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Dream Codes

Background and Origins

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Abstract

It's 1900, the beginning of a century of enormous upheaval in many areas of scientific knowledge, and Freud burst in with "The Interpretation of Dreams," provoking a combination of scorn, wonder, and ridicule. A masterwork of scientific observation, the 'dream book' marks the birth of a research method, though insufficiently appreciated then as now. Through deciphering the grammar and syntax of a 'primary process', laid out in detail in chapters six and especially seven, Freud arrived at his first *topographical* theory of mind, the cornerstone of psychoanalytic metatheory. Given these initial insights Freud fervently believed that his theory of dreams held enormous promise for the study of mental evolution. He remained disappointed to the end that the importance of this avenue of investigation was not fully recognized. In clinical practice we listen to verbal narratives of pictographic elements expressing sensory-affective experiences still tied to perceptual impressions and bodily feelings in the very process of being transformed into pre-cognized re-presentations. These iconic clusters, stretching from sensory-kinetic-emotive *physical* experiences, to memories, motives, fears, and desires; exhibiting proto-semiotic mechanisms of pre-linguistic tropes and cognition, obey laws that differ fundamentally from those of Aristotelian logic revealing a "psychic reality" that is idiosyncratic and highly personal. With its metaphorical and manifest/latent structure, the dream is our MRI, a "royal road" into the human unconscious, as sharp an investigative instrument into the forms and functions of this spontaneous, universal, human product, as can be found. Nowadays the range of detectable and interpretable unconscious meanings has expanded considerably thereby increasing self- and conscious-awareness. In the interest of generating an integrative paradigm linking body and mind this informal presentation also pursues a personal passion; namely, to continue where Freud left off regarding the scientific value of studying semiotic processes in dreams, viewing these, and the linguistic interpretation of their meanings, as a window into the evolution of the epistemologies of the human mind.

Introduction to Code Biology

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Abstract

Code Biology is the study of all codes of life with the standard methods of science. The genetic code and the codes of culture have been known for a long time and represent the starting point, the historical foundation, of Code Biology. What is really new in this field is the study of all codes that came *after* the genetic code and *before* the codes of culture. Some of these new codes have already been discovered, and it seems likely that many more will come to light in the future. The existence of many organic codes in Nature, however, is not only a major experimental fact. It is one of those facts that have extraordinary theoretical implications. The first is that most great events of macroevolution were associated with the appearance of new organic codes, and this gives us a completely new reconstruction of the history of life. The second theoretical implication comes from the fact that codes involve meaning and we need therefore to introduce in biology, again with the standard methods of science, not only the concept of information but also the concept of meaning. The third theoretical implication comes from the fact that the organic codes have been highly conserved in evolution, which means that they are the great invariants of life, the entities that must be perpetuated while everything else is changing. The study of the organic codes, in short, is bringing to light new mechanisms that have operated in the history of life and new fundamental concepts in biology.

Life as interplay of information and matter

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Abstract

Any sequence can be transformed into an equivalent one by alphabet change and/or encoding. Thus an information cannot be identified to a single sequence, but should be defined as the equivalence class among sequences with respect to such transformations, an abstract entity. It may be represented by its ‘information message’ defined as the shortest binary sequence in this class, whose length quantitatively measures the information. Any sequence must be borne by a physical medium, so information bridges the abstract and the concrete. Perturbations in the physical world result in random symbol errors, while information may instruct the assembly of physical objects by the agency of the semantics it bears. Information theory tells that errorless communication is possible provided a long and redundant enough error-correcting code is used. Conserving genomes over the ages needs error-correcting codes making their exact regeneration possible provided it is performed frequently enough. In engineering, such codes are conveniently defined by mathematical constraints tying symbols together, but constraints of any kind, defining ‘soft codes’, also do the job. The better conservation of old parts of the genome implies moreover that the genomic error-correcting codes are made of nested component codes. This scheme accounts for basic life features: need for successive generations, existence of discrete species with a hierarchical taxonomy, trend of evolution towards increased complexity, etc. Transcription of the genes and their translation into polypeptidic chains, becoming proteins when properly folded, are controlled by enzymes, which as proteins are needed for their own synthesis. A feedback loop results, referred to as ‘semantic’ since it implements the genetic code which tells the meaning of the genes. Once closed, it keeps its structure, thereby conserving the genetic code. The onset of a new semantic feedback loop originates an organic code in Barbieri’s meaning, which itself induces a new soft component in the system of genomic nested error-correcting codes by imposing new constraints to the genome. Due to the feedback, constraints on proteins affect the genome. Besides the synthesis of proteins, the assembly of living structures, as instructed by the genome, involves interwoven semantic feedback loops. Although closed, they do not prevent the genome lengthening, say by horizontal genetic transfer, which increases both the information quantity, hence its semantic specificity, and the redundancy, hence its error correction ability. Thus, closing semantic feedback loops does not prevent evolution: new structures can be appended with improved resilience to errors. Regeneration failure is very infrequent and results in a widely different genome which originates a new species if the phenotype it specifies withstands the Darwinian selection. A possible scenario for the origin of semantic feedback loops (hence maybe of life) is proposed.

Biological Autonomy, Regulation, Code: How are they related?

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Abstract

This paper aims at addressing some conceptual issues in the debate about biological regulation, code, minimal forms of meaning and interpretation. It does so from the point of view of a specific point of view on living systems, based on the theoretical framework of biological autonomy. According to this account - which has often been critical of the use of notions such as information and code in biology - living systems are metabolic self-producing systems able to self-maintain and keep the identity of their organization invariant through the continuous exchange of matter and energy with the environment. This approach stresses both the self-referential character of organisms as self-producing and self-maintaining systems, and the intrinsically interactive dimension of the autonomous organization of biological systems that cannot exist unless they maintain a continuous coupling with the environment. These ideas are at the basis of the thesis of the equivalence between life and cognition brought forth among the others by Piaget (1967) and Maturana and Varela (1980), according to which minimal cognition consists basically in the viable and meaningful interaction between an organism and its environment, rather than in the processing of information. Specifically, it resides in those adaptive mechanisms that are at the basis of the capability of organisms of modulating functionally their interactions with perturbations. Instead of characterizing meaning and interpretation capabilities (of internal and external variations) in terms of representations and information processing, this line of investigation associates them to internally generated operational schemes (meanings expressed in dynamical patterns of self-regulation) for variations perceived as perturbations.

