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Dream Codes III

Meaning's Vessel
Metaphor, the Matter of Mind

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> *... dreams are nothing more than a particular form of thinking, made possible by the condition of the state of sleep. It is the dream-work which creates that form, and it alone is the essence of dreaming—the explanation of its peculiar nature.*
> *S. Freud 1900, 506f.*

Alone in foreseeing the potential insights implied by his decoding of the language of the unconscious, Freud (1900) believed his dream book provided propositions from which "a number of inferences can be drawn that are bound to transform our psychological theories" (xxiv), holding enormous promise for future research. Yet already in the preface to the second edition (1911) he laments the general lack of awareness of the importance of these insights many of which have been confirmed by current cognitive studies.

Much has since been written on dreams in clinical psychoanalysis but almost no scientific advances beyond Freud's have been proposed regarding how the theory illumines the source-point, evolution, and accretion of representational and semiotic forms expressing meanings that are unique to the human 'mind.' I too believe that dreams hold a key to unveiling the prehistory and evolutionary ascent of human mentation and, through language, to conscious awareness. The development of these ideas, however, does not come without some revision and expansion of the model of mind in which Freud was operating in 1900 and a brief discussion of the epistemological framework.

The dream's compositional structure and primary process mechanisms reveal the multisensory motor and emotive source-points from which both presentational and denotational semiotic systems originate. Though disguised by pictographic form, these signifying mechanisms are the precursors of linguistic tropes and more abstract semiotic systems forming the embodied tissue out of which *meanings* in human cognition are generated, represented, and expressed. The dream's linguistic interpretation, negotiated contextually within a semantic of unconscious processes, further unveils the translation from primary to secondary process thought, as unconscious meanings are made conscious.

The central thesis in this presentation rests on revisiting the cognitive implications of Freud's theoretical analysis and understanding of dreams: what Freud called the "Dream-work," exhibits in *statu nascendi* proto-semiotic processes within an overall *Metaphorical* structure, expressing unencumbered personal wishes, fears, and current concerns. Why, then, did Freud not call this structure by name? I will propose an explanation as to why he didn't while examining the implications for human cognition of the dream's embodied metaphorical structure in light of contemporary understanding.

The Theoretical Challenges raised by Code Biology

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Code biology represents an important turn in the fundamental research in Theoretical biology. Especially the notion of artifact-making is a breakthrough. Nevertheless, the further reception by a wider scientific audience and the development of this framework need to deal with some important issues, about which extreme care, even from a terminological point of view, is mandatory. I list here some of the problems that need such a scrutiny: (1) The notion of (organic) information and its nature of observable (in fact, two observables, copying and coding), (2) The issue of the specificity of the sequence and its meaning, if any, (3) whether prebiotic chemistry lacks an informational dimension, (4) The possible connection between the notions of templates and types. I hope that such an examination can help to improve the strength of Code biology.

Origins of the First Cells

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The phylogenetic trees reconstructed from molecular data have revealed that all living creatures belong to three primary kingdoms (Archaea, Bacteria, Eukaya) and it is generally assumed that the first modern cells that appeared on the primitive Earth were the first representatives of these lineages. All known cells, on the other hand, contain a virtually universal genetic code, and this implies that that code evolved in a population of primitive systems that preceded the first modern cells and is collectively known as the *common ancestor* of all life. This gives us the problem of understanding how the descendants of the last common ancestor gave origin to the first modern cells. Here it is argued that the appearance of the genetic code allowed the ancestral systems to translate genes into specific proteins but their behavior was still ambiguous because they were unable to produce specific responses to the signals from the environment. To that purpose they needed to evolve *signal processing codes* and here it is proposed that it was precisely the origin of these codes that transformed them into the first modern cells.

How the Glycomic Code affects the Human Umwelt

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Plant metabolism is the machine that produces all the compounds that maintain food chains in nature, environmental equilibrium, agriculture and materials production. It becomes viable due to the protection of every plant cell by a cell wall. This is so because this extracellular matrix forms composites that offer, on one hand, the control of the mechanical properties of plant tissues, generating properties like the ones apparent in wood and food fibers and on the other hand protecting plant cells from the attack of predators. Therefore, plants and all ecologically related networks would not exist on Earth if plant cell walls did not exist. Recently it has been pointed out that the complex structure of interwoven polymers of the plant cell walls holds a Glycomic Code (Buckeridge and De Souza, 2014, Tavares and Buckeridge, 2015), which is encrypted by plant cells in a manner analogous to the DNA and histones in chromosomes. In this presentation we discuss how the Glycomic Code affects other entities' umwelts, specially the human. We propose that there should be a connection between the biological codes in the sense of Code Biology proposed by Barbieri with the philosophical approaches of semiotics (the Peircean view), in which habit formation is the result of a continuous process of triadic relations involving signs, objects and interpretants, where the patterns of the environment is the object to be represented, the code is the general sign that represents it and the several hierarchical relations among plants and other living beings are the interpretants. In this regard, the Glycomic Code (ultimately as a result of several other codes such as the Genetic code, the Splicing Code etc) affords plant diversity to emerge and indirectly impacts on the umwelts of all animals and microorganisms in nature, since it renders possible the existence of ecological networks. Moreover, being responsible for the existence of forests, food and medicines, it deeply affects (perhaps in part it even determines) human umwelt, bridging with its messages the realms of nature and culture.

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Genetic code engineering: A route towards the synthetic life with the genetic firewall?

