

# **Living as languaging: distributed knowledge in living beings**

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## **Abstract.**

We trace life at different levels of organization and/or description to the cohabitation of individuals within and between historically established lineages. Ways of such cohabitation depend on experience of particular guilds or aggregates; they cannot be easily foretold from any basic level of description, they are distributed across all levels, and across all members of the community. Such phenomena of interactivity constitute a lived world which, we argue, represents a genuine analogy with our domain of human cultures and languages. We draw an analogy with three levels of meaning as defined by Rappaport (2010) and show that life and languaging are virtually analogous.

## **Introduction**

Contributions to this volume show that cognition arises not only 'in the head', but also as the result of living in a network of interactions – in the medium of languaging. These may give rise to particular expectations about a given class of situations and, for example, various kinds of expertise. Following the same logic, language and languages cannot be separated from languaging (Steffensen, this volume); our joint activities make sense because of how we concert our doings in a culture or what Thibault (2011) terms a social meshwork. Outcomes of such doings often depend also on differences that people find as meaningful cues to perform expertly or to construe wordings in a particular way. In other words, much depends on patterns that are extracted by living beings that dwell in a historical world of bodily experience, and of the community into which they are rooted. Indeed, in the context, these ideas will not seem controversial; however, in what follows, we propose taking a further step: we propose that analogical processes help *all* inhabitants of the biosphere / semiosphere to become valuable members of living networks. Our approach may look as yet another contribution to the long list of holistic theories that compete without success with the reigning reductionist paradigm of biology. We, however, do not deny the explanatory power of contemporary biological theory: by stressing the role of historical bodily

experience and of the “cultural” role of communities we strive towards a fuller understanding of life phenomena, much along the line the linguists undertook from the vocabularies through semiotics up to languaging. We invite the reader to take an excursion from the “central dogma” and neodarwinian explanation of evolution, towards what we believe is a more complete view of the living, that extends through 9 orders of magnitudes (or “73 octaves of nature’s music“, as poetically expressed by M.-W. Ho 1993) and from nanoseconds to 4 billions of years. Our extension to the distributed view is to argue that what goes for cognition and language also applies generally to life.

### **Levels of meaning**

Biologists have much to gain from considering how human cultures exploit what have been termed various 'levels' of meaning. Here, we take inspiration and a leading thread in the book by R. A. Rappaport *Ritual and religion in the making of humanity* (2010); we shall exploit its paraphrase “Ritual in the making of species”, still by following Rappaport’s argumentation that was intended for human race only.

Rappaport invites us to acknowledge that human cultures as featuring three levels of meaning. Our paper will take the view that the kinds of systems that we find in molecular biology bear remarkable similarities. (1) *Low-order meaning* is based in differences that can be found in the everyday semantics: thus *rat* differs from both *mouse* and *rate* (in spelling as in pronunciation). Plainly, science is most comfortable with this kind of meaning, and we shall investigate some features of this level in biology. (2) In the *middle-order* of meaning, a person is able to make and construe “similarities hidden beneath the surfaces of apparently distinctive phenomena” (p. 71). While types may still appear, they are now associated with various kinds of metaphors and signs. This is the level of biosemiotics and biohermeneutics, and we took 4 casual examples how an individual construes its body and its *umwelt* at this level of meaning. Finally, (3) *high-order meaning* is “grounded in identity or unity, the radical identification or unification of self with other” (p. 71); in dealing with this, we look beyond models that depend on the regular appearance of discrete types and draw on what we think of as “experience of being” and our sense of belonging in a community. Rappaport concludes (caveat lector, he speaks about human condition!):

*“The distinctions of low order meaning, lodged in language, divide the world into discrete objects; the recognition of similarity constituting middle-order meaning*

*makes connections among those objects; high-order meaning unifies the world into wholeness. Middle-order and high-order meaning may thus prevail, at least from time to time, over the experiences of fragmentation and alienation that are, possibly, concomitants of language's objectifying powers, but it is important to note that the three levels of meaning do not always live easily together. Naive scientism and naive rationalism tend to deny the validity of middle- and high-order meaning, and it is ironically interesting that information may be the enemy of meaningfulness. Conversely, untempered commitment to middle- and high-order meaning may ignore crucial distinctions in the natural and social world.” (Rappaport 2010: 73, our emphasis).*

Let us explain the three levels on a Biblical parable: Ezequiel cites the Lord as declaring: “*I have no pleasure in the death of the wicked* (33, 11). While the verse may be new to some readers, it has been cited and interpreted in numerous sermons, moral debates and literary contexts. Yet, we suggest, none of hypothetical readers, naïve or learned, is likely to have considered the sentence in terms of the following syllogism:

*p*: God has no pleasure in the death of the wicked

*q*: Mrs. A is wicked

*p*→*q*: Mrs. A is immortal

Yet this what the sentence means in plain English. If language functioned like a unidirectional code, it would evoke Rappoport's low-order level of meaning. Why, then, do we not attribute immortality to Mrs. A? Our case is that the networks or paraphernalia of our civilization leads us to read the verse in relation to higher orders of meaning. This is not based on interpretation of the discrete signs at all: we *feel* that God would not grant such things; our cognitive biases link “death” with “damnation. Readers who are familiar with the Babylonian exile will place the prophet's words yet in another context that derives from our understanding of the original, our acquaintance with Middle Eastern realia, and our own cultural milieu. Still nothing of this will explain, why 2600 years after being written, the verses do still appeal to people in, for example, Central Russia or Arizona.

Middle- and high-level layers of meaning are often seen as bound up with hermeneutics, therefore as part of the humanities, as distinguishing humans from the rest of the biosphere. Biology, it is assumed, can be studied independently of history,

cultural contexts, language-like patterns, experience and so on. Yet, in the “*The chaos of everyday life*”, Rappaport suggests (2010, xvi), “*stability is bound up with the social facts of a shared collective existence*”. Not only do we depend on history, the reiteration of forms and experience but we also draw on, clichés, metaphors, ritualized activities and even strange assumptions. In Umberto Eco’s terms:

“...it is impossible to communicate without putting something into the background frame of mutual agreement and assuming that the other is able to access this presupposed knowledge. Otherwise, each speech event would require a complete restatement, with the result that there would be no time to say, or listen to, anything. This is clearly too great an extension for a presupposition as a sentence phenomenon, since the utterance of even the simplest sentence can presuppose all the world in this sense“ (Eco 1994, 228-9, our emphasis).