Is it possible, hence, to naturalize notions such as meaning and interpretation at the level of basic living systems - as adaptive autonomous systems - rather than considering them as prerogatives of complex organisms (e.g with a complex nervous system)? That is: is it possible to propose an operational characterization of them at a basic level? Our main thesis in this respect is that mechanisms of internal compensation for perturbations are those responsible for the emergence of a minimal form of “significance” and “meaning” (of some specific features of perturbations) for the organism. As we shall argue, regulatory mechanisms constitute a key theoretical tool for characterizing at the operational level, and therefore naturalize, notions such as world, meaning, significance etc., thus avoiding the risk of ultimately referring them externally, to the operations of an observer located outside of the system. Specifically, we will distinguish between two forms of regulation to which qualitatively different ideas of interpretation can be ascribed - dynamical stability and adaptive regulation - and we will show how the second implies a more complex form of dealing with variations and perturbations, and justifies a proper naturalization. We then propose a theoretical model of adaptive regulation characterized as the the capability of a system to mediate the effect of a perturbation by acting on its own internal dynamics through modulation or selection between distinct available internal regimes by means of a dedicated and *dynamically decoupled* subsystem.

We then explore the relationship between regulatory decoupling and code in order to establish whether or not there is a necessary connection between the two notions. We do so not only with respect to the classic models of genetic regulation such as the lac-operon but, especially - by leaning in particular on Di Giulio's version of the coevolutionary theory of the origin of the genetic code -with respect to the issue of why and how the genetic code originated.

Implications of the Existence of a Glycomic Code in Plant Cell Walls for Plant Biology and Biotechnology

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Abstract

Polysaccharides found in plant cell walls display a code that is produced as a result of polysaccharide branching and from fine adjustments of the biosynthetic machinery within plant cells. This code, here called “glycomic code”, confers chemical diversity to cell wall structure, this being one of the features responsible for differences among cells and tissues. The glycomic code generates semantics through the formation of composites (combination of different polymers) that display different chemical and physical properties. This generates multiple functions within the cell walls each with its respective function and biological meaning. For instance, the assembly of polymers will determine cell form as well as emergent properties of tissues and organs of the plant. The glycomic code regulates the resistance to hydrolysis so that in order to disassemble the cell wall of a plant, a given organism (including microorganisms, herbivores and the plants themselves) has to possess a decoding (or decrypting) key. Whereas some fruits can “relax” the glycome code and allow organisms to have access to the interior of cells so that this service will be exchanged by seed dispersion, other tissues can lock the glycomic code (the xylem in the vascular systems for ex.) so that microorganisms would seldom gain access to the sugars in the cell walls. Essentially, as the cell walls are an important barrier between the cytoplasm of plant cells and the exterior, the existence of the glycomic code is likely to be one of the reasons why plants can exist as stable organisms in Nature. Here I present evidence that the fine structure of all classes of hemicelluloses known display fine structural variability consistent with the existence of the glycomic code. On this basis, I present evidences from literature on how the glycomic code is used to give rise to biological meaning for several phenomena in plant biology. Finally, I will present some ideas on how the understanding of the glycomic code and its semantic implications can be used in plant biotechnology.

The Coding of Nature and Art – Aristotle’s Mimesis Revisited

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Abstract

On this auspicious occasion of the inauguration of Code Biology as an academic discipline, it is only appropriate for Marcello Barbieri, the man who has conceived of his brain-child, delivered it, and christened it to introduce the concept. Not a biologist by training, but an unabashed veteran semiotician, I shall first attempt to rehearse a few commonplaces of the thorny issue of ‘code’ by referring to a discursive tradition that links two eminent semioticians, Umberto Eco (1976, 1984) and Barbieri (2003, 2013), and then try to revisit some Aristotelian texts to see how the first biologist and semiotician in the West encoded Nature (φύσις) and art (τέχνη). For all its popularity--and confusion--today, the word ‘code’ was never used by the precursor of biosemiotics Jakob von Uexküll, nor, for that matter, was it discussed by Ferdinand de Saussure except once only in passing. Uexküll’s description of the interaction between receptor and effector in the functional circles can be encoded to represent an elementary semiosis, involving a basically monoplanar codification. Advances after him, in particular, cellular biology and molecular biology, when coupled with semiotics, may shed light on his project. However, to date not much has been done in this regard, but the process of sign-function is often prematurely shifted from syntactic (i.e., formal) code to semantic code (Chang 2003). Barbieri’s definition (2003) as ‘a set of rules that establish a correspondence between two independent worlds’ (Barbieri, 2003: 94) serves to identify the principle of equivalence governing inter-systemic relations. The author further provides a biological instance to illustrate code as an operative category. It means the existence of a real organic code is based on (and can be inferred from) the existence of organic molecules--called adaptors-- that perform two independent recognition processes. In the genetic code the adaptors are the transfer RNAs, but it will be shown that adaptors also exist in splicing and in signal transduction, which means that there are at least other two organic codes in real life (Barbieri, 2003: 93). Barbieri’s organic codes are presumably an advancement of the genetic code, which bridges the world of nucleic acids and that of proteins through the mechanisms of transcription and translation. There is no doubt that the genetic code involving the transcription process from DNA to RNA qualifies as a *bona fide* code, but as Eco (1984) observes, it is characterized by ‘a process of steric stimuli’ (Eco, 1984: 183) in which ‘every element ... interprets a previous one, and, in doing so, makes the process grow’ (Eco, 1984: 184). In terms of Peircean interpretation, it is a case of semiosis, but not unlimited, and the kind of exclusive reliance on the internal syntax without semantic correlation is *monoplanar* and what Eco terms an *s-code* (1976: 36-40; 1984: 169). More or less in the same way Barbieri questions Shannon’s ‘sequence information’ as purely syntactic and non-semantic and, as such, has limited relevance to biology (Barbieri 2013: 39). Even though the concept of coding is not traceable to dates prior to the rise of modern linguistics and information science, as far as semiotic modelling is concerned, it is perfectly legitimate to revisit the Corpus Aristotelicum, especially the so-called Organon, in terms of the modern concept of sign and the related concept of code. Therefore, the second part of the paper will examine how Aristotle applies his methodology of naming and classification in *Categories* and *De Interpretatione* to his studies of poetic genres in *Poetics*, animals in *History of Animals*, *Parts of Animals*, and physiognomy in the forged but fecund *Physiognomics*.

