 forming a papilla then this synaptic cell-to-cell communication is terminated. (b) Alternat-  
 39 ively, the intruder might penetrate deeply into the host plant cells and then immunological  
 40 plant synapses support haustorial complexes and mycorrhizal arbuscles. (c) During the initia-  
 41 tion of a Rhizobia-plant symbiosis, bacteria organize infection threads, the tips of which  
 42 represent immunological plant synapses specialized for transporting bacteria deeply into root  
 tissues' (figure 1 and text in Baluska et al. 2005: 108).

#### 4 G. Witzany

1 The *second* type of plant synapse resembles the immunological synapse  
2 of animal cells and allows plants to respond to pathogen and parasite at-  
3 tacks (Baluska et al. 2005) as well as to establish stable symbiotic interac-  
4 tions with rhizobia bacteria and fungal mycorrhiza (Baluska et al. 2005;  
5 see also Estabrock and Yoder 1998; Yoder 1999; Keyes et al. 2000; Kah-  
6 mann and Basse 2001; Engelberth et al. 2004; Imaizumi-Anraku et al.  
7 2005).

8 A limited number of chemical messenger substances is available to  
9 maintain and simultaneously conduct the communication between (a)  
10 root cells of three different types, (b) root cells and microorganisms, (c)  
11 root cells and fungi, and (d) root cells and insects (Bais et al. 2004; Call-  
12 away 2002; Dessaux 2004; Dunn and Handelsman 2002; Teplitski et al.  
13 2000; Walker 2003; Fleming 2005). The communication process in the  
14 root zone is generally intra-, inter- and metaorganismic and requires a  
15 high communicative competence in order to be successfully interactive  
16 on all three levels and to distinguish messenger molecules from ‘noise’  
17 (Federle and Bassler 2003; Hirsch et al. 2003; Sharma et al. 2003). Here,  
18 the *Mitwelt* term is useful: its objects are primarily rule-governed sign-  
19 mediated interactions, which depend on coherence of signs and three-  
20 leveled rules, and not on natural laws alone.

21

22

#### 23 2. The epigenetic a priori of semioses

24

25 As in the case of semiotics, biosemiotics also depends on the a priori of  
26 bodies, i.e., living organisms: without living organisms there are *no* intra-  
27 inter and metaorganismic semioses, transcription, translation, copying,  
28 coding, splicing, self-splicing (group I and group II introns), i.e., the  
29 whole complexity of semiotic processes. Rule-governed sign-mediated  
30 interactions depend on living bodies in principle. Living bodies are the  
31 *epigenetic a priori of semioses*. Only in rare exceptions living bodies are  
32 monads, but they are in any case involved in a commonly shared rule-  
33 constituted genetic set up with their descendants.

34 If signs are used by humans, there is, according to Peirce, a non-  
35 reducible three leveled relationship between (1) the sign-user/sign-  
36 interpreter and (2) the signs which designate (3) (some)thing. According  
37 to Morris the relationship: (a) between sign-user/sign-interpreter and  
38 signs is subject to pragmatic rules, (b) between signs and the designated  
39 (some)thing is subject to semantic rules (c) between signs and signs is  
40 subject to syntactic rules. According to Wittgenstein (1968) rule obeying  
41 sign-users/interpreters are never *solus ipse* subjects (as with Descartes,  
42 Kant, Hegel, Husserl, Carnap, Frege, Russel, Tarski, and Popper) but

1 always *performative participants* of communicating communities. Using/  
2 interpreting signs is social interacting.

3 Integrating this pragmatic turn thinkers we are able to avoid the main  
4 problem of all variations of philosophy of consciousness: how to make  
5 the move from a state of *solus ipse* consciousness to a state of mutual  
6 agreement, coordination and cooperation.

7 Therefore, semiotics as well as biosemiotics are really social sciences  
8 (Witzany 2005b). Their research is directed towards signs, their use, their  
9 meaning, their syntactic combinations (Noeth 2000; Kull 2005). Because  
10 one sign alone is not a sign and without a sign-using community there is  
11 neither meaning, nor interpretation or linguistic action, i.e., active sign  
12 use, the social component is the decisive one. In Wittgenstein's language  
13 game it is the analysis of obeying rules, in Peirce it is the 'ultimate opin-  
14 ion' of an 'indefinite community of investigators' which refutes the *solus*  
15 *ipse* subject of knowledge of Descartes and Kant in principle.<sup>1</sup> It is never  
16 the role of an interpreter, because 'the interpreter' as *solus ipse* subject  
17 doesn't exist (Witzany 2005b). Interpreting is a social action, and the 'in-  
18 terpretant' is an internalized commonly shared background knowledge of  
19 a historically evolved linguistic community.