In turning to how language and cognition play out ‘in the wild’, such ways of meaning appear less exotic. Human actions are situated in a normative world where bodies use learning (and other interactional products) to co-ordinate internal and external structure. People, moreover, do this collectively as ‘co-acting assemblages’ (Cowley & Vallée-Tourangeau 2010: 469). Persons-embedded-in-action and/or-interaction resemble to a “field force”, built and rebuilt continuously by inhabitants of a “field” that was inherited from those who long since passed away. Heidegger (1982, 1995) calls this Being-with-others (*Mitsein*) in a Country (*Gegend*). This country is molded by, on the one side, tectonic forces and, on the other, efforts by those who share their being in the here and now. In this way, a countryside or culture is able to evolve across innumerable generations. If this is indeed the basis of cognition, it cannot be traced to simple encodings. This is because, in coming up with thoughts, people draw on distant factors – like the words of an ancient prophet in our example above. Can we, however, generalize from human experience to biosphere, without committing the flaw of anthropomorphization?

In what follows, we show that biological codes such as the DNA script, intracellular and intercellular signal systems and ecological cohabitations; also have a strange duality. While participating in unidirectional processes, they also inhabit a ‘country’ of messages and lineages. The “scientific” treatment of “biological syllogisms” applies in artificial, laboratory settings. Like thinking and sense-making, living processes and their evolution depend on interactivity, a process Kirsh (2010) defines as a *back and forth process where a person alters the outside world, the*

*changed world alters the person, and the dynamic continues* (p. 441). Many challenge such a view: in line with the central dogma (see below), many focus on the lowest Rappaportian level. It is hoped that higher levels of meaning are emergent phenomena that can be explained by focusing on such a lowest level of description. It is as if, in studying life, one can ignore the role of living beings. Yet, in Western culture and, thus, the humanities, this view is common; even Rappaport, who should know better, concurs: “*Non-human systems are organic systems constituted largely by genetically encoded information. Human systems are cultural-organism systems constituted by symbolic (linguistic) as well as genetic information.*” (2010:10) In challenging this, we aim to rescue the study of life itself from the no man’s land that lies between sciences and humanities.

## **THE LOW ORDER**

In biology, by adopting the so called “Central dogma”, the focus has fallen exclusively on the low order of meaning (see any modern textbook in molecular or cell biology, e.g., Alberts et al. 2008; the reader who is acquainted with basics of molecular biology can safely skip this section). It claims that information flow in biological systems is unidirectional, from script encoded in DNA to proteins to higher levels of organization. Hence, the basic level of description of any living being is its master copy of DNA containing “data” and “programs” how to build the body. Even instructions how to construct the “hardware” (or better, wetware) of the body must be in its entirety encoded in the genetic script (its “wording” is called *genotype*). In the process of *transcription*, parts of DNA information (about 30.000 “genes”, constituting about 2-4 per cent of DNA in human cells) are transferred to much shorter strings of RNA; one class of RNAs (messenger or mRNAs) serves for *translation* of information into a string of a particular *protein* (more about proteins see below). The translation rules – the genetic code – extend the realm of chemistry: the code was established in evolution by *natural conventions* (Barbieri 2008ab). Several thousands of different kinds of proteins constitute the lowest level of cellular agency (higher levels being multiprotein complexes, membranes, organelles, and other structures) responsible for metabolism, locomotion, cell division, but above all for the extremely reliable *replication*, i.e. copying of DNA master copy, to distribute it to daughter cells, and, of course, also for the transcription and translation processes described above. The assembly of agencies and structures constitute cells, and cells build multicellular bodies; how such an

assembly looks like, i.e. what is its *phenotype*, is *primarily* the function of the genetic script implemented in DNA. To repeat again: there is *no reverse flow of information* – no feedback from the world or flesh into the script (see, e.g. the classical treatise *Chance and necessity* by J. Monod 1970). Phenotypes, and other structures of biosphere web, essentially obey, as if verbatim, the genotypic instructions.<sup>1</sup> There are no pterodactyls in contemporary biosphere, because no pterodactyl genotypes operate in contemporary cells, they were lost long ago. Flaws and paradoxes of the theory came to light relatively early (see, e.g. Hofstadter 1979), yet the debates on the topic often end with a mantra “In principle the central dogma holds”. The problem, of course, lies in the fact that all living beings have been born of living beings, they do not start from scratch like crystals, flames, neither they are products of assembly lines. Bodies and their genetic scripts are coextensive, neither is “primary” or more basic.

The contemporary neo-Darwinian paradigm, however, draws on the Central dogma. Replication of DNA is highly, but not absolutely reliable (typos, and even more serious disruptions may occur due also to external factors), hence, genes in a population may come out in slightly different “spellings” called *alleles* (likewise, “program” and “programme” represent two alleles of the same word). Alleles (and coalitions of alleles) build phenotypes slightly differing (in this or that respect) from other phenotypes, and such differences may influence the *fitness* of a particular body – in terms of the amount of its descendants. The body (phenotype) is, then, a vehicle to transmit its burden of alleles into the next generation: the fitter the vehicle, the higher the frequency of particular allele(s) in the population in next generation. The fitness is determined by *natural selection* in the external environment: Because of the Central dogma, natural selection acts on the carnal vehicles, whereas the gist of evolution is in transferring pure information as inscribed in DNA. For more succulent version of the story see e.g. Dawkins (1976, 1982).