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Sketch for a theory of evolution based on coding

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Abstract

With the discovery of DNA and the mechanisms of transcription and translation, molecular biology has revealed that at the heart of life lay two mechanisms: copying and coding. Copying is generally considered to be more fundamental, because the logic of evolution by natural selection does not require coding, only differential replication, and because replication is mostly conceptualized as instantaneous copying. At best, coding is seen to provide a one-way bridge from genotype to phenotype, mostly if not completely under control of the genome. As a result, the phylogenetic aspects of macroevolution are brought to the front, and ontogenetic aspects are easily overlooked. This picture is but a crude approximation however, which is being challenged by an increasing number of empirical and theoretical findings. The underlying reason is that in reality replication, and therefore evolution, is not primarily based on copying alone but always involves coding. When a theory of evolution is built on the notion of coding instead of copying, a coherent picture arises that sheds new light on some of the controversies and open questions in contemporary biology, such as what is the nature of replication, what are the roles of phylogeny and ontogeny in evolution, and how to characterize the increase of biological complexity in evolution. It is therefore not just an interesting idea, but a scientific necessity to develop a biology that acknowledges the crucial and ongoing role of coding in evolution.

My contribution to the first gathering in code biology will be a sketch of how such a code biology might look like. I start by introducing basic notions and terms. As more terms are introduced, a theory unfolds that culminates in a coherent and unifying picture of macro evolution that is sketched at the end of the talk. Borrowing the words of Valentin Turchin whose work together with that of Marcello Barbieri, Ross Ashby and many others has profoundly influenced my own, “[p]roperly speaking, to define a particular science is the same as introducing its basic concepts, for all that remains to be added is that a description of the world by means of this system of concepts is, in fact, the particular, concrete science.” Meaning operates at the core of addiction, at many different levels of analysis. Since research has shown fairly decisively that addiction depends upon brain plasticity and learning, it is clear that biological codes are central to addiction considered at the neurological level. Less attention has been paid to the function of biological coding at the social level in the development, understanding, and treatment of addiction. This, then, will be the focus of the present paper. The development of differing systems of meaning among addicts and non-addicts results in impediments to interpersonal relationships between addicts and their close social connections, as well as in sometimes insurmountable problems for treatment professionals. The very possibility for addiction arises because of the meanings that mind-altering experiences create for the addict; indeed, part of what we are saying when we say that someone is addicted is that for that individual, the preferred substance or activity has come to mean something different, and much more significant, than it does for others. Nevertheless, there is a consistent, regular relationship between certain street corners, paraphernalia, and people, and the addict's mood, alertness, and thought patterns, which those who have been addicted thoroughly understand. The meanings of the sights, sounds, and accoutrements associated with the addict's use are different, on the other hand, for her children, parents, and other people in her life, relative to what they are for the addict, but there is a systematic relation between two worlds in the former group's case, as well. The differing and even incommensurable codes of the addicted and the non-addicted provide a powerful tool for elucidating the frustrating and sometimes seemingly hopeless rifts between addicts and those who would care for them. Non-addicts try to understand addicts' actions in terms that make sense of what seems to be obviously self-undermining and otherwise irrational behavior. Addicts, on the other hand, often feel that they aren't understood, and, as a result, that they are being judged, threatened, or dismissed for something that is clearly not their fault. The two groups use similar sentences, but they seem to fail at communication, because the respective sets of sentences reflect different models of the world, based on different experiences of people, places, and objects, as well as of stress, pleasure, danger, and value. Consideration of these problems in terms of code biology reveals a more promising future for addressing them than has been heretofore available.

Molecular Codes

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Abstract

We present a formal method to assess the semantic capacity of a chemical reaction network, aiming at distinguishing chemical systems that are able to process meaningful information from those that are not suitable for information processing. The basic idea is to measure how easy it is to implement with this network a molecular code, which is a mapping between species that cannot be inferred from knowing only the species. We analyzed models of real chemical systems (Martian atmosphere chemistry and various combustion chemistries), bio-chemical systems (gene expression, gene translation, and phosphorylation signaling cascades), as well as random networks and artificial chemistries. We found that different chemical systems possess different semantic capacities. Basically no semantic capacity was found in the atmosphere chemistry of Mars and in all combustion chemistries, i.e., with these chemistries, organic codes cannot be implemented (in the way we defined them). Whereas the bio-chemical systems possess very high semantic capacities, with (hypothetically) increasing capacity from metabolic networks, signalling networks, to gene regulatory networks. Random networks possess a semantic capacity for a specific relatively low density of reactions. However, we have found high density artificial reaction networks with significant semantic capacity in artificial chemistries based on a structure-to-function mapping. We conclude that our approach can be applied to evaluate the information processing capabilities of a chemical system and may thus be a useful tool to understand the origin and evolution of meaningful information, e.g., at the origin of life. It may also serve as an example how abstract, semiotic concepts can be grounded on data through an intermediate formal modeling layer that integrates physical experiments.