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Genetic encoding in living systems is based on highly standardized chemistry composed of the same number of “letters” or nucleotides as informational polymers (DNA, RNA) and the 20 alfa-amino acids as basic building blocks for proteins. The universality of the genetic code enables the horizontal transfer of genes across biological taxa which afford a high degree of standardization and interconnectivity. Since the basic chemical constitution of all living organisms in the context of carbon-based chemistry consists from a limited number of small molecules and polymers - all deep chemistry changes within living systems tend to be generally lethal.[1]

Until the 21st century, biology was mainly an analytical science that has now reached a point where it merges into a synthesis science (synthetic biology). From this perspective, I will argue that the primary objective of such bioengineering is to try to change the chemical composition of living cells i.e. to create an artificial biological diversity of life. To perform such a far-reaching experiments, we need a deeper understanding how incorporation of different noncanonical synthetic amino acids affects e.g. translation machinery, protein folding and cell survival in general. I will exemplify this with chemical evolution of bacteria recently done in my group that lead to changes in the amino acid set of the genetic code of *Escherichia coli* resulting in new-to-nature amino acid composition.[2] In the other words, we provided an approach for the evolution of synthetic cells with alternative biochemical building blocks.[3] Therefore, I anticipate future experiments that combine chemistry, physics and biology in the context of controlled evolution experiments. Doubtless, this will enable the partial or full redirection of informational flow in biology to achieve "new version" of the genetic code. In this context, one of the great challenges for 21st century bioscience is the development of a strategy for expanding the standard basic chemical repertoire of living cells to achieve biocontainment by man-made or naturally evolved changes in the genetic code. Indeed, approaches to alter the meaning of the genetic information stored in DNA as informational polymer by changing the chemistry of the polymer (i.e., xeno-nucleic acids) or by changes in the genetic code have already yielded successful examples.[4] In the future, this should enable us not only to generate ‘new’ version(s) of the genetic code and related technologies but also enable us to start to navigate away from the ‘old‘ [5] biological world.

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Smell as a valuable acquisition between unmediated presence and mediated absence

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Senses are generally considered as separate entities: touch, hearing, sight, smell and taste – the classical "five senses" – as distinct modalities to cope the complexity of the phenomenal world, extracting the peculiar information that can drive life's experience. But analyzing the way these senses work, it clearly appears that they are intermingled, they collaborate, the boundaries that are supposed to separate them are apparent: senses are logically separable, but not separate. The sensorial system is a cohesive and interrelated continuum in which senses act in synergy, even trying to replace each other depending on the context and on possible impairments. Senses – of distance, proximity and contact – detect, perceive and process information of different nature in order to allow organisms to live, interact and communicate.

Among the senses, smell presents some intriguing peculiarities. Depending on species, smell organs have different location, distribution and acuity. In many species, in humans too, smell chemically work decoding microportions of matter detached from the objects, which remain suspended in air until a breeze or an intentional act take them to the olfactory mucosa, where the chemical decoding reactions happen. Olfactory information is material, it is intimately linked to the material composition of the subjects/objects, to nature, behaviour and state of the organisms; it is a trace of their materiality, revealing some of their inner peculiarities. Olfactory information is some sort of an emanation of things, of bodies, of the surrounding environment. Through smell the living intimately gets in fine touch with what is outside its body, literally breathing it, melting with its material emanation.

Odors are unavoidably tied to the emitters, to living or inanimate matter, and can reveal information about the state and condition. Smell is related to memory, intimacy, instinctuality, sexuality. In nature animals spread odors, or, conversely, try to hide them. Smell has a profound emotional relevance in humans, who have developed ways of hiding odors (deodorize) and adding invented smell information (perfumes). While odors are peculiar and personal, perfumes are additions, they can be created, (ex)changed, given; in semiology odors could be considered as indexes and perfumes as signs.

Smell information can be created or simulated by chemically assembling the molecules responsible of scents and preserving them from degradation through processes like microincapsulation, which is used in advertising to "print" smells. Odors, perfumes, fragrances, aromas and scents are also widely present in the arts, but they can only act in direct communication forms: smell – as well as taste and, in part, touch – does not fit into the mediascape, which is largely based on sight- and hearing-related information. It seems humans have accepted to communicate more rapidly, remotely, pervasively, in increasingly affordable and economic ways, but in exchange for an impoverished communication. In fact there have been recurrent attempts to add smell to media narratives, to video, films, computer-related interactions, but all of them have failed to date, although they have proven the importance of smell.

Are we entering into an anosmic future or should we re-evaluate smell information, considering its natural, communicative and aesthetic relevance with regard to the direct interaction with the unmediate material environment and to the physical presence and location of bodies? How can smell information represent a valuable acquisition towards the virtual bi-sensory environments?

Directed self-assembly: genomic assembly complexity and the dialectic of information and structure

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Biology uses dynamical mechanisms of self-organization and self-assembly, but it also choreographs and directs these processes. The difference between abiotic self assembly and a biological process is rather like the difference between setting up and running an experiment remotely on the space station compared to doing it in one's own laboratory: on the space station everything must be set up beforehand to let the experiment run 'hands off', but in the laboratory one can intervene at any point in a hands on approach. It's clear that the latter approach, of directed self-assembly, can allow far more complicated experiments and produce far more complex structures. This control over self-assembly is exercised at certain key points along a trajectory and the process may be quantified in terms of the genomic assembly complexity.