What is important for our further exploration is the fact that the Central dogma and neo-Darwinism models presuppose the concept of a ‘basic level’ in description of the living. Living beings are viewed as passive machines that are designed to transfer their “software” into their progeny. One way of countering such views is to exploit the language metaphor of life (Markoš & Faltýnek 2011; Markoš et al. 2009; Kleisner & Markoš 2005, 2009). Rather than dwell at the lowest level of meaning, we look beyond

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<sup>1</sup> The analogy with how some Jewish or Christian denominations treat the Scripture is astonishing.

models that depend on discrete types and, in so doing, show the relevance of higher levels of meaning to the realm of living. We argue that living systems draw on ecological (or oiko-logical) aspects of meaning. It is our view that recognition of their historical basis is necessary to placing life in a coherent system of knowledge that brings out the continuities that link it with the many human worlds that unfold within a cultural meshwork. As there is no external agency steering the living processes and their evolution, life acts as its own designer (Markoš et al. 2009) – the lowest level of meaning will not satisfy the task.

### **THE MIDDLE LEVEL**

One way of countering such views is to exploit the language metaphor of life (Markoš & Faltýnek 2011; Markoš et al. 2009; Kleisner & Markoš 2005, 2009). Rather than dwell at the lowest level of meaning, we look beyond models that depend on discrete types and, in so doing, show the relevance of higher levels of meaning to the realm of living. In so doing, we face opposition from both the sciences and the humanities (see, e.g. Heidegger 1995). However, we see no need for this: accordingly the paper aims to show that, in contrast to views associated with the kind of logic associated with the central dogma, living systems draw on ecological (or *oiko-logical*) aspects of meaning. It is our view that recognition of their historical basis is necessary to placing life in a coherent system of knowledge that brings out the continuities that link it with the many human worlds that unfold within a cultural meshwork.

We pursue the “language metaphor of life” beyond human beings into communities of living entities. In arguing that it is essential, we show that history and experience matter to intracellular processes, cells living in a body, members of a species and even ecosystems...). Biology depends on cultures or, in Kauffman’s (2000) terms *biospheres* made up of populations of cooperating *autonomous agents*. Many of the properties of languaging (Markoš 2002, Markoš et al. 2009, Markoš & Švorcová 2009, Markoš & Faltýnek 2011) appear in communities or guilds of living entities: the processes that sustain life are *radically distributed in that they depend on ‘memory’ that is inseparable from their surroundings*. Living beings are not produced or created but, like crystals or tornadoes, merge into being: they are *born* into already present “biospheric fields”. Other living things give birth to beings that develop in a domain of rules, values, heuristics and ways of doing things. Hence, besides the genetic script and the body that harbors its patterns, we emphasize the third factor – the community. We

now focus our approach around four examples: (1) the intracellular “ecology” of the protein world; (2) epigenetics; (3) symbiosis and symbiogenesis; and (4) the new science of evolution-development, affectionately known as evo-devo.

### **1. Proteins as agents at the molecular level**

In our view it is difficult to understand life without considering properties of the protein community. For a readerships who are not biologists, therefore, we pinpoint some of its key features below (see Box 1).

#### **Box: On proteins**

Proteins are huge molecules. By comparison, if we treat the “size” of a hydrogen atom as 1 and that of water as 18, a protein averages at about 40.000 (10-100.000). Each of their “building blocks”, an amino acid, has a size of around 100. Proteins are always synthesized as linear chains consisting of aperiodic sequences that are constituted by 20 different species of amino acids. In turn, their sequencing is determined by a sequence of DNA building blocks. Parts of the DNA (genes) are copied (transcription) into messenger RNA; is the products are translated in accordance with a sequence of instructions (the genetic code) into the amino acid chain that constitutes the protein. Thus some proteins copy and transfer DNA to their progeny and others copy its content into RNAs. These are relatively easy processes. However, the protein chain or machinery that translates mRNA into complex protein and RNA structures can only arise from translation (not copying). (On copying & coding, see Barbieri 2003.)

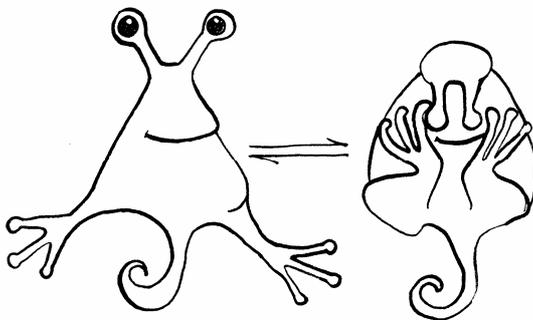
The resulting chain shows sensitivity to a particular train of amino acids by wrapping onto itself and creating a 3D molecular protein molecule. Given the view that all necessary information is contained in the DNA (e.g. Monod 1972, Anfinsen, 1973) many thought that a one-dimensional codon sequence unequivocally determined both the chain and the shape of the molecule. On this view, since proteins are the “basic building blocks” of the cell, the shape of cells and multicellular beings is to be traced to the code of a genetic script. In fact, the shape of the protein molecule may be largely determined by its actual environment (see the main text).

Most proteins function to bind a tiny shape (one or more ligands) to different parts of the protein molecule. As a ligand, it may serve a molecule (sugar, hormone), specific parts of other proteins, nucleic acids, or of cell structures). On binding the ligand, the molecule *does* something: it may change the chemical nature of the ligand

(enzyme), bind in an antigen (antibiotic), transfer molecules across a membrane (channels, pumps); pass or amplify signals (receptor); etc. etc. These are not coding processes (based on input-output relations) but rather *performances* that change the protein molecule's shape by binding its ligand(s). The set of possible protein shapes is enormous – and never singular. Finally, every protein depends on being able to change its shape.

A mammalian cell contains about 30.000 genes of which, in a given cell, 10.000 are typically 'read'. However, the set of actual protein shapes in the cell is much larger: as explained below, this depends on the protein ecosystem into which new proteins are born. (for more detail and self-explanatory cartoons, see Alberts et al., 2008).

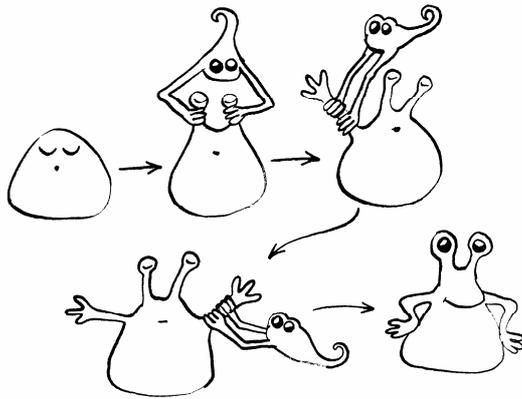
A protein molecule is a string of amino acids that can attain an astronomic number of different shapes. In a given case, however, their embedding in a cellular environment will ensure that only a limited (“meaningful”) number are attained, (Fig. 1). Misfoldings are quickly repaired, or removed – by the cell's protein assembly apparatus.