Carrying Pieces of Information in Organocatalytic Bytes

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Abstract

It's quite consolidated that biological polymers like DNA, RNA and proteins enclose information. A less conspicuous fact is that the very order in which the atoms are arranged in a small (monomer) molecule also encloses information. For instance, even short carbon chains might present chiral or saturated carbons whose substituent groups might assume one between two possibilities giving raise to (S/R, CIS/TRANS) isomers. Shannon and Weaver (1949) defined information as one selection between two possibilities (as 0 selected between 0 and 1 in a binary code). This is also true for L or D in an isomer. For instance, a "hexose nyble" code could be created based in the left (L), right (D) relative position of hydroxyls in its chiral carbons: D-allose (DDDD), D-altrose (DDDL), D-glucose (DDL D), D-manose (DDL L), D-gulose (DLDD), D-idose (DLDL), D-galactose (DLLD), D-talose (DLLL), L-talose (LLLL). Diastereomers present distinct chemical topologies and might present even distinct melting points, although the single difference among them is the specific positions of its atoms among the other possibilities i.e. information. Autopoiesis, the ability of produce their own boundaries and components, is a universal property of living beings (Maturana and Varela 1972). Minimum autopoietic systems able to self production and reproduction have been built (Luisi and Varela 1990, Bachmann et al. 1990, 1991, 1992). However, these artificial autopoietic systems are unable to evolve because they are not able to preserve information (Luisi 2007). Living beings preserve their self-production instructions throughout reproduction in codified biopolymers. As this process is subject to errors their dissimilar offspring entails evolution through natural selection. A catalyst is a chemical topology which establishes weak interactions with chemical compounds reducing the activation energy (the energy necessary to overcome its intrinsic stability). In opposition to unselective transition metal catalysts used in industrial applications, biological catalysts are selective, catalyzing reactions only from cognate molecules. Their selectivity is given by stereochemical blockages and fittings which delimit substrate topologies able to make catalytic interactions. These properties are made possible thanks to the huge size of enzymes and ribozymes. However, the emergence of these huge polymers from smaller ones faces logical matters as the Eigen's paradox. Organocatalysts are organic compounds which exhibit catalytic properties. Although they present lower selectivity, their turnover and enantioselectivity are comparable those of enzymes in a way that asymmetric catalysis is said to be a tripod formed by biocatalysis, organometallic catalysis and organocatalysis (List, 2007). Proline is an example of organocatalyst able to catalyze a wide range of reactions including aldol additions and α -aminations, but other amino acids have been shown to be able to catalyze asymmetric reactions (Paradowska et al. 2009). The enantiomeric excess of organocatalyzed reactions implies that part of organic information might be preserved during organocatalysis. Molecules as proline and other amino acids occur in prebiotic environments (Miller 1956, Ring et al. 1972). In addition to their catalytic properties, it is plausible to expect that in a rich reducing chemical environment, they can generate spontaneous autopoietic systems similar to those designed by Luisi's group, but able to conserve catalytic information. These considerations suggest that organocatalysis may have had a role in the origin of life and suggest a roadmap for testing it.

On the Structure and Generative Capacity of the Lexicon: a contribute to the characterisation of natural codes

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Abstract

Cognition is the capability of every life form to evolve in a specific environment identifying and responding to essential environmental stimuli (Maturana 1978; Ferreira 2007, 2010). The capacity to identify specific environmental features springs out naturally whenever life forms interact with their environment, defining specific semiotic relations. That disposition seems to rest upon a significant degree of innate “knowledge”- a “know how”, which all organisms possess, and which is the result of the experience of biological predecessors and a consequence of their adaptive efforts to adequately respond to environmental conditions and changes. Triggered out by the urge to satisfy the life form’s internal state(s), this “know how” guarantees the identification of the right environmental features, as well as the choice of the adequate behaviour from a repertoire that is already pre-established according to typical contextual frameworks.

As posited by Ferreira (2007, 2010), independently of the type of cognition or the level of semiotic complexity involved, meaning is always a value- a structured entity. In the entity’s meaningful world, the Umwelt (Uexküll 1926), meaning always comes structured according to paradigms of significance that determine not only the conditions of their occurrence or co-occurrence but also define possible variations according to different contextual frameworks. These structured paradigms of significance are usually defined as codes. Being highly structured entities, code units carry a semantic potential that will determine the role to be played by the unit in larger structures of significance . Plus, code units carry in themselves a high generative power responsible for the economy and elegance of the whole system. It is this generative power that is responsible for its capacity to adapt to new contexts and that guarantees the coherence and integrity of the code even when variations occur within existential frameworks. The present paper takes as a stand point the structure of the lexicon in natural languages, highlighting the structure of meaning and its generative potential aiming, this way, to contribute to a larger discussion on the nature and structure of biological codes.

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Trinucleotide n-circular Codes and their Corresponding Amino Acids

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Abstract

The main aim of this talk is to investigate the barrier which makes it impossible to encode all twenty, or just nineteen amino acids, using codes with the best known error correcting properties.

We introduce five hierarchically ordered classes of trinucleotide codes including the well known comma-free and circular codes. Using combinatorics we show that it is impossible to encode all twenty amino acids with codes from four out of the five classes that have the strongest error correcting properties, a fact that was previously known only empirically for comma-free and circular codes. However, it is possible to encode all twenty amino acids using codes from the largest class with the weakest coding properties.

Additionally, we will give examples of classes of trinucleotide codes which include the primeval code that are automatically circular and we will list which amino acids they can code for.

Dichotomic classes, short range correlations and entropy optimization in coding sequences

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Abstract

In this talk we introduce and study dichotomic classes, quantities that arise naturally from the mathematical model of the genetic code introduced in Gonzalez(2004) and further investigated in Gonzalez (2008), Gonzalez et al.(2008, 2009), Giannerini et al.(2012).

Dichotomic classes can be defined as nonlinear functions of the information contained in a dinucleotide, that is, a group of two adjacent bases. Interestingly, such classes, that represent precise biochemical interactions, emerge naturally from the mathematical model. Moreover, dichotomic classes possess precise symmetry properties and can be put in a group theoretic framework.

We use the dichotomic classes as a coding scheme for DNA sequences and study the mutual dependence between such classes. We obtain meaningful tests for dependence by using an entropy based measure possessing many desirable properties together with suitable resampling techniques. We find universal strong short-range correlations between certain combinations of dichotomic classes. These correlations point to the existence of a local structure that might be related to the mechanisms of error correction and entropy optimization in the management of genetic information.

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“What is life 2.0” playing the sudoku with a new tool box: Metabolic Holons, Codepoiesis, and Optionality

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Abstract

In 1944 with his seminal work “what is life?” Schrödinger dropped the bomb of an epistemological revolution associated with non-equilibrium thermodynamics into the discussion about life. To stress the special status of living systems he (one of the most reputable physicists of his time!) invented a scientific non-sense – “negative entropy” (entropy can only be positive in classic thermodynamics!) – to describe what makes it possible life. Obviously, he was looking for “something completely different” capable of explaining the existence of a double mechanism of self-organization (order from order plus order from disorder) across different scales. The huge success of molecular biology in the 60s muddled the issue for a while. In fact, the mechanism of DNA replication was used to explain the stability of life forms while mutations could explain the variability driving evolution. This simplistic mono-scale explanation given by molecular biology was quite weak but it was the best available. Since then many scientists, operating in different fields have been working to integrate within a more robust and complex theoretical framework the discussion of the mechanisms explaining the existence of life.