Man-made and organic coding

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The paper uses the work on languaging and the brain to pursue two major themes. First, it introduces Morse as exemplifying a man-made code and, having done so, asks how codes use writing systems and their products (with reference to versions of the Roman alphabet). Brief attention is given to how these are mastered by people with experience of literacy that is grounded in face-to-face language-activity. It is emphasised that, taken together, codes, writing systems, and human skills both stabilise and extend the 'human ecology'. Second, man-made codes are contrasted with how Marcello Barbieri describes brains/ organic coding and, by so doing, I address whether his models throw light on how brains enable vocalisation that occurs under a multi-scalar set of bodily, emotive and contextual constraints (i.e. face to face language or vocal activity in which wordings play a part). Second, the question is asked on their role in relation to how brains contribute to a person's skills in using literacy (and "uttering" visible words and sentences). This is done by focusing, on the one hand, on Anderson's (2010) and Dehane's (2009) work on neural re-use and, on the other, insights from a tradition that can be traced to Bernstein and Ukhtomsky.

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A minimal model for the evolution of codes

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One of the main open questions in code biology is how codes evolve. In earlier work I have argued that coders are the result of metasystem transitions [1,2]. These correspond to the establishment of novel self-regulatory systems or "coders". Coders are self-regulatory in the sense that they are systems regulating their further persistence as a system. Regulation requires variety, which is a measure for the amount of distinctions present in a system [3]. In other words, coders effectively realize distinctions [4].

Another way to see this is starting from the fact that codes are arbitrary equivalence relations between meanings and signs [5]. Meanings and signs, the elements of the equivalence classes induced by the coding relation, are the distinctions realized by the activity of coding.

Our understanding of the origins of codes should thus benefit from a proper understanding of the nature and origin of distinctions. In this paper, I present a minimal model for the evolution of a novel distinction. The model consists of a population of agents undergoing evolution by natural selection. Initially, the agents are "unaware" of their environment. The evolution of "awareness" requires two things. Firstly, that a novel distinction is made, and secondly that the distinction is coupled to a regulatory action, in turn leading to increased fitness.

In this way, the model illustrates how the notions of distinctions, codes, coding, coders and self-regulation are intertwined and captures a concrete (albeit still rather abstract) scenario for the evolution of codes.

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Towards Measuring Molecular Codes

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Recently, a formal method to assess the semantic capacity of a chemical reaction network to process "meaningful" information has been suggested (Görlich/Dittrich, PLoS ONE, 8(1), e54694, 2013). The basic idea is to measure how easy it is to implement with this network a molecular code, which is an arbitrary (contingent) mapping between species, that is, a mapping that cannot be inferred from knowing the species alone. A preliminary computational analysis of various chemical systems revealed a quite large spectrum of different semantic capacities. Basically no semantic capacity was found in the atmosphere chemistry of Mars and combustion chemistries, whereas bio-chemical systems posses very high semantic capacities. From this, the hypothesis has been derived that life over the course of evolution is gaining access to (chemical) systems with increasing semantic capacity. So far, in order to compute the semantic capacity, a quite complete reaction network model of the respective chemistry is required; which is in general difficult to obtain. This contribution presents an approach that should be able measure the semantic capacity of a chemical system without requiring the reconstruction of a reaction network, nor is it even required to identify the chemical species. This is achieved by using a chemical finger printing method, like mass spectroscopy, together with algebraic techniques from set and lattice theory. These techniques exploit the fact that the chemical finger printing methods posses properties that allow to formulate natural union and intersection operators. With those operators a criterion for a molecular code can be formalized and computationally implemented. The feasibility of the method is demonstrated by using computer simulation. In conclusion, the hypothesis on the increase of the semantic capacity in the course of evolution appears to be experimentally testable with a reasonable effort.

Semiopoiesis: Life as the Fundamental Semantic Network

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Any system out of equilibrium – as a marble thrown into a bowl – tends to equilibrium, i.e. to decay to a lower state of energy – in the example, the button of the bowl. However, some systems as dices, roulettes and switches present more one state of equilibrium equally stable. Mankind has been using such polystable systems to store and process information in commutable devices as abacus, relays and flip-flop circuits. Biological copolymers like DNA, RNA and proteins are also polystable structures in which any sequence of monomers is equally stable. Living beings also use the commutability of chemical polymers to store and process (genetic) information. In most physical processes and chemical reactions, each set of reactants produces only one set of products (e.g.: $NaOH + HCl \rightarrow NaCl + H_2O$). However, in living beings, the same set of reactants can generate *more than one* set of products. For instance, in a given cell, a specific codon of mRNA determines the amino acids residue sequence in a polypeptide. This relationship is determined by the presence of tRNAs, which adapts specifically to a codon sequence on mRNA to deliver a specific amino acid at the catalytic site of the ribosome. However, not all organisms present identical tRNAs. In different organisms the same codon can specify a different amino acid residue. Even in a same organism an organelle as mitochondria transcription machinery is known to use a code distinct from that used in the nucleus. In other words, in different contexts the same reactant set (monomers, mRNA, tRNA) produces a distinct product set (proteins). So, to describe the operation of the system, besides the physicochemical principles, we must include the *local rules of correspondence,* i.e. the *codes*. In the case of the transcription machinery, the correspondence is defined by the tRNA anticodon, which was defined in each organism by natural selection. In 2013, Görlich and Dittrich (G-D) developed a method to evaluate the *semantic capacity* of a chemical network. Mining chemical and metabolic network databases, they assessed the capability of each chemical system to implement a *code*. To this, a set of reactants must be able to produce more than one set of products. Evaluating several chemical networks (various combustions and Martian atmosphere chemistry) they demonstrated that aside metabolic networks, no other chemical networks exhibited significant semantic capacity. Analyzing the G-D semantic test I observed that, while for most reactants is virtually impossible to produce more than only one set of products, when I employed commutable molecules as copolymers (or even functionalized carbon chains) it became *very* easy. These pieces of evidences strongly suggest that *life is the fundamental semantic network* in the Universe. Living organizations, although obey to laws of physics, are not determined by them. The freedom to determine more than one product (e.g. specific polymer sequences) using the same reactants (e.g. the same monomers) gives to living beings (and quasispecies) the power to select products whose properties *make sense* to the organism stability (internal organization necessary for survival and reproduction). In other words, the fundamental *meaning* of molecular *information* is to perform a *function* in the system's *self-syntax* (semiopoiesis). Only secondarily, information gets relevance as a *message*, in a process of communication when the function becomes to induce some action in another being.