**Fig. 1** Two possible conformations of a protein molecule.

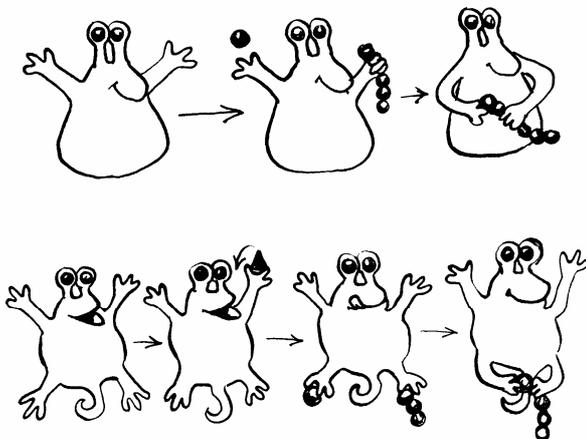
In order to attain proper shape a great many nascent proteins depend on “chaperons” (Rutherford & Lindquist 1998; Bergman & Siegal 2003; Taipale et al. 2010; Fig 2). The set of chaperon proteins thus become major regulatory “hubs” that, in different regimes, regulate the cell's crowded protein network by means of fine-tuning (Taipale et al. 2010). In a broader context, not only chaperons but all pre-existing structures and protein assemblages can play formative roles in the environment where a protein molecule is born (e.g., Good et al. 2011). Hence the decision of the context in which the protein is to work is by no means local; it results from the ecosystem of cell

“inhabitants”. Thus, without any need for central control, proteins function as a meshwork of complex system.



3. **Fig. 2** The action of a chaperone on the nascent protein (in many cases, contact with a chaperone is required across the whole lifetime of a given protein).

Shape transitions are necessary to protein function. To perform a specific action each must take on a conformation that gives exquisite sensitivity in distinguishing and binding its ligand. On binding, the conformation changes and, by so doing, sets off special operations on or with the ligand (see Box 1). It may, for example, be chemically transformed or transported; a change in conformation may switch a signaling pathway or, perhaps, set off protein-protein binding. The changing conformation can prompt a functional complex to perform a task. The effects of such a change are sketched in Figure 3 below. During such functions, the protein’s performance (speed, efficiency, etc.) may be fine-tuned by the protein ecosystem. While about one tenth of proteins in the cell are bound to “housekeeping” functions (e.g. respiration, food intake, or special syntheses), the others act as a regulatory, information processing network that make subtle responses to whatever happens to the cell.



2. **Fig. 3** In the top row a given protein functions by adding a molecular element to a growing chain. The protein has binding sites to both ligands (the monomer and the chain). Thus, when ligands bind onto specific sites, they induce unifying changes in conformation. In the lower row a protein molecule couples with an energy source that enables the inactive conformation to attain the receptive shape required for work (if ligands are available and bound to

appropriate sites). In such cases, sites depend on –not codes –but how functions are distributed.

The function of protein is *distributed* in that it does not rely on predetermined features alone; it also draws on historical (evolution, ontogeny) and *ad hoc* contingencies (e.g. temperature, mating season, etc.), or, in short, on the *experience* of the cell and organism. Such a statement somewhat complicates the straightforward model of evolution described above.

Fig. 4-1

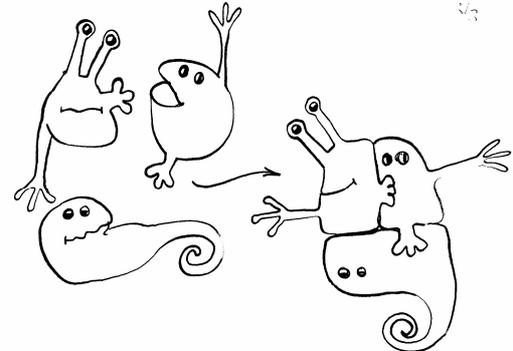
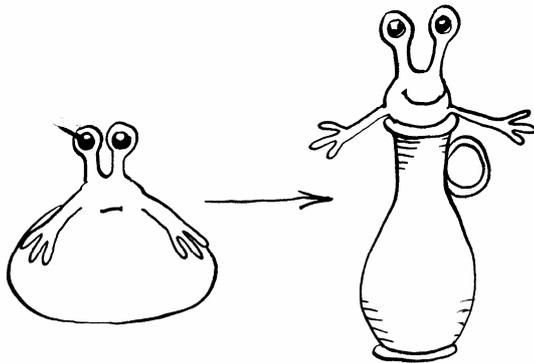
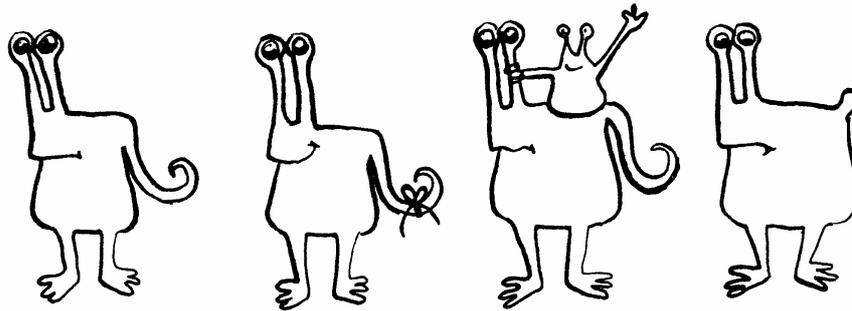


Fig. 4-2

Fig. 4-3

Fig. from 4-1 to 4-3 The performing conformation can be also attained by embedding protein into a structural and/or functional context of a specific environment, or can be delicately (or less delicately) and reversibly modified by specific action from its environment.