In this paper, I follow the same strategy adopted by Schrödinger when writing “what is life”. That is I stand on the shoulders of an additional wave of giants that provided in the last decades new key theoretical concepts for further developing his original ideas: (i) dissipative systems (Prigogine school); (ii) autopoiesis and metabolic patterns stabilized through informed autocatalytic loops (Maturana and Varela, Morowitz, H.T. Odum); (iii) order-for-free (Kauffman); (iv) complexity theory and anticipatory systems (Simon, Rosen); (v) centripetality and teleology in theoretical ecology (Ulanowicz); (vi) holons and holarchies (Koestler, Allen); (vii) fund-flow model for analyzing patterns across multiple scales (Georgescu-Roegen); (viii) biosemiotics (von Uexküll, Pattee); (ix) codepoiesis (Barbieri) (x) optionality – how to win when deciding in face of uncertainty when it is impossible to get reliable predictions (Taleb).

After briefly explaining these concepts the paper uses them to explain the special ability of life. Life expresses a process capable of learning how to take advantage of favourable boundary conditions for reproducing itself while building up resilience and adaptability. In relation to this point three concepts are extremely useful: *metabolic holons*, *codepoiesis* and *optionality*. Using these new concepts it is shown that life in metabolic networks – e.g. ecosystems – is capable of handling distinct types of information at different scales (very large, large, medium, local, micro), as in several Sudoku games run one inside the other.

The Codes of Literacy

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Abstract

It has been proposed that thoughts occurring in the minds of humans exist in linguistic form. In writing, thoughts in mind are inscribed on material such as paper in linguistic code. It is evident that in literate humans coded thoughts in mind/brain can be rapidly transformed into the codes of written text. In writing, thoughts are produced by the brain one coded element at a time in sequences that are meaningful to both the writer and literate reader. How is this accomplished? How are thoughts in mind organized in brain before and during the writing process? An important task for biosemiotics is to investigate the nature of the structures and processes that enable human brains to instantiate linguistic codes. Questions to be addressed include: what is the nature of the linguistic codes; where do they originate and how are they installed in the human brain; what is the process by which linguistic codes in mind/brain are transformed during writing into the codes of written text? Is it possible, through a code-based analysis of writing, to distinguish processes of mind from processes of brain?

It can be reasonably assumed that the body and brain of humans that lived in the period immediately prior to the invention of writing were the same as those who lived in the subsequent period in which literacy took hold. No genetic changes in brain or body were necessary for the invention of writing and the development of the codes of literacy. The acquisition of literacy by a child is a time consuming and tedious learning process, a burden that is readily accepted by most members of a literate society. This learning process entails installing the codes of literacy into the brain of the developing child. Investigation of this installation process can provide important clues as to how the content of a linguistic utterance can be encoded in written text, and how the content of the written form of linguistic content in mind can subsequently be reconstructed with reasonable accuracy in the mind of a literate reader.

Spoken language acquisition occurs naturally when a child is raised in an oral society but literacy, the ability to read and write, cannot be naturally acquired by a child in an oral and literate society. Evolutionary changes occurring in head and neck morphology and the brains of the ancestors of *Homo Sapiens* were necessary for the evolution of spoken language, and spoken language is the necessary foundation for literacy. Literacy, however, is an invention of mind that appeared relatively abruptly in human society on the order of a mere 5K YBP.

This presentation will propose the development of a theory of literacy that has a neurobiological element. It will require the examination of the essential differences between the human and nonhuman primate brain that allows only humans to be literate. Literacy is clearly dependent on the invention of codes that can be inscribed in a medium external to the human brain. These inscriptions can be viewed as the encoding, for export, of thoughts that exist in the mind of the writer. What it is about the human brain that uniquely enables it to instantiate these codes and to manage their transfer from brain to text (writing) and then back into brain (reading)?

A mathematical model of the genetic code, the origin of protein coding, and genetic code conservation

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Abstract

We present a mathematical model of the mitochondrial genetic code that explains exactly its degeneracy distribution (1). The same approach, which is based on redundant integer-number numeration-systems (non-power systems), has been previously used for explaining the degeneracy distribution of the *Euplotes* nuclear genetic code (2). The mitochondrial model suggests a possible origin for protein coding on the basis of the symmetries of primeval adaptors connecting the world of nucleic acids with the world of amino acids. In the optics of code theory we are interested in investigating if some characteristics of primeval genetic codes have been conserved through evolution and, consequently, if such characteristics should be observed in present ones. The results are very surprising: i) we observe a perfect conservation of the degeneracy distribution of the mitochondrial code (note that such property allows to change the meaning of some codons without altering the degeneracy distribution), ii) some primeval degeneracy properties (as for example the Rumer's anti-symmetric transformation) are exactly conserved in present codes, iii) the nuclear codes can be included in the mitochondrial class as a particular case of symmetry breaking. In fact, the main differences between mitochondrial and nuclear codes are due to post-transcriptional modifications, iv) the comparison of all known variants of the genetic code allows to uncover that particular classes of codons are prone to variation. Such unstable codons are described in our model by discrete symmetries involving a lesser number of codons (less constrained codons). Such codons are mutually related by a global symmetry: the palindromic symmetry. Using these properties a hierarchy of codon stabilities can be obtained. The previous results point to two main conclusions: 1) the genetic code emerge as highly conserved, much more that though until now because of the fact that most known variants are compatible with the conservation of the degeneracy distribution; this result enforces one of the main postulates of code biology, 2) the degeneracy distribution seems intimately tied with important, but yet to be determined, biological functions (degeneracy distribution is much more conserved than the assignments codon/amino acid). Some interesting possibilities for such functions include: error correction control (point mutations (1-3) and frame synchronization (2-4)), protein synthesis regulation (5), and control of protein folding (6).