20 From this point of reflection we can describe sign use in non-human  
21 nature also. But not from an monological *solus ipse* perspective as a cog-  
22 nitive simulation of an (quasi-) extraterrestrial observer, but with the  
23 knowledge that living bodies are involved in social lifeworlds which de-  
24 pend on social lifeworlds of (a) the same and parallel (b) other species,  
25 genera, organismic kingdoms. All living organisms of the eukaryotic  
26 superkingdom *depend decisively* on functioning symbioses with microbial  
27 social lifeworlds. In examining the cells of the human body, 10 percent  
28 stem from the human individual and up to 90 percent are symbiotic mi-  
29 croorganisms (Blech 2000).

30  
31

### 32 **3. Evolution of the eukaryotic superkingdom by genomic integration**

33

34 Another example applying the *Mitwelt* concept is the Serial Endosymbi-  
35 otic Theory. The SET is so revolutionary because it reversed the evolu-  
36 tion vector from ramification to unification. Eukaryotic cells, according  
37 to Margulis, are the result of merging several different ancestor genomes,  
38 that of (1) thermoplasmic archaeobacteria with (2) motile spirochaeta-like  
39 eubacteria. This was followed by a merging with (3) aerobic organisms.  
40 The final step was the merging with (4) photosynthetic bacteria. One inte-  
41 grated genome was sufficient in the merger of archae- and eubacterium.  
42 In the protocista two integrated genomes were necessary, in the fungi

1 three, in animals at least four, and in the plant kingdom (350 million years  
2 ago) at least five. (Margulis 1996, 1999, 2004; Margulis and Schwartz  
3 1988; Margulis et al. 2000; Margulis and Sagan 2002; Cavalier-Smith  
4 2002; Stechmann and Cavalier-Smith 2003).

5 From the biosemiotic point of view this symbiogenetic process was  
6 a change *from metaorganismic* communication, i.e., rsi's between two in-  
7 dividuals who lived in symbiosis, to an *intraorganismic* communication  
8 process. In the latter, two different genomes integrated into one at the  
9 correct sequences, at the correct genome ratio, (i.e., the genome architec-  
10 ture). It had to involve a correct integration of entire gene-blocks. The  
11 SET demonstrates that complex genomic makeups can be passed on di-  
12 rectly and not through step-by-step development via chance mutations  
13 (Witzany 2005b). One scenario of how this integration process of two dif-  
14 ferent genomes could take place can be imagined by the phenomenon of  
15 horizontal gene transfer (Wagner et al. 1999; Wolf 1999, 2000; Jain et al.  
16 1999; Jain et al. 2003; Xie et al. 2004; Timmis et al. 2004). As suggested  
17 (Witzany 2005a, 2005b, in press) these (symbiogenetic and HGT) pro-  
18 cesses are not changes in aggregate status solely but undoubtable bio-  
19 semiotic ones: They are highly competent DNA textprocessing proce-  
20 dures (Frost et al. 2005; Bordenstein and Reznikoff 2005; Gogarten and  
21 Townsend 2005). Thomas and Nielsen identified 17 steps of integration  
22 performance (see Fig. 2).

23 The DNA transfer between prokaryote cells include transformation,  
24 transduction and conjugation which depend on certain mobile genetic  
25 elements such as plasmids, bacteriophages and transposons. In this  
26 processes that 'agents' are the 'natural genetic engineers' (Frost et al.  
27 2005).