The Ecoacoustic Event Detection and Identification (EEDI): A New Tool to decoding Soundscapes

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We define ecoacoustic events (represented by geophonic, biophonic, and technophonic sounds and their combinations) as inclusive portions of soundscape, at which we recognize distinct roles and/or meanings. Their identification results in great assistance to decode the ecosemiotic complexity of soundscapes.

We propose an ecoacoustic event detection and identification (EEDI) model articulated in the following three successive steps:

1) Processing acoustics files by adopting the acoustic complexity index (ACIf and ACIt) methodology.

2) Combining ACIf with its temporal evenness ($\mathrm{ACIf_e}$) in an Euclidean space, which we call ecoacoustics event space (EES), after the assumption that the value of ACIf found in a temporal interval (e.g., one minute) may have a different temporal distribution inside the sampled time. For instance, heavy rains are characterized by high values of ACIf and ACIfe, while background isolated calls of a bird are characterized by low values of ACIf and ACIfe. The application of empirical thresholds to both the metrics can restrict the identification process to events of interest.

3) Searching for significant correlations between the selected events and a library of classified acoustic signatures (ACIt) to complete the identification process.

Due to the capacity to process and to classify a large amount of acoustic data in a short time, EEDI, powered by the Soundscape Meter 2.0 software, results in a new tool for analysis of large data sets from long-term monitoring programs of soundscape surveys.

Crick was not wrong: reminiscence of a role of comma-free codes in present circular codes

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In 1957, Francis Crick suggested an ingenious solution for solving simultaneously the problem of amino acid coding and frame maintenance. The idea was based on the notion of comma-free codes. Trinucleotide comma-free codes have very strong error detecting properties, but have not yet been proved to be used in nature. Nevertheless, we can state now that Crick's theory was not completely wrong.

In the present talk the decompositions of di- and trinucleotide circular codes in comma-free codes will be discussed. Our results show that on the dinucleotide level, the maximal circular codes are generated by the comma-free codes. Although this connection for trinucleotide codes is not existent in the same form as it is for dinucleotide ones, we can show that at least for each of the maximal self-complementary C3-codes, which build a very important subclass of common circular codes and were found in nature, there is always a large subcode that is comma-free and encodes almost all the amino acids that are coded by the code itself.

Our results can be seen as another hint for an evolutionary process that developed the current standard genetic code from an ancient genetic code that satisfied a weaker version of Crick's hypothesis about codes without commas.

The non-power model of the genetic code: an universal description of degeneracy and degeneracy evolution

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A new mathematical approach to the genetic code based on non-power representations of integer numbers allows to describe the degeneracy distribution of both the nuclear and the mitochondrial variants of the genetic code. Recently has been showed that the possibility that an arbitrary degeneracy distribution admits a non-power representation is extremely rare (Gonzalez et al. 2016a). In this contribution we analyse different degeneracy distributions in relation to the actual tRNA implementation in different organisms and in different variants of the genetic code (data from Grosjean et al. 2010). Surprisingly, all the extreme cases used in extant organisms, that is, all the cases implemented by a minimum number of adaptors, are exactly described by a correspondent non-power representation. Moreover, proposed evolutionary steps of the genetic code are also well described by alternative non-power representations. The rarity of degeneracy distributions that should be described by non-power representations together with a new biological hypothesis on the origin of degeneracy based on the same rationale (Gonzalez et al. 2012, 2016b), strongly supports the idea that non-power representations are a key aspect of genetic coding and that they are related to primeval symmetry properties of the molecules involved in protein translation.

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A new perspective on the heterogeneous nature of language

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This paper treats neither individual languages nor human language as natural or artificial codes. Rather, “language” can be used to indicate both systems for making graphical traces and vocal participation in face-to-face coordination. The first of the senses is dependent on the second; vocalization has slowly been integrated (over evolutionary time – and, furthermore, slowly *becomes* integrated over ontogenetic time) into most forms of co-action, as a way of aligning the timing of one’s activity with that of conspecifics while sharing and shaping specific aspects of the experience, and exerrting a form of control. One such form of co-action is the use of graphical marks as organizational techniques that, if standardized in a community, become an easy perceptual and conceptual reference point for engaging with vocalizations. It is with marking systems, and ways of talking about them, that the study of “language” has historically been concerned (Linell 2005).

In a fundamental sense, language relies on vocalization in organising human action and co-action. Vocal tract activity is constrained by processes on several timescales. One such source of constraint are articulatory synergies, coherent and repeating patterns of movement involving articulators that are flexibly strung together into structured streams (Fowler 2014; Goldstein & Fowler 2003). (For instance, “b” and “p” sounds are brief stoppages of airflow made by pressing the lips together while also vibrating one’s vocal cords, or not, and keeping the tongue lowered; together, the movements are an “articulatory synergy”.) Other constraints are prosodic, as when pitch change is used to direct another person’s vocalizing (e.g., to do “turn taking” or to question), or attending is regulated by stress and emphasis (e.g., Cummins 2009; Port 2008). Vocalization is also organized by bodily effects of emotion (e.g., hormonal and other neurochemical changes, changes to breathing rate) and attention. And of course, literate speakers sometimes organize articulatory activity to “match” a graphical form in ways described as “uttering” particular words or sentences. Understanding language thus depends on at least (1) how the organizational flexibility of brains allows humans to engage with these various constraints, and (2) how graphical systems are used to reflect, and then to re-organize, vocal activity. These topics are addressed later in the workshop.