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Realization of Molecular Codes By Protein Complex Formation

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Abstract

Molecular codes, such as the genetic code, are situated at the central information processing subsystems of the cell. The recent development of a formal framework for molecular codes and of algorithmic approaches for code identification allows us to analyze different kinds of systems for molecular codes. While the code based analysis of the gene translation system, the genetic code, as the prototypic molecular code has been described before the analysis of “non-genetic” codes is one of the major current research topics. Here, we are interested in codes that are mediated by protein assembly processes, which are facilitated by the cell in many regulatory processes. In particular, we analyzed a rule-based model of the human inner kinetochore assembly and study how protein complex formation in general can give rise to molecular codes. The analysis of 105 reaction networks generated from the rule-based inner kinetochore model in two variants: with and without dissociation of complexes showed that codes can be found only when some but not all complexes are allowed to dissociate. We show that this is due to the fact that in the kinetochore model proteins can only bind at kinetochores by attaching to already attached proteins and cannot form complexes in free solution. Using a generalized linear mixed model we study which centromere protein (CENP) can take particular roles in a molecular code (sign, meaning, context). By this, associations between CENPs (CenpA, CenpQ, CenpU and CenpI) and code roles are found. We observed that, e.g., CenpA is a major risk factor (increases probability for a code role) while CenpQ is a major protection factor (decreases probability for a code role). Finally, we show, using an abstract model of copolymer formation, that molecular codes can also be realized solely by the formation of stable complexes, which do not dissociate. For example, with particular dimers as context a molecular code mapping from two different monomers to two particular trimers can be realized just by non-selective complex formation. We conclude that the formation of protein complexes can be utilized by the cell to implement molecular codes. Living cells thus facilitate a subsystem allowing for an enormous flexibility in the realization of mappings, which can be used for specific regulatory processes, e.g. via the context of a mapping.

BDA-generated Models of the Genetic Code

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Abstract

In this talk we introduce the concept of a BDA-generated model of the genetic code which is based on binary dichotomic algorithms (BDAs) [1]. A BDA partitions the set of 64 codons into two disjoint classes of size 32 each and provides a generalization of known partitions like the Rumer dichotomy [2] or the Parity class dichotomy [3]. We investigate what partitions can be generated when a set of different BDAs is applied sequentially to the set of codons. An algorithm is developed that scans for interesting BDA-generated models. The search revealed that those models are able to generate code tables with very different number of classes ranging from 2 to 64. It is analyzed whether there are models that map the codons to their amino acids. A perfect matching is not possible. However, we present models that describe the standard genetic code with only little errors. There are also models that map all 64 codons uniquely to 64 classes showing that BDAs can be used to identify codons precisely. This could serve as a basis for further mathematical analysis using e. g. coding theory. The hypothesis that BDAs might play a role at the decoding center of the ribosome is discussed.

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On Formal Representations of Organic Codes

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Abstract

In past Gatherings of Biosemiotics I have reported on progress in the development of a linguistic model for self-fabrication couched in terms of a formal system that writes its own production rules (such a system would be ‘closed to efficient causation’, to use the criterion that Robert Rosen regarded as necessary for life). The model is based on a structural hierarchy of letters, words, sentences and paragraphs that are analogous to chemical elements, metabolites, macromolecules and macromolecular assemblies. Production rules are ‘active’ sentences that join words together and are analogous to enzymes. A “metabolism” is modelled by a set of these active sentences that construct the words that the sentences themselves are constructed from. A key result that follows from the logic of the model is that it can only be made to be self-fabricating by assuming the existence of an internal representation of the sequence of words in each sentence and an algorithm (mechanism) for decoding this information, which, of necessity, must be written in another language. This logical need for a code to translate between the two languages directly confronted me with the problem of formally representing this code in such a way that it conforms to Barbieri’s definition of an organic code, i.e., the decoding rules, like molecular adaptors, must themselves be implemented and produced within the system as adaptors that link the two independent languages of the code.

In this talk I shall consider my solution to this problem and contrast it to other representations of codes. For example, in terms of formal language theory a code is a mapping between the elements of a finite source alphabet and to elements of a set formed by sequences of symbols from a target alphabet. The Morse code is an example of such a mapping. What is often not considered is that the physical decoding of a source symbol entails the recognition of the symbol by an agent and the subsequent translation into its meaning by using the relevant rule, i.e., the code mapping can be decomposed into a recognition mapping and a translation mapping. In an organic code the adaptor must do both.

I shall also touch on other uses of the term ‘code’, as for instance in information science and computer science. This discussion should link to other interesting contributions to this conference, such as Gérard Battail’s nested soft codes and Dennis Görlich and Peter Dittrich’s molecular codes in a reaction network.

From genetic code symmetries and quadratic forms over different fields to protein structure prediction

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Abstract

Symmetries by base substitutions for degeneracy in the genetic code were identified by Rumer. The complete set of symmetries was characterized more recently (1). A rationale accounting for these symmetries relies on codon substitution matrices of importance in molecular evolution and their corresponding quadratic forms over the field of p -adic rational numbers (2).

Further, quadratic forms over the field of rational numbers were associated to kinetic energy conservation for polypeptide chains in molecular evolution: the consistency of this finding with the codon arrangement within the genetic code will be discussed (3). A method to predict edge strands in beta-sheets from protein sequences was derived (4). Based on the same formalism, another method to predict amino acids at proximity of beta-sheet axes from protein sequences was reported (5).

These relations between protein sequences and structures allow applications to be envisioned for the next CASP (Critical Assessment of techniques in protein Structure Prediction) challenges. Such methods shall facilitate large-scale computational approaches in structural genomics.

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Is the histone code an organic code?