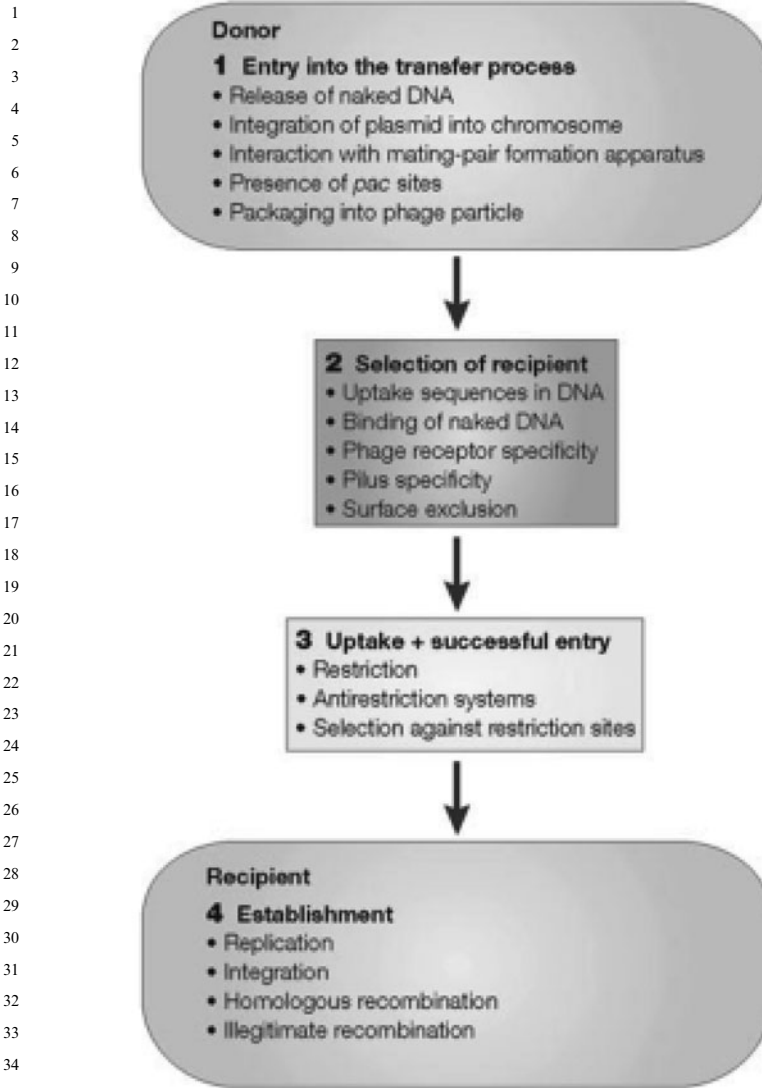
28  
29

#### 30 **4. Analog — symbolic (prokaryotic genome — eukaryotic genome)**

31

32 The step from prokaryotic to eukaryotic cells and the recombination of  
33 up to 5 (or maybe even 7) different genomes into one, as occurred in the  
34 evolution of plant cells was also the step from a nearly complete analog  
35 proteinencoding DNA to a genome architecture of analog and increas-  
36 ingly symbolic sequences (Witzany 2005b). As higher-developed eukary-  
37 otic multicellular organisms show, this analog/symbolic ratio changed  
38 into a proportion in humans, for example, of 3 percent proteinencoding  
39 DNA (which is nearly identical to that of mice, namely 99 percent) and  
40 97 percent non-proteinencoding DNA.

41 Ten years ago this non-proteinencoding DNA was not the center of  
42 research interests and therefore named 'junk' DNA. While there is no



36 Figure 2. *'The process of horizontal gene transfer. A schematic outlining the stages through*  
37 *which DNA must go on its journey from donor to recipient bacteria. The process begins with*  
38 *DNA in a potential donor cell becoming available and ends when this DNA becomes a func-*  
39 *tional part of a recipient cell's genome' (figure and text in Thomas and Nielsen 2005: 719).*

1 relation between the complexity of organisms and the quantity of protein-  
2 coding DNA, but an obvious relation between complexity of organisms  
3 and non-protein coding DNA, this 'junk' DNA became interesting. It  
4 does not code for proteins but for RNAs, especially for a type of micro-  
5 RNAs (Cavalier-Smith and Beaton 1999; Mattick 2001, 2003, 2005; Mat-  
6 tick and Gagen 2001; Shapiro and Sternberg 2005). These micro-RNAs  
7 are as competent as proteins in DNA/RNA editing. Some may term this  
8 discrete structure of eukaryotic DNA (that doesn't indicate analogous for  
9 what it codes) digital (Emmeche and Hoffmeyer 2005). But this informa-  
10 tion theoretical description is a more or less technical term, whereas 'sym-  
11 bolic' is a better description for the phenomena as such (Cvrcková and  
12 Markos 2005; Witzany 2005b).

13 Some of the discovered tasks of these micro-RNAs are co-suppression,  
14 suppression of transposition, position effect variegation, start-stop sig-  
15 nals, RNA interference, imprinting, chromosomal methylation, transvec-  
16 tion, transcriptional and posttranscriptional gene silencing along with  
17 numerous other RNA-DNA, RNA-RNA (trans-acting RNAs), RNA-  
18 protein interactions (Mattick and Gagen 2001). Today we may say that  
19 cellular differentiation and phenotypic variation results primarily from  
20 variations in this high-order regulation, not in the proteins themselves,  
21 thus non-protein coding DNA bears the architecture of eukaryotic com-  
22 plexity (Mattick 2001).