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On Rosen's Paradox, Formal Cause, and Codes

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In 1959 Robert Rosen published a paper [1] in which he described a logical paradox in John von Neumann's kinematic self-reproducing automaton [2]. The core of this automaton is a general purpose constructor, A, that builds a machine x from component parts S according to $\varphi(x)$, the blueprint for x. When A is supplied with its own description $\varphi(A)$ it builds a copy of itself. Rosen interpreted Von Neumann's description in terms of a system of sets and mappings and pointed out that in the situation where A is supplied with its own blueprint the range of the mapping A contains A itself, which is logically impossible: on the one hand, no mapping can be defined before its domain and codomain are stipulated; on the other hand, the codomain, since it contains the mapping itself as an element, cannot be stipulated before the mapping is given. Thus, in the words of Rosen, "neither the mapping A nor its range can be specified until the other is given."

I shall show that this logical paradox is only apparent, arising from the particular way that Rosen used mappings to describe the Von Neumann architecture. In essence, this follows from the realisation that, contrary to Rosen's interpretation, A by itself is not a mapping, and needs to be combined with a blueprint to become one. There is no logical paradox in a mapping $(A, \varphi(A))$ containing A in its range, A on its own just being an inert object. There are two general questions that arise from this. First, how should one incorporate formal cause (here the blueprint $\varphi(A)$) into a mapping? One of Rosen's great contributions was to show how Aristotle's four causes can be formalised in terms of a mapping, but I disagree with his treatment of formal cause when it is a separate object from the efficient cause. Second, if the formal cause is a separate object that contains encoded information there exists a logical necessity for a decoding system, something that Von Neumann to my knowledge did not explicitly consider in his description of self-reproducing automata.

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From code to translation – What could be the role of the first peptides

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We know a lot about how genetic information is translated into peptides. We also know an increasing amount about how the genetic code underlying translation could have evolved. But the evolutionary path leading from a genetic code to peptide synthesis is still shrouded in the mist of unknown.

One way to tackle this problem is to find what could the first peptides used for. As mRNA (i.e. information coded in RNA) is not yet available, peptide synthesis could had been non-template dependent. We know that present day peptide enzymes are superior (or can be superior) to ribozymes. But can primitive peptide enzymes be superior to established ribozymes? Probably not.

So what could a peptide composed of a few amino-acids do that ribozymes could not? RNA cannot traverse a lipid membrane, albeit it can change the permeability of it. Peptides can protect RNA like nothing else (cf. capsids of viruses). Peptides can scaffold ribozymes, like in the ribosome. We look at amino-acid frequencies of various peptide functions outside of traditional enzymes to look for functions in which small, apolar amino-acids, believed to be abundantly available in prebiotic setting, could play a dominant role.

Embodiments of interaction: In search for dynamic mechanisms

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A variety of hypotheses and concepts have been recently proposed to rethink the question of structure/function relationships in the brain to account for its capacity for language and higher-order cognition in humans. We consider several related frameworks, as recently proposed with the concepts of “neural reuse“ (Michael Anderson), “shared circuits“ (Susan Hurley) and “neuronal recycling“ (Stanislas Deheane), as well as pointing out some of the difficulties that remain in accounting for the dynamic, interaction-driven aspects of cognition as a basis for language use. In this context, the concepts of synergies and functional organs/systems are introduced with reference to the neurophysiological schools of Anokhin (1984), Bernstein (1967; 1984) and Ukhtomsky (1978), as well as Peter Tse’s (2013) recent concept of criterial causation. Drawing on the above frameworks may help to specify some of the mechanisms resonsible for fast, flexible organization of cognitive processes as a prerequisite for interaction, and frame the problems of language production and language codes from an embodied and “interactivist“ perspective. We hope this approach may also help to analyze the problem of “artifact construction“ in the nervous system in line with the code biology approach to cognition, while focusing on its anticipatory aspects.

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Slow Down and Smell The Birds: Chemistry, Avian Biology and Natural Selection

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For nearly 150 years, biologists studying the avifauna of the Hawaiian islands have noted that one class of birds – the Drepanididae, consisting of about 16 honeycreepers – have a strong, disagreeable and almost overpowering odor. Many naturalists up to the present day have contemplated this matter and speculated about both the source and the function of this smell. Writing to R.C.L. Perkins in 1892, Alfred Newton wrote to British naturalist RCL Perkins, working on the Big Island of Hawaii: “Do conceive some theory or two or three theories to explain the common odour that is so remarkable. Can’t you bottle us a little of the stink that we may enjoy it too?” Later naturalists have described the smell as “simply overpowering,” and even persistent in the birds’ nests long after they have been vacated.