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Abstract

The system that comprises post-translational histone modifications, their biological effects, and the proteins that instantiate these effects has been described as the 'histone code'. Independently, Barbieri used the term 'organic code' to describe biological codes in addition to and including the genetic code. He also provided the defining criteria for an organic code, but to date the histone code has not been tested against these criteria. Furthermore, the use of the term 'code' has seen a number of uses, not all of which conform to the precepts given by code biology. It would be useful therefore, to investigate these uses and contrast them with the term as it is defined in code biology. A perspective on codes will be given that also allows the synthesis of this concept with that of information, so providing a useful platform for the investigation of both concepts in the molecular world. The bulk of the presentation will be an investigation of whether the histone code is a *bona fide* organic code according to the criteria provided by code biology. Drawing on our current knowledge of the major histone post-translational modifications and of the specific protein binding domains that recognise and translate these into specific biological effects, it will be shown how the histone code system fits into the context of an organic code and fulfills the criteria for an organic code, so giving it the same standing as the genetic code. In short, the marks produced on histones by processes such as acetylation and methylation act as organic signs that are translated into unique biological effects, which are the biological meanings of the signs. These translations are accomplished by effector proteins that consist of a binding domain that recognises a specific histone mark and a regulatory domain that mediates the biological effect. Crucially, these domains can be experimentally interchanged between different effector proteins, thus altering the rules that specify the relationships between sign and meaning. The effector proteins therefore fulfill the role of adaptor molecules that instantiate the conventional rules of the histone code.

Are ‘Archetypes’ Biological Codes?

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Abstract

Analytical Psychology is understood as a depth psychology. In fact, Carl Gustav Jung aimed to understand the profound (bio)logic of the mind and thought finding this depth in ‘archetypes’ (which can be understood as a very old code, or codes — a small set of biological rules — surreptitiously influencing human behaviour); a concept akin to another: ‘instinct’.

In a sense, we can state that: (1) archetypes appeared after the genetic code and before the codes of culture; (2) the existence of archetypes and the collective unconscious are both in line with the mechanistic view: (a) ‘archetypes’ as *codes*; (b) ‘collective unconscious’ as our *phylogenetic heritage shared by all* (by no means a metaphysical entity); (3) the archetypes showed a trend towards conservation (a code conservation system). Thus, Psychology cannot ignore these ‘archaic codes’ to really comprehend the human mind; in equal measure, clinical practice in (Analytical) Psychology cannot ignore the ‘archetypes’ if aims to be truly useful/salutogenic.

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Eco-acoustic Codes of Borneo Primary Forest

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Abstract

Through a case study of field recordings collected in Brunei’s undisturbed rainforest within the scope of Monacchi’s long-term project “Fragments of Extinction”, this presentation will focus on the interpretation and representation of acoustic codes of a primary ecosystem. Soundscapes were recorded with innovative three-dimensional microphone systems set-up in remote and challenging habitats, where the rate of biodiversity loss will be increasing. The result is one of the most vivid sound portraits possible with current hi-definition technology, providing a detailed example of the current state of Bornean biophony. This will be a critical reference point for future conservation studies and policies.

After an introduction of the cross-disciplinary project, the presentation will focus on specific analyses of a 27 hour (dusk to dusk - included) continuous recording. Data are being evaluated with different methodologies to assess the ecosystem richness and variability through an entire circadian cycle. A careful dissection of species’ sonic languages within the three-dimensional recording domain is followed by bioacoustic species mapping, to then outline the 24-hour eco-acoustic behaviour of life cycles. In parallel, data are examined with Acoustic Complexity Indexes as important ecological meters of information, and acoustic codes are traced with several methodologies. Within the aim of the study two questions are posed: how do soundscape data represent significant ecological indicators for revealing the interconnected equilibrium of these primary natural systems? How can the specific recording techniques employed preserve essential information for the investigation of acoustic communities?

In consideration of the *Acoustic Niche Hypothesis* (Krause 1987), engaged here to interpret and frame one of the most diverse soundscapes on Earth, we think that the different degrees of complexity found in the communication codes of insects, amphibians, birds and mammals reflect evolutionary mechanisms of long-term cross-adaptation confirmed by extreme acoustic efficiency, niche partitioning, and systemic behaviour.

Histone Code running on a Chromatin Computer

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Abstract

Heritable instructions to build and "run" an organism are encoded in DNA, a sequence of characters taken from a four letter alphabet. In eukaryotic cells, DNA is in complex with histone proteins forming chromatin. This has two major consequences for information storage and processing. First, DNA is partitioned into segments of about 200 nucleotides in length each wrapped around one histone complex. Second, histone complexes carry modifications. Over 200 different marks can be placed onto histone complexes. Specific combinations of histone marks have been associated with particular regulatory functions giving rise to the Histone Code Hypothesis. For two reasons, the chromatin modification state should not only be viewed as an index structure of the genome. Furthermore, the chromatin state is independent of the underlying DNA, at least in theory. Second, the chromatin state is not static like the DNA sequence. Instead it changes dynamically and fast in response to modification enzymes in the narrow and cellular signals in the broader sense. In this contribution I will show that eukaryotic chromatin can act as a cellular computational device. With a set of read-write rules that act non-deterministically on chromatin and the capability of self-modification the chromatin computer shows striking similarity to amorphous computing. A threat to the chromatin computer and the cellular memory is replication. To date it is unclear how histone marks are propagated across cell division. In general, replication is associated with loss of information. Computer simulations can demonstrate that simple patterns can be re-computed after cell division with some error remaining. I will discuss how this relates to cellular plasticity, cell differentiation and aging. A glimpse into the past will help us to gain understanding of how a complex and dynamic regulatory system as the chromatin computer could come about. With an evolutionary analysis spanning the tree of life I will demonstrate that the emergence of protein domains able to specifically recognize histone marks is likely to be a major eukaryotic innovation in gene regulation.