23

24

##### 25 **5. Structural (protein-code-) vocabulary and its higher-order regulation**

26

27 The phenotypic variation in complex organisms is then the result of a *dif-*  
28 *ferent use* of a set of protein coding core components. We can say that in  
29 higher eukaryotic organisms we find 3 percent protein coding DNA as the  
30 structural vocabulary and 97 percent non-protein coding DNA which has  
31 higher-order regulatory and constitutional functions that are decisive for  
32 expression, differentiation, development, (i.e., coordinated expression in  
33 time). I postulated these higher order regulatory and constituting func-  
34 tions as a consequence of the pragmatic philosophy of biology approach  
35 already in 1993 and in a further developed version in 2000 in terms like  
36 'innovation-code, text-generating-code, evolution-code' (Witzany 1993b,  
37 1997, 2000).

38 In an article in S.E.E.D. Journal (Witzany 2005b), I put it in concrete  
39 as the genome-editing *MetaCode*. This non-protein coding *geMetaCode*  
40 has regulatory and constituting functions in chromosomal methylation.  
41 These functions decide about different signaling pathways of the same  
42 genetic setups through different rules of gene silencing and special start



1 and stops via alternative splicing. With this chromosomal methylation,  
 2 organisms are able to handle ‘multiple protein meanings’ (Ast 2005) of  
 3 one and the same genetic data set. As shown by some epigeneticists, these  
 4 (*geMetaCode*-) functions are influenced and altered by environmental  
 5 and other influences which are heritable but *do not involve or depend on*  
 6 *mutations* of the DNA itself (Jenuwein and Allis 2001; Spotswood and  
 7 Turner 2002; Sternberg 2002; Turner 2000, 2002; Jaenisch and Bird 2003;  
 8 True et al. 2004; Wang et al. 2004; Waterland and Jirtle 2004).

9 The proposed *geMetaCode* integrates the features of (1) non-  
 10 proteincoding DNA, (2) DNA which codes alternatively for (micro)RNAs  
 11 and proteins, which depends on situational contexts and (3) the protein-  
 12 coding DNA. This enables the (epigenetic) body and genome to interact  
 13 *in time* over the whole lifetime, in the expression pathways of early devel-  
 14 opment, the body axis, extremities, up until the adult individual. Or, as in  
 15 plants, the endless growth and development (Trewavas 2001, 2003, 2005)  
 16 based on *one and the same* protein coding vocabulary. The latter is used  
 17 depending on the developmental context as epigenetic orientation of the  
 18 plants, and therefore by the non-proteincoding regulatory, constitutional  
 19 and generating functions of *geMetaCode*.

20

21

## 22 6. Genetic backup insurance against mutational faults

23

24 Plants can overwrite their genetic code they inherited from their parents  
 25 and revert to that of their grand or great-grandparents (Lolle et al. 2005;  
 26 Weigel and Juergens 2005; Pearson 2005). This contradicts traditional  
 27 DNA textbook conviction that children simply receive combinations of  
 28 the genes carried by their parents. Now a backup code was found that  
 29 can bypass unhealthy sequences inherited from the parents and revert  
 30 to the healthier sequences possessed by their grandparents or great-  
 31 grandparents. As shown by a research team, plants are able to replace ab-  
 32 normal code sequences of their parents with the regular code possessed by  
 33 earlier generations.

34 Is it therefore necessary that not only the genetic setup of the parents is  
 35 inherited but also that of the grand-parents and former ancestors? What  
 36 is proposed is that higher order regulating micro RNAs — which func-  
 37 tion as expressions of *geMetaCode* — ensure ancestor genome structures,  
 38 which overrule proteincoding DNA under certain circumstances like  
 39 stress. Such stress situations that could be dangerous for survival, could  
 40 trigger plants to revert to the genetic setup of their ancestors which per-  
 41 haps is more competent to deal with this circumstances than that of their  
 42 parents.

1 It means that the (pragmatic) situational context of a living plant body  
2 (neuronal, hormonal, inflammatory, immune, stress) may induce epige-  
3 netic intervention on *geMetaCode*, i.e., active micro-RNA's activate a  
4 certain signaling pathway network which is able to restructure semantics  
5 of a genetic setup. By initiating methylation- and histone-modifications,  
6 certain silencings, start and stops, alternative splicing processes constitute  
7 alternative sequences, so that in existing genome architecture not the in-  
8 herited parental sequences are translated and transcribed but the backup  
9 copy of grand or great-grandparents.