The smell lingers in collections of these birds after death, lingering for at least five to ten years, and in numerous cases, for many decades. A number of scientists have proposed an interdisciplinary solution to the problem, and several have identified the ideal helpmate for this work: an analytical chemist with the tools necessary to sample the VOCs (volatile organic compounds) being emitted from the bird. Identifying the materials constituting the odor is half of the solution, because once the compounds have been identified, we can identify their source on the bird (skin? feathers? preen glands?) and reach informed conclusions about the evolutionary function of this odor. Various reasons have been proposed for the smell, ranging from defense against predation (an early adaptive response to strong selection from a community of bird predators), or sexual selection (potential mates are attracted to the smell). I have recruited an analytical chemist at Pomona College and we are attempting to borrow some specimen material to begin testing to begin solving this problem.

Color Systems are Categories that Carry Meaning in Visualizations: A Conceptual Metaphor Theory Approach

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This paper will show how color systems can be used to visualize meaning in the diverse field of biosemiotics. Historically, scientists have leaned on Newton's prismatic colors to differentiate different values in visualization, but there are many more possibilities when different complex color systems are mapped to linguistic systems. Donald Favareau defines biosemiotics at www.biosemiotics.org as "the study of the "myriad forms of communication and signification observable both within and between living systems." I will outline the beginning of my plan to color map the molecular blending of natural, airborne, olfactory elements within a given natural environment, to be seen in a virtual reality environment.

Color is an ecologically organized, dynamic sign system. Color can be used as communication not just for representation of other things, but is also a sign system itself. Each object inside the category (or domain) of color carries attributes. This includes image schemas, which are dynamic patterns, often connected to objects, emerging from embodied experiences. Image schemas are essential to the process of abstract conceptualization and reasoning. We will see how image schemas manifest themselves in color sequences during the section on the interaction of color. This part focuses on the 20th Century Bauhaus artist, Josef Albers. Albers researched and taught how ordered colors interact with each other and carry both quantitative and qualitative meaning, such as less or more than, and pictures continuums of changing values. He created an interactive language than can be used and expanded for scientists who are visualizing semiotic values.

The concept of color as a category is important. We categorize in order to construct thoughts. Even infants categorize; one cannot engage in intelligent thought and action without this capacity. Categories consist of entities that share similarities in varying degrees. The psychologist, Eleanor Rosch, approached and qualified color as a natural category. Berlin and Kay, started the Universalist, evolutionary view of color categorization in 1969, and anthropologists have added to this tradition ever since. Germany, during the first twenty years of the 19th Century, saw an explosion of systematic color thinking: Goethe published *Zur Farbenlehre* in 1810 (*Color Theory*), Arthur Schopenhauer produced *Über das Sehn und die Farben* in 1816 (*On Vision and Colors*), and Philipp Otto Runge created his *Farbenkugel* (*Color Sphere*) in 1810.

Goethe, in the second volume of his color theory, was responding in a negative way to Isaac Newton's *Opticks* from one hundred years earlier (1704). He did not agree with the scientifically accepted “received knowledge” from Newton on the colors of the prismatic spectrum—the refraction of light. He also wrote two short essays called *Contributions to Optics* on this subject. The part of his treatise on color that is meaningful for this research is in the first volume, where Goethe's attention is applied to how color appears; these concepts are categories with dynamic relationships between the individual category members. I focus here because of its functionality in mapping information from other domains. One can refer to this area of Goethe's research as qualitative: "the dynamic observing subject itself became the locus of the research.

In this paper I will show examples of color mappings that can be described accurately and clearly using the language and thinking of conceptual metaphor theory and conceptual blending theory. To this end I follow a particular conceptual route through the domain of color. The path begins in the nineteenth century with Goethe and Runge and their methods of organizing color through geometry and different qualities, such as transparent, translucent, mat or shiny. Goethe, Wittgenstein and Westphal explored color separately from the optics of Newton, and they opened the door to the semiotics of color. It is this concept that I explore in relation to how color systems can be used more effectively in today’s scientific visualizations.

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Applying eco-field and the General Theory of Resources to bark beetles: Beyond the Niche Construction Theory

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A new perspective in landscape ecology is the application of the term Eco-Field together with the General Theory of Resources. In this paper, we describe the putative eco-field in bark beetles as a spatial configuration with a specific meaning-carrier for every organism-resource interaction. Bark beetles are insects with a relevant role in matter and energy cycles in conifer forests and they are involved in significant changes of forestry landscapes when plague outbreaks occur.

Bark beetles are conveyed by the recognition of semiotic signals towards host trees using a specific eco-field. These signals are mainly a group of scents, which have been called odourtope. The interactions with other organisms (fungi, bacteria, nematodes, predators, etc.) takes place through sharing relevant information of the eco-field networks (representamen networks) in the forestry ecosystem.

The eco-field networks let an expansion of the realized semiotic niche of the bark beetle towards the potential semiotic niche. Also if different organisms end up showing an interdependence of the eco-field, the niche construction process can be initiated. Subsequently, if this interdependence becomes crucial the process can lead to the establishment of mutualistic relationships. This is an example on how evolutionary processes are initiated by the recognition of signals by a network of eco-fields.

Memes: A Literature of Hogwash

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Since the release of Richard Dawkins' 1976 book *The Selfish Gene*, some philosophers, anthropologists, and communications scholars have popularized a the idea of memes as cultural analogs to genes. Based on a small side comment in Dawkins' book, defenders of this idea have run with the concept of memes to argue for a particular understanding of how culture maintains itself and develops. Despite the fact that Dawkins himself has backed away from the notion of memes, or at least expresses himself very ambivalently with regard to them, a large literature has arisen claiming that such things as language, manners, artifacts, and cultural arrangements (including religion in particular) are carried forward through the mechanism of memes.