Undoubtedly, evolution draws on random change mutation in the genetic script. As described in every textbook, this leads to alterations in the sequence of protein-coding or regulatory areas of DNA. As a result of change in the region of coding, a protein may alter its performance; mutations in the regulatory sequences may also place proteins in new contexts by, for example, altering the timing of ontogenetic gene expression. Changes in the setup of protein network (ecosystem) can have far-reaching

consequences for a cell, an individual's likeness and, indeed, for the ecosystem in which it lives. There is, moreover, a second kind of evolutionary change. A whole network of proteins may be induced to change its performance by external agents such as temperature, nutrition, toxins, epidemic, etc. that change the appearance and performance of its bearer. If the whole population is the target of such a change, an unaltered genetic script may nonetheless present a new "attitude towards the world" (see, Matsuda 1987, Hall et al. 2004). Given these two modes of evolution, the network has distributed functions. This is important because, contra the central dogma of biology, this *cannot* be traced to inscriptions in genetic code, Indeed, it depends on non-local factors that are co-dependent with biochemistry, molecular configurations, function and evolutionary effects. If epigenetic causation (often reversible from the beginning) takes many generations it may even come to be fixed by genetic algorithms (e. g. Waddington 1975, Rutherford & Lindquist 1998). Next, therefore, we turn to how cells develop.

## **2. Epigenetics in the lives of a cell**

Not only the protein ecosystem that shapes the "construction of meaning" through cellular epigenesis. Accordingly, we shift our focus from distributed control to consider how a cellular system attunes its current needs by using the 'wording' of genetic texts. We find a sophisticated process that is reminiscent of the subtle use alternations that "accent" an alphabet's basic letters (e.g. 'a') by marking them as (for example) á, ä, à, â, ã, å, Æ, Æ, etc. While from the point of view of the original Latin such modifications look bizarre, they perform many functions. Even if the differences do not matter at one level (e.g. in e-mails), there are substantial differences at others (e.g. in German, Bar/Bär are different words as are tacher/tâcher in French). In the cell, marks are (reversibly) placed onto DNA or proteins and thus altering the "text" that influences how proteins perform.

Epigenetic use of a diacritic like process is far from simple. They ensure, for example, that cells which inherit the same basic 'text' from the zygote can develop into, say, a liver or a brain. As different sets of proteins contribute to the relevant epigenetic processes, organ formation depends on the highlighting and suppression of different parts of genome and/or proteome. There are two key processes in the cell nucleus that

help cells (and cell lineages) to remember their spatial and temporal coordinates.<sup>2</sup> The first of these adds chemical marks (i.e., “diacritics”) to DNA molecules. These alter how the script is treated, read and/or understood. The second process uses the organization of the cell’s nucleus or scaffolding structures known as nucleosomes. Both processes are tightly interwoven, and deeply influence the cell’s orientation and workings.

### **DNA markings and genomic imprinting**

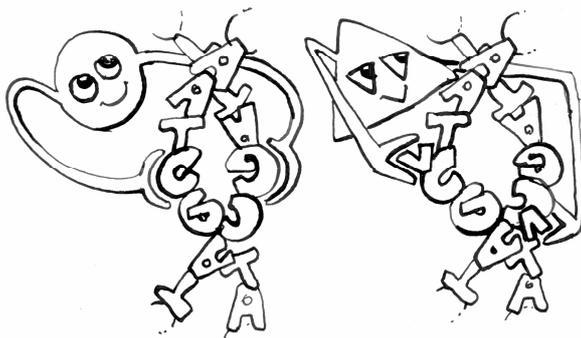
One-dimensional molecules of DNA are often compared to a letter string written in 4 “characters” A, C, G, and T (chemically - nucleotides). On this linear model, the chemical modification of characters resembles human use of diacritics. The commonest of these modifications (methylation) applies to the C character or cytosine in the DNA string. For some mechanisms, nothing has changed (e.g. DNA replication uses the 4 bases); however, for others, the string features a fifth character in the string. Such modifications are reversible in the sense that another battery of enzymes can remove the “diacritics”. The method allows methylation to influence the accessibility – and transmissibility – of specific DNA strings. In a reading metaphor, it enhances or hides the text from the performing proteins (Fig. 5). The reversible process of DNA modification can profoundly influence a cell’s internal milieu. This is because it is only by binding proteins to regions of a DNA string that the encoded ‘message’ can be transmitted to the body-world. Thus, if the functionality of a region is enhanced or hidden, major changes can occur. Such processes therefore function, not only at the level of the cell, but in the organism as a whole. While some epigenetic changes are programmed (as in creating liver cells), others draw on an individual’s lived experience. Thus, in identical twins, the pattern of DNA expression is similar early in development. However, across the lifetime, a cascading set of epigenetic effects will draw on processes such as DNA methylation.

In other cases, genetic material remembers its maternal or paternal origin. This leads to manifestations in the overall likeness of an individual and is especially well known in so-called genomic imprinting. In mammals, all females are genetic “chimeras” because, in their cells, only one (of two) X chromosomes functions. In a

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<sup>2</sup> Such processes are especially important in the context of multicellular organisms and their ontogeny. It is important that some of them may outlive even to the next generation, thus transferring the experience of parents.

given cell lineage whether this is maternal or paternal is determined at random. If the active chromosome bears an debilitating mutation, the effect cannot be mended in spite of the second (but inactivated) X chromosome has the right gene. Serious mental diseases may develop when maternal/paternal imprinting gets erased or impaired (e.g. Prader-Willi or Angelmann syndromes). In some groups (plants, and perhaps also animals), imprinting enables parents to transmit information to their offspring about the environment they are likely to encounter (e.g., Gilbert and Epel 2009; Allis et al. 2007).