10 Under normal conditions, genetic setup is in use, which stems from the  
11 parents. These research results are indications that not only a combina-  
12 tion of parental genes is inherited, but also ancestral genome-regulating  
13 features in 'non-coding' DNA, which enables alternative splicing path-  
14 ways, i.e., a *different use and multiple protein meanings of one and the*  
15 *same genetic data set* (Lolle et al. 2005; Weigel and Juergens 2005; Pear-  
16 son 2005).

17

18

## 19 7. Conclusions

20

21 This contribution could be an approach to resolve the contradiction of  
22 neo-Darwinism and neo-Lamarckism: The protein-coding DNA is not  
23 subject to evolutionary remodifications that lead to new abilities or new  
24 organisms, but is subject to chance mutations which can alter *existing*  
25 genotypes. The non-protein coding DNA, with its higher-order regulatory  
26 functions is subject to evolutionary remodifications *that are heritable but*  
27 *also reversible* and that regulate the structural vocabulary of protein-  
28 coding DNA. The *geMetaCode* is subject of encoding acquired abilities,  
29 i.e., to higher-order regulatory and constitutional functions, which may  
30 reorganize *and generate* new and altered genotypes with phenotypic con-  
31 sequences by alternative use of *one and the same* protein-coding DNA.

32

33

## 34 Note

35

- 36 1. The 'ultimate opinion' of the 'indefinite community of investigators' of Peirce doesn't  
37 resolve the discrepancy between (artificial) scientific languages and the ultimate meta-  
38 language of everyday language. Only the pragmatic action theory was able to found and  
39 justify rule-governed sign-mediated interactions as the a priori of the intersubjective-  
40 communicative character of thought, research, progress of knowledge, *and* everyday  
41 language. In contrast with Peirce, the pragmatic action theory doesn't focus on the inter-  
42 preter of signs in a process of interpretation, but on the *preconditions* for his ability to  
interpret, i.e., his a priori reliance on a social lifeworld that was the basis for his learning

1 to speak and to act communicatively. In my opinion, Josiah Royce with his 'community  
2 of interpretation' followed by George Herbert Mead and his 'community of universal  
3 discourse' were more radical in reaching a post-Kantian communicative community as  
4 subject of knowledge.  
5

## 6 References

- 8 Ast, G. (2005). The alternative genome. *Scientific American*, April.
- 9 Bais, H. P., Park, S. W., Weir, T. L., Callaway, R. M., and Vivanco, J. M. (2004). How  
10 plants communicate using the underground information superhighway. *Trends in Plant  
11 Science* 9 (1), 26–32.
- 12 Baluska, F., Volkmann, D., and Menzel, D. (2005). Plant synapses: Actin-based domains  
13 for cell-to-cell communication. *Trends in Plant Science* 10 (3), 106–111.
- 14 Blech, J. (2000). *Leben auf dem Menschen. Die Geschichte unserer Besiedler*. Hamburg: Ro-  
15 wohlft Taschenbuch Verlag.
- 16 Bordenstein, S. R. and Reznikoff, W. S. (2005). Mobile DNA in obligate intracellular bacte-  
17 ria. *Nature Reviews Microbiology* 3, 688–699.
- 18 Callaway, R. M. (2002). The detection of neighbors by plants. *Trends in Ecology and Evolu-  
19 tion* 17, 104–105.
- 20 Cavalier-Smith, T. (2002). Chloroplast evolution: Secondary symbiogenesis and multiple  
21 losses. *Current Biology* 12, 62–64.
- 22 Cavalier-Smith, T. and Beaton, M. J. (1999). The skeletal function of non-coding DNA: new  
23 evidence from ancient cell chimeras. *Genetics* 106, 3–13.
- 24 Cvrcková, F. and Markos, A. (2005). Beyond bioinformatics: Can similarity be measured in  
25 the digital world? *Journal of Biosemiotics* 1, 87–105.
- 26 Dessaux, Y. (2004). Biological communications and interactions in the rhizosphere. Paper  
27 presented at the Rhizosphere 2004 Congress, Munich, Germany, September 12–17.
- 28 Dunn, A. K. and Handelsman, J. (2002). Toward an understanding of microbial commu-  
29 nities through analysis of communication networks. *Antonie van Leeuwenhoek* 81, 565–574.
- 30 Emmeche, C. and Hoffmeyer, J. (2005). Code-duality and the semiotics of nature. *Journal of  
31 Biosemiotics* 1, 48.
- 32 Engelberth, J., Alborn, H. T., Schmelz, E. A., and Tumlinson, J. H. (2004). Airborne signals  
33 prime plants against insect herbivore attack. *Proceedings of the National Academy of  
34 Sciences* 101 (6), 1781–1785.
- 35 Estabrook, E. M. and Yoder, J. I. (1998). Plant-plant communications: Rhizosphere signal-  
36 ling between parasitic angiosperms and their hosts. *Plant Physiology* 116, 1–7.
- 37 Federle, M. J. and Bassler, B. L. (2003). Interspecies communication in bacteria. *Journal of  
38 Clinical Investigation* 112 (9), 1291–1299.
- 39 Fleming, A. (ed.) (2005). Intercellular communication in plants. *Annual Plant Reviews* 16.
- 40 Frost, L. S., Leplae, R., Summers, A. O., and Toussaint, A. (2005). Mobile genetic elements:  
41 The agents of open source evolution. *Nature Reviews Microbiology* 3, 722–732.
- 42 Gogarten, J. P. and Townsend, J. P. (2005). Horizontal gene transfer, genome innovation  
and evolution. *Nature Reviews Microbiology* 3, 679–687.
- Hirsch, A. M., Dietz Bauer, W., Bird, D. M., Cullimore, J., Tyler, B., and Yoder, J. I.  
(2003). Molecular signals and receptors: Controlling rhizosphere interacting between  
plants and other organisms. *Ecology* 84, 858–868.
- Imaizumi-Anraku, H. et al. (2005). Plastid proteins crucial for symbiotic fungal and bacte-  
rial entry into plant roots. *Nature* 433, 527–531.