Using Dawkins' particular understanding of how genes work, writers in this area would have it that memes are mechanisms that reproduce themselves through the behavior of their "hosts". That is, the ideas themselves are things that duke it out for existence. This paper argues that the concept of memes is incoherent for at least three reasons. First of all, Dawkins' notion of "the selfish gene" doesn't work even at the gene level, and so *a fortiori* cannot explain anything based on an analogy to that mechanism. It is not genes that are selected for in evolution, but traits. Genes do not represent a sufficiently large level of organization to either fit or not fit a given environment. Therefore one could not use the idea of memes to account for cultural evolution; rather, one would have to look for whole patterns that are either successful or unsuccessful at replicating themselves. Second, it would be completely otiose to appeal to a non-empirical, metaphysical entity such as memes to explain cultural processes, when every human activity and artifact can be explained naturally, without appeal to them. Ordinary biological processes can account for learning and transfer of ideas and practices at every level of sophistication. The whole notion of memes, in short, flagrantly violates Occam's Razor. Third, taking memes seriously as an analog to genes would mean at the very least that these entities should share the hallmark characteristic of genes: their function according to code. On any understanding of memes, though, there is no set of rules establishing a correspondence between objects of two different worlds. Memes instead are said to be reproduced by imitation or 'contagion'.

The notion of contagion here, first of all, is anything but clear; it seems to be a mere metaphor for the idea of spreading, but spreading can take many forms. Yawns, for example, are contagious, as is laughter, but these are somehow understood to by the defenders of memes as "innate," and not to count as the right kind of contagion. The criterion for such a judgment is just what is missing, however. As for imitation, it need not involve any adaptors performing independent recognition processes, as genetic transmission of information does. Imitation can be accomplished with no signaling happening at all. Signaling involves *meaning* in an important sense; it involves recognition at both ends of the transmission, and so requires adaptors, in addition to something that is "encoded." Therefore, if memes are supposed to explain the most obvious examples of social coding, including language, morals, and law, then they are total failures.

DNA computing: from simple rules to supervised learning

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The development of engineered biochemical circuits capable of adaptive behavior is a key goal of synthetic biology and molecular computing. Such circuits could be used for long-term monitoring and control of biochemical systems, for instance, to prevent disease or to enable the development of artificial life. I will describe a novel molecular circuit architecture for implementing adaptive algorithms using DNA strand displacement reaction networks that are able to compute arithmetic functions, store behavioral parameters, and adapt their behavior in response to signals from the environment. As a proof of concept, we use this architecture to design and simulate a DNA circuit for supervised learning of a class of linear functions by stochastic gradient descent.

Our architecture uses buffered DNA strand displacement gates. Briefly, a buffered DNA strand displacement gate is one where the gates are initially present in an inactive form, and must be activated by a precursor input strand. This extension enables the inactive gates to be present in excess and called up as required to carry out computation. By designing the circuit so that availability of these activating strands can be controlled by another gate, we can implement buffered gate networks with feedback loops that adjust future circuit behavior in response to past stimuli.

Our example circuit uses buffered strand displacement gates to implement supervised learning of a class of linear functions using stochastic gradient descent, which is a well-known and well-studied machine learning algorithm. We use computational simulations to demonstrate that the DNA circuit correctly implements this learning algorithm and to characterize its learning performance for a range of initial conditions and learning targets, and in the presence of noise in the inputs. Thus, this work offers a route to an experimental realization of adaptive molecular computing systems using DNA strand displacement.

Linear codes

and the mitochondrial genetic code

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The origin of the genetic code can certainly be regarded as one of the most challenging problems in the theory of molecular evolution. Thus the known variants of the genetic code and a possible common ancestry of them haven been studied extensively in the literature. In [1] Gonzalez, Giannerini and Rosa developed the theory of a primeval mitochondrial genetic code composed of four base codons. These were called {\it tesserae} and it was shown that the tesserae code has some remarkable error detection capabilities. In our talk we will show that using classical coding theory we can construct the tessera code as a linear coding of the standard genetic code and at the same time it can be deduced from the code of all dinucleotides by Plotkin's construction. The result has some interesting implications on the existence and construction of so-called {\it circular codes} in the world of tesserae.

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From Typical Sequences to Typical Genotypes

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The idea of *typical sets* in information theory is central to the design of efficient coding schemes for digital communication. In my talk I will describe novel conceptual and mathematical links between this core information-theoretic notion with its associated asymptotic properties, and properties of genotypes as long sequences of polymorphic markers sampled from multiple populations. Standard population-genetic considerations such as *linkage equilibrium* within populations, the availability of large data sets of *single-nucleotide-polymorphisms* (SNPs), and the typically low *minor allele frequencies* for such polymorphisms, translate under a typical set framework into considerations on statistical independence of time-sequential signals, the *asymptotic* nature of set-typicality, and the qualities from relatively low *entropy rates*, respectively. I will also demonstrate that a population assignment scheme based on exclusive set-typicality of sequences is theoretically viable, and moreover of potentially practical interest especially in cases of ’noise’ introduced from small sample sizes.

Proto-language in wolves

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Like several other animals (and human infants), wolves have proto-language. In human development, proto-language precedes and is the foundation of the child's development of the adult language. In animals, proto-language forms an important part of their communicative repertoire. In animals and humans alike, proto-language is characterized by the absence of grammar, and is directly tied to internal bodily states and/or to aspects of situations. In other words, actual use of proto-language is often action-related, for instance by directing attention. In terms of the tripartite Umwelt model (Tønnessen, based on Uexküll), animal interjections can be associated with the conceptual aspect of Umwelt, where in the human case linguistic practices are placed. In animals too, the conceptual Umwelt is characterized by predicative reasoning, i.e. the habitual, mental attribution of specific features to someone or something. However, the mediated aspect of Umwelt also comes into play as far as mediation, e.g. anticipation and memory, enters the picture, as is typically the case with emotions, which are often at the basis of interjections.