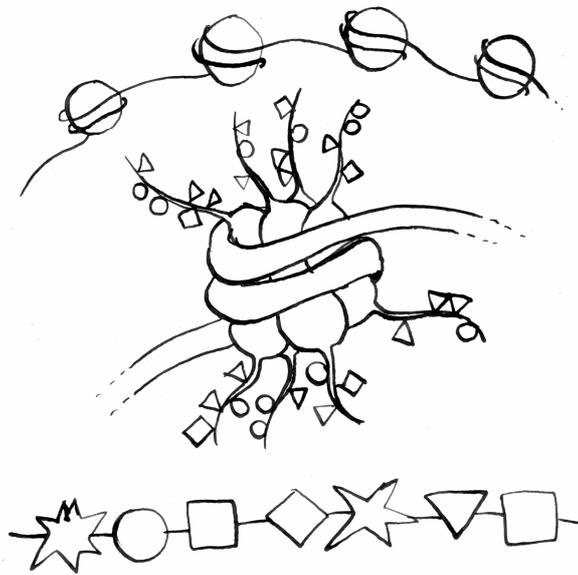
**Fig. 5** Epigenetic marking: changing some characters affects the overall shape of a section on DNA. If the section AGCTAA represents a *ligand* for a specific regulatory protein (a), a modification (to AGCTAA) turns it into *another ligand*; it becomes the target of a protein (b). The complex DNA-protein participates in the cell's protein network by influencing its

ability to read other parts of the DNA script: the “reading machinery” behaves differently in cases a and b.

### *Nucleosomes*

DNA strings (billions of “letters” – in mammals) can be compared to a linear text or a multilevel structure containing hundreds of different proteins. DNA is organized into structures of higher order called *chromatin*: its lowest level of structuration is a “rosary” of *nucleosomes* containing about 147 DNA “characters” wrapped around 8 proteins (doublets of 4 different *histones*, Fig. 6). While stabilizing the strand of DNA, these also enable or deny proteins access to particular sections of genetic material. This depends on functions that are independent of central control. Rather the actions of specific proteins (e.g. methylation, phosphorylation, acetylation), give rise to modifications (and erasures) of histone proteins whose end tails stick out from the nucleosome (e.g. Allis et al. 2007). The modified surface of the nucleosome can thus serve as binding site for proteins that constitute a chromatin ecosystem. Furthermore, such a modification affects all other proteins. It results in a network of interactions that maintains cell differentiation (e.g. as liver cells or neurons) while

favouring quick and reversible response to external or internal cues. For example, some genetic material becomes walled up in a given cell lineage or during A developmental stage. By modifying both the DNA and histones, the system acts as an attractor that silences part of the DNA string – possibly thousands of nucleosomes in a row. In other cases, protein assemblies organize regions to produce a given cell lineage. In most cases, even long-lasting modification may (or should) be reversible in circumstances such as regeneration or, gametogenesis. This view of the cellular ecosystem as akin to reading is shown in the nucleosome pictured in Figure 6 below.



**Fig. 6** The nucleosome.

**a.** DNA is wrapped around 4 kinds of histone proteins. **b.** Histones are prone to binding by regulatory proteins; epigenetic marking (symbols on protruding “tails”) can change the set of proteins that bind to a particular part of a histone. Such a change may switch the whole protein network into a different setting. **c.** Each nucleosome (plus proteins attached to it) thus represents a unique, fine-tuned complex that decides how and when the genetic script at that position is to be read. (After Allis et al. 2009)

Elsewhere Markoš and Švorcová (2009) draw an analogy to a natural language that emerges in a natural community of living protein players (“speakers”). This, we argue, cannot be reduced to a fixed code that depends on executing a program. The parallel is striking: while a histone code can be described in terms of (grammatical) rules, it draws on a dynamical, experience dependent ecosystem or, simply, the total protein milieu. It is argued that any formal language defined as a set of character strings and determinate operations (Searls 2002) is merely derivative of natural language, i.e. it was created by individuals (proteins, cells or humans) who live in the natural world. Developing a consensus on how to read these codes is historical and based on the experience of a community of natural speakers: as Nigel Love (2004) suggests, it

consists in second-order constructs. Although rules can be described by formal languages, these do not *constitute* natural languages. Just as there are no transcendental laws or rules of human language, biological codes are unlikely to depend on by a deeper formal language. Rather, just as in human languaging, biological meaning is extracted by natural ‘speakers’ who dwell in a historical world of bodily experience.

If the correlation between the DNA script and the shape of the protein is contextual, and experience dependent, then emancipation from the genetic script is likely to go further at “higher”, supramolecular levels. Accordingly, we now trace parallels between the interactions of biological systems and the metabolic and symbolic aspects of language and, beyond that, what are usually regarded as different language-systems.

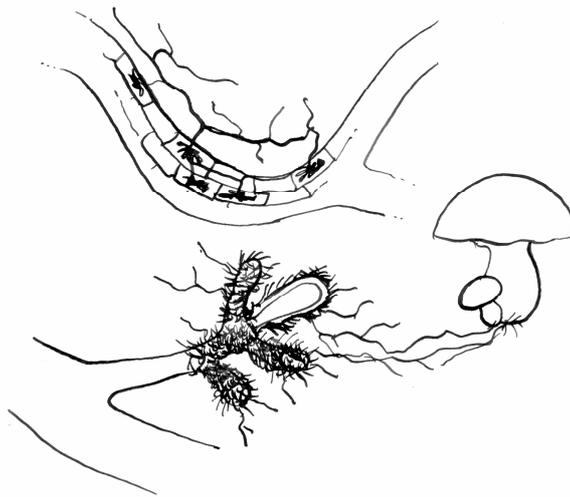
### **3. Symbiotic interactions**

In biology, there is often intimate coexistence between two or more lineages of organisms (Sapp 1994, 2003). This *symbiosis* includes endosymbionts that have been long established within the cells (e.g. the mitochondria or chloroplasts that are viewed as integral to eukaryotic cells), ones living inside other bodies (e.g. bacterial communities in bowels) and the more floating interactions that constitute ecosystems. Symbioses are ubiquitous: they serve the biosphere in that, for example, symbiotic bacteria perform activities that their hosts require. They manage photosynthesis, sulphur metabolism, nitrogen fixation, cellulose digestion, and the production of nutrients (e.g. Hoffmeister & Martin 2003). Symbiosis is thus mainly understood as persistent mutualism or, as “associations between different species from which all participating organisms benefit.” Symbiotic interactions are not marginal, academic topic but, rather, resemble the distributed cognitive systems that allow humans to use artifacts and institutions to extend their cognitive powers. In the terms proposed by Douglas (2010):