- 1 Jaenisch, R. and Bird, A. (2003). Epigenetic regulation of gene expression: How the ge-  
2 nome integrates intrinsic and environmental signals. *Nature Genetics Supplement* 33 (3),  
245–254.
- 3 Jain, R., Rivera, M. C., and Lake, J. A. (1999). Horizontal gene transfer among genomes:  
4 The complexity hypothesis. *Proceedings of the National Academy of Sciences* 96, 3801–  
5 3806.
- 6 Jain, R., Rivera, M. C., Moore, J. E., and Lake, J. A. (2003). Horizontal gene transfer  
7 accelerates genome innovation and evolution. *Molecular Biology and Evolution* 20 (10),  
1598–1602.
- 8 Jenuwein, T. and Allis, C. D. (2001). Translating the histone code. *Science* 293, 1074–  
9 1080.
- 10 Kahmann, R. and Basse, C. (2001). Fungal gene expression during pathogenesis-related de-  
11 velopment and host plant colonization. *Current Opinion in Microbiology* 4 (4), 374–380.
- 12 Keyes, W. J., O'Malley, R., Kim, D., and Lynn, D. G. (2000). Signaling organogenesis in  
13 parasitic angiosperms: Xenognosin generation, perception, and response. *Journal of Plant  
Growth Regulation* 19, 217–231.
- 14 Kowallik, K. V. (1999). Endosymbiose — ein Motor der Evolution. *Biologen heute*, [http://  
15 www.vdbiol.de/content/e3/e132/e2219/index\\_ger.html](http://www.vdbiol.de/content/e3/e132/e2219/index_ger.html).
- 16 Kull, K. (2005). A brief history of biosemiotics. *Journal of Biosemiotics* 1, 1–34.
- 17 Lolle, S. J., Victor, J. L., Young, J. M., and Pruitt, R. E. (2005). Genome-wide non-  
18 mendelian inheritance of extra-genomic information in *Arabidopsis*. *Nature* 434, 505–509.
- 19 Margulis, L. (1996). Archaeal-eubacterial mergers in the origin of Eukarya: Phylogenetic  
20 classification of life. *Proceedings of the National Academy of Sciences* 93, 1071–1076.  
21 — (1999). *Die andere Evolution*. Heidelberg: Spektrum Akademischer Verlag.  
22 — (2004). Serial endosymbiotic theory (SET) and composite individuality. Transition from  
23 bacterial to eukaryotic genomes. *Microbiology Today* 31, 173–174.
- 24 Margulis, L., Dolan, M. F., and Guerrero, R. (2000). The chimeric eukaryote: Origin of  
25 the nucleus from the karyomastigont in an amitochondriate protist. *Proceedings of the  
National Academy of Sciences* 97, 6954–6959.
- 26 Margulis, L. and Sagan, D. (2002). *Acquiring Genomes. A Theory of the Origin of Species*.  
New York: Basic Books.
- 27 Margulis, L. and Schwartz, K. V. (1988). *Five Kingdoms*. New York: W. H. Freeman.
- 28 Mattick, J. S. (2001). Non-coding RNAs: The architects of eukaryotic complexity. *EMBO  
Reports* 2 (11), 986–991.
- 29 — (2003). Challenging the dogma: The hidden layer of noncoding RNAs in complex organ-  
30 isms. *BioEssays* 25 (10), 930.
- 31 — (2005). Das verkannte Genom-Programm. *Spektrum der Wissenschaft* 3, 62–69.
- 32 Mattick, J. S. and Gagen, M. J. (2001). The evolution of controlled multitasked gene  
33 networks: The role of introns and other noncoding RNAs in the development of complex  
34 organisms. *Molecular Biology and Evolution* 18 (9), 1611–1630.
- 35 Noeth, W. (2000). *Handbuch der Semiotik*. Stuttgart: Metzler.
- 36 Pearson, H. (2005). Cress overturns textbook genetics. *Nature* 434, 351–360.
- 37 Shapiro, J. A. and Sternberg, R. von (2005). Why repetitive DNA is essential to genome  
38 function. *Biological Review* 80, 1–24.
- 39 Sharma, A., Saghal, M., and Johri, B. N. (2003). Microbial communication in the rhizo-  
40 sphere: Operation of quorum sensing. *Current Science* 85 (8), 1164–1172.
- 41 Spotswood, H. T. and Turner, B. M. (2002). An increasingly complex code. *Journal of Clin-  
ical Investigation* 110 (5), 577–582.
- 42 Stechmann, A. and Cavalier-Smith, T. (2003). The root of the eukaryote tree pinpointed.  
*Current Biology* 13 (17), 665–666.