We will analyze a data set from Wolf Park (USA) involving captive, socialized wolves, aiming to identify animal interjections performed in a range of situation types. We will be looking for patterns and variation, e.g. between different groups (packs), with a view to determining the range of meanings and situations in which different interjections occur. We hypothesize that since interjections are very likely to some extent conventionalized, there will be systematic, observable variations grounded in the lived experience of social relations, whether intra–pack, or human–animal. Of interest here is the extent to which these calls or interjections are not merely expressive of internal states but serve communicative and thus social functions such as coordinating relations between individuals in the group. Our assumption is that interjections are often learned through experience, in a social setting. By comparing instances of interjections in wolves, we will also consider how the individual and social agency of wolves is enacted through these vocalizations, and how it contributes to individual and group development. This implies that socialization is always in part self-socialization (i.e. that socialization always involves individuation).

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Downwind

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The Downwind installation (2013) combines art, engineering and science research and is composed of twenty pods that sense human presence and respond by breathing smells on the audience. Downwind explores our differences in olfactory sensitivity and selectivity due to the genetic basis of human olfactory variability and the perception of odiferous sequences in changed contexts.

Not only are synthetic olfactory molecules changing perception of the world, but technologies are changing perception. Is a visceral comprehension possible in a sanitised and deodorised olfactory environment suffused with new synthetic olfactory molecular architectures for smell and taste? Whether natural, synthetic or engineered, they are the olfactory cyphers of change, yet sensing them is defined by a combination of genetics and personal experiences. To increase our ability to perceive the information of new chemical signals not just with the nose but with the gut it may be necessary to retrain one's olfactory observation and to note the feelings and emotions that arise from olfactory materials.

At first the phenomena of smell may seem insignificant but humans are bound up in the transpiration and consumption/absorption of olfactory particles. Emerging as vapours into the troposphere, fragrances arise from cultural, social and political systems that have engineered the landscapes and thus mindscapes into settlements, habitations, fields, factories, front lawns and streets. Synthesised and novel particles may affect microbes and thus by implication the immune system which establishes a distinction between self and other which eventually transforms the behaviour of living beings.

Humans, animals and insects are immersed in an atmospheric ocean of olfactory cues which are in dynamic flux with olfactory perception. The smell compounds used in Downwind are ones known to elicit specific anosmias (loss of sense of smell) for some, and not for others. The revolutionary wind of genetic discovery suggests that we may not all be perceiving the same reality.

Odor in the land
An undervalued aspect in human history and heritage

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In this paper I address one of the more transitory signs in the land that even more as sound, has been mostly absent from consideration in the reconstruction of the narrative of our species: odor of the land.

Within the field of archaeology/anthropology investigation of a number of signatures, straddling quantitative and qualitative methods are used to understand human behavior and document human history. Archaeologists for example employ a wide range of methods to understand signs and indices to add, complement, or contradict stories represented in human written and visual languages. For instance, scientific methods such as C_{14} dating and other chemically based dating techniques are use ubiquitously. Cross-referencing of cultural and natural materials such as ceramics and tree-ring records are used to provide insight in the relationship between human behavior and environmental conditions.

My interest and research in human spatial thinking has provided insight in how differences in spatial thinking among groups result in different land design and management strategies. Notably, differences in the ontological foundation of languages demonstrate this diversity in thinking regarding our surroundings. Words and categories that indicate knowledge of landscape sounds and smells are more prominent in certain languages. Knowledge based on these signals has long been undervalued in the current visually dominant society. Recently, research in other sensory-based knowledge is regaining attention. This is not just important for our current understanding of environmental changes, but can also broaden our insight into past behavior and land management from which we stand to gain in our present world.

Past smells and sounds are difficult to investigate, but even today technological developments toward understanding signals other than visual lag behind those of visual information. I recently initiated an experimental project to investigate an approach for representing sense-able modalities of the land**. It** specifically focused on vegetation scent, which like sound, is considered an ephemeral quality. I propose that these qualities, that constitute sensory signatures in the *semiosphere*, are crucial components of biodiversity and therefore important to understand from a scientific as well as artistic perspective.

The expected outcome of the proposed experiment is the start of a library of scents of the land, is a step toward new opportunities for scientific research, for artistic exploration and experience of cultural and natural heritage within E-culture –immersive- environments, thereby crossing the art -science boundary.

The non-Darwinian quasi-species bifurcation mechanism of code evolution

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When a system like the genetic code relies on the products of its own operation to synthesise the components of its functional machinery it cannot evolve through simple Darwinian adaptation based on genetic selection. The products of codes required for the bio-computational interpretation of genetic information are only able to confer selective fitness as a result of their “chance” association with the genes that newly encode them. However, there exist elementary physico-chemical mechanisms, like Turing reaction-diffusion coupling, whereby the “selective isotropy” of co-localization and movement through physical space serves to maintain an association between information (genes) and its interpretation (catalysts) sufficient to support their coevolution, with the concomitant elimination of destructive "parasitic" species. These problems will be discussed within the context of Eigen’s theory of quasi-species and the symmetry-breaking bifurcations that resulted in the pre-LUCA phylogenies of the amino acyl-tRNA synthetases, especially the initial split into paired Class I and II sets of “statistical proteins”, but also the progressive reduction in coding ambiguity as far as the 61-codon, 20-amino acid “universal” genetic code.