“Plants and animals live in a microbial world. *Their surfaces are colonized by microorganisms (bacteria and protists) from which they generally derive no substantial harm. Some plants and animals, however, live in specific and coevolved relationships with particular microorganisms, and these associations have profound impacts on the ecology and evolution of the taxa involved and, in some instances, also on entire ecosystems. In particular, animal or plants symbioses with microorganisms dominate most terrestrial landscapes, certain coastal environments and the immediate environs of*

deep-sea hydrothermal vents. [...] *Symbioses are important not just because they are widespread and abundant, but also because the acquisition of symbiosis can dramatically alter the evolutionary history of some lineages and change the structure of ecological communities.*” (Douglas 2010, 19–23, our emphasis).

Although symbiosis can be compared with many aspects of human cognition, we focus on its ecological and evolutionary consequences. As an ecological force, symbiosis ensures that species are bound to cohabit. For example, terrestrial plants typically have an intimate symbiotic connection between their roots and fungi. The most ancient and widespread partnership is *arbuscular mycorrhiza* that dates back ca 460 million years and applies to 250 000 living plant species (Redecker et al. 2000 Fig. 7). Fungi benefit plants by mobilizing nutrients from organic substrates while also delivering water. This is because fungal hyphae are thinner and thus permeate soil better than root hairs. In return, plants subsidize fungi by organic matter.



**Fig. 7** Mycorrhizal symbiosis – tight cohabitation of fungal mycelium with roots of most plants. Two of many possible configurations are shown: **a.** Endomycorrhiza – fine mycelial protuberances invade the plant-cell cytoplasm and create an elaborated network. **b.** Ectomycorrhiza – while also very intimate, hyphae do not invade the interior of cells. The fungus interconnects trees within its reach, i.e. the whole forest may be networked in this way, the network involving many

species of plants, fungi, and other organisms like bacteria.

Symbiosis influences biological evolution profoundly. For example, new lineages of organisms can be engendered by the fusion of previously symbiotically living systems. Symbiogenesis is thought to have given rise to eukaryotic cells that draw on a conglomerate of different bacterial partners (see theory of serial endosymbiosis by Margulis 1993; Margulis & Sagan 2002). Indeed, even those who posit that nature is controlled by something like fixed codes admit that (at least) two kinds of cell organelles – mitochondria and plastids – originated from free-living microbial ancestors. (Douglas 2010,; Margulis & Fester 1991; Overmann 2006; Paracer & Ahmadjian 2000; Sapp 1994, 2003). What is remarkable on symbioses is not the fact

that different beings, like Russian dolls, share a composite body. Rather, what matters is that, unlike Russian dolls who are indifferent to each other, symbiosis involves mutual understanding between partners who spent even billions of years as separate lineages.

The moral of the story is becoming clear. In biology, wherever we look, we find interactive communities that “somehow” modify what first seems simple. Once we look “below the skin” of a cell, we find an ecosystem of cellular proteins that bend, prune, decorate and tattoo (but also clear away) other proteins: their existence is dependent on a genetic script but their fate depends on the field beyond. The same pattern appears at other levels: although all genes are present in every cell, their expression is distributed through the workings of structures and processes that will put down epigenetic markings. The unpredictability of the outcomes, i.e. the history of evolution comes to the fore when unrelated lineages enter intimate cohabitations. The same picture applies to ontogenies, i.e. patterning multicellular bodies. Development of a multicellular individual is a fascinating process especially when we trace its historical dimension across lineages and begin to consider what the biosphere has to say about such essentially intimate process.

#### **4. Ontogeny**

Many who discuss evolution echo the central dogma in claiming that *the potential of a species to evolve new traits is constrained by its genome or the set of genes it has available. For example, Poe writes: “It might be evolutionary advantageous for your progeny to have wings, but it’s simply not possible given the genes H. sapiens has to work with”*. (Poe, 2011: 8). Whatever the truth of the claim its evolutionary basis cannot be what lies in the genome. Indeed, such a view is the biological counterpart of “written language bias” in linguistics (Linell 2005). Just as written letter strings are sometimes seen as basic, even primary, forms of language, DNA strings can be viewed that way. Function is ascribed to static, reproducible, and rational entities that can be seen and known in totality. Written language bias influenced molecular biology in the 1950s and 1960s (see Markoš & Faltýnek 2011) and, even today, some regard “linear biology” as biological common sense. Just as texts can be reduced to sequences (successions) of letters, DNA conforms to sequences of bases in nucleic acids and proteins. On this view, formal syntax lies ‘behind’ living phenomena – both language and the likenesses of living bodies. Indeed, the “central

dogma” takes the extreme view that information is never ambiguous and flows from a script to the body.

The evidence presented above shows why we reject linear models in biology. First, simple proteins do not derive unequivocal shapes from nucleotides sequences. Second, distributed knowledge contextualizes script by assembling cells whose histories contribute to different lineages and organs. Third, members of different lineages use context to construct a world where cohabitation is widespread. Perhaps, then, we should return to our claim that Ezequiel’s meaning cannot be extracted *solely* from a sequence of letters. In denying peace to the wicked (if that was his aim), the likeness (of a message, or of a body) is not a function of a sequence, program, or algorithm. Rather, it draws on a context that belongs to a given lineage, group, organism... – and often does so creatively. Members of different species ( $\equiv$  cultures) treat identical (or very similar) scripts ways that are quite specific: understanding a text is not a passive crystallization or decoding.