- 1 Sternberg, R. von (2002). On the roles of repetitive DNA elements in the context of a  
 2 unified genomic-epigenetic system. *Annals of the New York Academy of Sciences* 981,  
 154–188.
- 3 Teplitski, M., Robinson, J. B., and Bauer, W. D. (2000). Plants secrete substances that  
 4 mimic bacterial *N*-acyl homoserine lactone signal activities and affect population density-  
 5 dependent behaviours in associated bacteria. *Molecular Plant-Microbe Interaction* 13,  
 6 637–648.
- 7 Timmis, J. N., Ayliffe, M. A., Huang, C. Y., and Martin, W. (2004). Endosymbiotic gene  
 8 transfer: Organelle genomes forge eukaryotic chromosomes. *Nature Reviews Genetics* 5,  
 123–135.
- 9 Thomas, C. M. and Nielsen, K. M. (2005). Mechanisms of, and barriers to, horizontal gene  
 10 transfer between bacteria. *Nature Reviews Microbiology* 3, 711–721.
- 11 Trewavas, A. (2001). How plants learn. *Proceedings of the National Academy of Sciences of*  
 12 *the USA* 96, 4216–4218.
- 13 — (2003). Aspects of plant intelligence. *Annals of Botany* 92, 1–20.
- 14 — (2005). The green plants as an intelligent organism. Paper presented at the First Meeting  
 on Plant Neurobiology, Florence, Italy, May 17–20.
- 15 True, H., Berlin, I., and Lindquist, S. L. (2004). Epigenetic regulation of translation reveals  
 16 hidden genetic variation to produce complex traits. *Nature* 431, 184–187.
- 17 Turner, B. M. (2000). Histone acetylation and an epigenetic code. *Bioessays* 22, 836–845.
- 18 — (2002). Cellular memory and the histone code. *Cell* 111, 285–291.
- 19 Wagner, E. et al. (eds.) (1999). *From Symbiosis to Eukaryotism. Endocytobiology VII: Pro-*  
 20 *ceedings of the International Congress on Endocytobiology, Symbiosis and Biomedicine.*  
 Freiburg/Geneva: University of Freiburg/University of Geneva.
- 21 Walker, T. S. (2003). Root exudation and rhizosphere biology. *Plant Physiology* 132, 44–51.
- 22 Wang, Y., Fischle, W., Cheung, W., Jacobs, S., Khorasanizadeh, S., and Allis, C. D. (2004).  
 23 Beyond the double helix: Writing and reading the histone code. In *Reversible Protein Ace-*  
 24 *tylation* (= Novartis Foundation Symposium 259), G. Bock and J. Goode (eds.), 3–20.  
 London: Wiley.
- 25 Waterland, R. A. and Jirtle, R. L. (2004). Early nutrition, epigenetic changes at transposons  
 26 and imprinted genes, and enhanced susceptibility to adult chronic diseases. *Nutrition* 20  
 27 (1), 63–68.
- 28 Weigl, D. and Juergens, G. (2005). Genetics: Hotheaded healer. *Nature* 434, 443.
- 29 Witzany, G. (1993a). Zeichenprozesse als Bedingungen der Möglichkeit von Leben und Evo-  
 30 lution. *Zeitschrift für Semiotik* 15 (1/2), 107–125.
- 31 — (1993b). *Natur der Sprache — Sprache der Natur. Sprachpragmatische Philosophie der Bi-*  
 32 *ologie.* Würzburg: Königshausen and Neumann.
- 33 — (1995). From the ‘logic of the molecular syntax’ to molecular pragmatism. *Evolution and*  
 34 *Cognition* 1 (2), 148–168.
- 35 — (1997). Semiosis and evolution. In *Semiotics Around the World: Synthesis in Diversity,*  
 36 *Proceedings of the Fifth Congress of the International Association for Semiotic Studies,*  
 37 *Berkeley 1994,* I. Rauch and G. F. Carr (eds.), 977–980. Berlin: Mouton de Gruyter.
- 38 — (2000). *Life: The Communicative Structure. A New Philosophy of Biology.* Norderstedt:  
 39 Libri Books on Demand.
- 40 — (2002a). Reduction of biological phenomena? Deficits of systems theory and the alterna-  
 41 tives. In *Processes in Complex Systems, Proceedings of the Seventh International Congress*  
 42 *of the International Association for Semiotic Studies, Dresden 1999,* W. Schmitz (ed.), 303–  
 307, Berlin: Mouton de Gruyter.
- (2002b). Sprache und Kommunikation als zentrale Struktur- und Organisationsprinzi-  
 pien belebter Natur. In *Körper-Sprache-Weltbild. Integration biologischer und kultureller*