Vertebrates, arthropods, earthworms and even echinoderms have lost the two-sided symmetry of their ancestors. In the evolution of these *Bilateria*, all species have the same basic body plan (antero-posterior and dorso-ventral axes, left-right symmetry, etc.; see Švorcová 2012): differences arise from localized expression of ancient, conservative genes. The body plan is set by embryogenesis long before the appearance of body parts. Since bilaterian phyla have evolved independently for more than 500 million years, it is striking that the basis script remains unchanged. While the genes in each lineage underwent changes in “spelling” as some were duplicated, others deleted or otherwise modified, even unrelated lineages have much in common. For example, deletion of a single gene in the genome of fruit fly can be deleterious or lethal; however, the consequence can be experimentally reversed – by transferring a gene from the genome of a mouse (Gehring 1999). Although proteins coded by such homologous genes differ in many parameters, the message is ‘understood’: the fly embryo steers the homologue towards a normal developmental pathway. And, of course, “normal” is interpreted as flies (not mice). Thus, if one deletes the gene that initializes eye development in the fly embryo, blind flies will be born. However, a mouse gene restores the development of eyes-those of an insect not a mammal. Thus, a particular protein serves as a tool for establishing a developmental pathway: it does not determine the end product (the eye). Plainly the digital representation of genes (an inscriptional form that may be shared by fruit flies, mice and humans) does not determine how gene

works. Rather, this is understood in the “cultural” context of the lineage (species, culture: at the lowest level of description, it depends on an embryo that grows in an ecosystem of interacting proteins (cells and tissues). This complexity allows the same genes to be used in many ways while nonetheless preserving (and transferring) the essentials of the proteins involved. The resulting patterns, ontogenetic outcomes, depend on bodily or lineage memory (see below), not on a linear string that enshrines a memory in a store or depot.

Just as in the Biblical story, the genes are written in an ancient script that is open to non- arbitrary interpretations. Understanding depends on both the individual *and* how the outcome is settled in a given population. The results depend on both situated and non-local factors. To illustrate this matter, one might consider the notorious comparisons between chimp and human genes. While now widely known that their genomes are 98% “similar”, there is debate what such a number means (see, e.g., Marks 2002). Our comparison with reading mechanisms of book of life can be further elucidated by examples of inscriptions: thus an ancient philosopher’s name is rendered as “Aristotelés” in Czech and “Aristotle” in English.<sup>3</sup> Is his message different for both communities? If it is not, as some will argue, this depends on the history of individuals and populations –not spelling.

Examples such as these may appear trivial. However, we should not assume that, in both life and culture, small changes can have large effects. Changing even a fraction of a percent of genetic material can make a difference – especially if the a mutation affects a genomic control centre (Davidson 2006; Carroll 2005). In presenting our case, we show only that it is naïve to posit the existence of virtual body plans that are attained (and perhaps even foreseen) by a single “keystroke”, or a mutation that creates a “hopeful monster”.<sup>4</sup>

## **THE HIGH LEVEL OF MEANING**

We approach the most speculative part of our paper. Rappaport argues (p. 15):

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<sup>3</sup> \* Versions of written US and UK written English may differ in the spelling in 2 percent of strings. Does this explain the differences between two nations? Remarkably, this line of thinking is pursued by those who seek a genetic Word that is “responsible” for differences in flesh.

<sup>4</sup> In European history, a single “mutation” – insertion of word *filioque* into the Christian creed (and Son) in the 6<sup>th</sup> century – is often seen as the main “cause” of schism between Orthodox and Western Christianity.

„The survival of any population, animal or human, depends upon social interactions characterized by some minimum degree of orderliness, but orderliness in social systems depends, in turn, upon communication which must meet some minimum standard of reliability if the recipients of the message are to be willing to accept the information they receive as sufficiently reliable to depend upon.“

We came to similar conclusions earlier when we compared the coherence of members of a biological species to a culture (Markoš 2002). Yet, Rappaport goes even further: his “standard of reliability” lies in rituals shared (albeit not always necessarily respected) by all living members of the community: it is the tie that defines it. Ritual, for him, is “The performance of more or less invariant sequences of formal acts and utterances not entirely encoded by the performers” (p. 24). In other words, it sculpts the “fashion” according to which “we” behave, even if there is no logical necessity to perform exactly in such a way, but it “constructs” the present, as well as the eternity of a given community. “Societies must establish at least some conventions in a manner which protects them from the erosion with which ordinary usage – daily practice – continuously threatens them.” (p. 323) “Universal sacred postulates” in rituals serve as such eternal constant that are not to be questioned, not even interpreted in various ways. Yet, they have their evolution across generations. May it be that biological species also constitute such a community kept together by the ritual inherited from the predecessors? Even if rituals seem eternal, they change in subsequent generations as the *umwelt* or “worldview” of a given lineage shifts in this or that direction. With a very similar “sacred texts”, i.e. genome, we have – after 8 millions years of separation – two cultures of humans and chimps. If the parallel between languaging and life should be fruitful, we should be prepared to think in similar lines. How we look like today is the matter of our genes *and* of the ways how we make use of them in the ever-changing world.

## **Conclusion**

Life cannot be subsumed under physico-chemical principles (even expressible through mathematical notation) because, as Simon (1971) argues, biology and physical science have different objects. Simply said, physical systems lack *meaning*. The fact was first recognized in systems theory and cybernetics (e.g., Bertalanffy 1968); however, no scientific concept of meaning has been developed or needed by the exact and empirical sciences. It is possible, of course, that this is logically impossible or that

it just cannot be achieved in quantifiable ways. However, organisms are both ontological and historical: they are products of phylogenetic and evolutionary history. Not only is their multi-scalar nature likely to contribute to the complexity of meaning but this is likely to depend on how relationships use hereditary material to develop over time. As we have seen, this depends on the spatial conformations of DNA molecules and interrelations between them (e.g. DNA-RNA, RNA-protein, protein-protein, etc.) that gives the living world has a character of a network or a web of interactions. To grasp the ‘core’ properties of biological entities, we always need to know about their exact setting. Conversely, it is *far from enough to rely on knowledge of the structure* of their elements. In developing the language metaphor of life (Markoš & Faltýnek 2011; Markoš et al. 2009; Kleisner & Markoš 2005, 2009), we challenge the view that only the lowest level of meaning is accessible to science. Rather, we examine higher levels, where “meaning” gradually becomes applicable to the realm of living. It is our view that this is the most appropriate basis for explaining life and placing it in a coherent system of knowledge that also gives do weight to the complexity of human worlds that unfold within a cultural meshwork.

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