14 G. Witzany

- 1 *Interpretationen in der Medizin*, L. Albers and O. Leiss (eds.), 87–96. Stuttgart/New  
2 York: Schattauer.  
3 —(2005a). Serial Endosymbiotic Theory (SET): The biosemiotic update 2005. Paper pre-  
4 sented at the First Meeting on Plant Neurobiology, Florence, Italy, May 17–20.  
5 —(2005b). Natural history of life: History of communication logics and dynamics. *S.E.E.D.*  
6 *Journal* 5 (1), 27–55.  
7 —(in press). From biosphere to semiosphere to social lifeworlds. Biology as an understand-  
8 ing social science. *Journal of Biosemiotics* 2.  
9 Wittgenstein, L. (1968). *Philosophical Investigations*. Oxford: Basil Blackwell.  
10 Wolf, Y. I. (1999). Evolution of aminoacyl-tRNA synthetases — analysis of unique domain  
11 architectures and phylogenetic trees reveals a complex history of horizontal gene transfer  
12 events. *Genome Research* 9, 689–710.  
13 —(2000). Genome alignment, evolution of prokaryotic genome organization, and prediction  
14 of gene function using genomic context. *Genome Research* 11, 356–372.  
15 Xie, G., Bonner, C. A., Song, J., Keyhani, N. O., and Jensen, R. A. (2004). Inter-genomic  
16 displacement via lateral gene transfer of bacterial *trp* operons in an overall context of ver-  
17 tical genealogy. *BMC Biology* 2, 15.  
18 Yoder, J. I. (1999). Parasitic plant responses to host plant signals: A model for subterranean  
19 plant-plant interactions. *Current Opinion in Plant Biology* 2, 65–70.  
20 Zook, D. (1998). A new symbiosis language . . . *ISS Symbiosis News* 1 (3), 1–3.

21 Guenther Witzany (b. 1953) is the founder of and free philosopher at telos-Philosophische  
22 Praxis <witzany@sbg.at>. His research interests include universal pragmatics, biosemiotics,  
23 plant neurobiology, microbiology, and theory of science. His recent major publications  
24 include *Life: The Communicative Structure. A New Philosophy of Biology* (2000); *Natural*  
25 *History of Life: History of Communication Logics and Dynamics* (2005); and ‘The Logos of  
26 the Bios. Contributions to the foundation of a three-leveled biosemiotics’ (in press).  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42