Transcriptome and proteome analyses show alternatively coded peptides, by codon expansion and nucleotide exchanges, in the bacterial genome of *Tropheryma whipplei*

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Abstract

Recent analyses of mitochondrial transcripts show that RNAs not corresponding to any genome region exist. These match the mitochondrial genome assuming systematic nucleotide exchanges ('swinger' RNAs, 23 different exchange types exist, i.e. A<->C). Two independent RNAseq runs of *Tropheryma's* transcriptome detect 11 and 16% swinger RNAs among all reads mapping on *Tropheryma's* genome, spanning on average 2.8% of the genome's length and matching regions covered by regular transcription. *Tropheryma's* trypsinized proteome, assuming swinger transcription, yields on average 205 peptides (range: 148-312 peptides) of 14 residues (range of mean lengths: 12.5-15 residues) per exchange type. These peptides map more frequently than randomly expected on swinger RNAs: transcriptome and proteomic evidences converge, confirming the existence of exchange coding, at least for short polypeptides. Proteomic analyses assuming codons expanded by one or two silent positions (tetra- and pentacodons) detect approximately 200 peptides matching these alternative ways of decoding *Tropheryma's* genome (for various nucleotide exchanges). For at least one exchange type (analyses of further exchanges ongoing), A<>T+C<>G (corresponds to inverted 3'-to-5' RNA), tetra- and pentacoded peptides map preferentially on regions matching detected 3'-to-5' RNA. Different exchange types cover sequences characterized by different nucleotide frequencies, high G frequencies characterize regular and 3'-to-5' transcriptions. Questions remain open on the existences of: a) complete proteins, rather than short peptides, coded by nucleotide swinging and/or expanded codons; b) promoter-like sequences regulating the different swinger transcriptions; and c) regulation of tetra- and pentacoding. These results indicate that any DNA or RNA sequence has the potential of coding according to three codon sizes (larger sizes not yet explored), and 24 types of transcription. Hence genes include 72x more information than considered until now, and 72 alternative translations. Relatively few peptides/transcripts correspond to each of these unusual coding systems, but taking all together, they represent sizeable proportions of the transcripts and peptides detected by classical methods. Their detection depends solely on analyzing data according to the predictions of the various coding hypotheses.

Code Biology and Addiction

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Abstract

Meaning operates at the core of addiction, at many different levels of analysis. Since research has shown fairly decisively that addiction depends upon brain plasticity and learning, it is clear that biological codes are central to addiction considered at the neurological level. Less attention has been paid to the function of biological coding at the social level in the development, understanding, and treatment of addiction. This, then, will be the focus of the present paper. The development of differing systems of meaning among addicts and non-addicts results in impediments to interpersonal relationships between addicts and their close social connections, as well as in sometimes insurmountable problems for treatment professionals. The very possibility for addiction arises because of the meanings that mind-altering experiences create for the addict; indeed, part of what we are saying when we say that someone is addicted is that for that individual, the preferred substance or activity has come to mean something different, and much more significant, than it does for others. Nevertheless, there is a consistent, regular relationship between certain street corners, paraphernalia, and people, and the addict's mood, alertness, and thought patterns, which those who have been addicted thoroughly understand. The meanings of the sights, sounds, and accoutrements associated with the addict's use are different, on the other hand, for her children, parents, and other people in her life, relative to what they are for the addict, but there is a systematic relation between two worlds in the former group's case, as well. The differing and even incommensurable codes of the addicted and the non-addicted provide a powerful tool for elucidating the frustrating and sometimes seemingly hopeless rifts between addicts and those who would care for them. Non-addicts try to understand addicts' actions in terms that make sense of what seems to be obviously self-undermining and otherwise irrational behavior. Addicts, on the other hand, often feel that they aren't understood, and, as a result, that they are being judged, threatened, or dismissed for something that is clearly not their fault. The two groups use similar sentences, but they seem to fail at communication, because the respective sets of sentences reflect different models of the world, based on different experiences of people, places, and objects, as well as of stress, pleasure, danger, and value. Consideration of these problems in terms of code biology reveals a more promising future for addressing them than has been heretofore available.

Graph Grammars and the Analysis of Large (Bio)chemical Networks

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(joint work with Jakob Lykke Andersen, Daniel Merkle & Christoph Flamm)

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Abstract

Chemical reactions, including but not limited to the complex biochemical reactions catalyzed by enzymes within a cell, can be described and understood as graph transformations corresponding to the application of rules that in turn are formal statements of chemical reaction mechanisms. The framework of graph grammars allows the generation of very large chemical reaction networks in a manner that is not only computationally efficient but that can also incorporate experimental constraints such as known intermediates. Graph grammars also form a computationally framework in which rule composition and binding operations provide natural means of coarse grainings and abstractions. One may ask, for example, whether an abstract reaction scheme such as an auto-catalytic cycle has an implementation over a collection of reaction mechanisms and whether it is reachable from a particular set of initial molecules. At an abstract level, chemical reaction networks are directed hypergraphs whose vertices are molecules. At this level of description one can define key (bio)chemical concepts such as catalysis or auto-catalysis as structural properties of directed hypergraphs. In practice, this leads to ILP formulations very similar to problems of network flow on hypergraphs that can be solved efficiently to detect such structures in very large networks. The ambiguities in the relationship between organizational structure of a reaction network, i.e., its “logic” and over-all transformations and the underlying implementation in terms of actual molecular transformations allows, at least in principle, to encode information on internal status as well as environmental of an organism (or prebiotic system) in the form “metabolic states” and to process such information. It seems worthwhile to explore to what extent such capabilities of complex chemical reactions systems are actually utilized in modern biological entities.

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Karl Popper, Forensic Science, and Nested Codes

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Abstract

This paper utilizes the framework of Karl Popper's 3-world ontology to make the case that forensic science is a specialized coding system that establishes meaningful connections between the world of biology (world 1) and the world of human society (world 3). Forensic science is a cross-disciplinary endeavor that uses scientific methods to determine what transpired in a crime so the legal system can determine how to prosecute the offender(s). On a Popperian analysis of forensic science, world 1 consists of evidence gathered at the crime scene, which enables investigators to develop a detailed reconstruction of the incident for consideration under the legal and ethical codes of society, which are products of world 3. Understanding forensic science in this way serves two purposes: first, it extends Marcello Barbieri's code biology into the realm of philosophical considerations in science, law and ethics; and second, it situates forensic science within the larger context of debates in contemporary philosophy of science.

On Barbieri's model of semiosis, organic codes are nested within neural codes and both organic and neural codes are nested within cultural codes. Accordingly, organic codes and neural codes in some sense constitute cultural codes; and likewise cultural codes would not exist without their evolutionary foundation and history in organic and neural codes. This idea is philosophically similar to Darwin's theory that complex features evolve through the modification of simpler features and functions so that the evolution of biological complexity in nature is cumulative. Forensic science too can be understood as a system of codes within codes in that the human codes of world 3, i.e., those associated with the forensic process, are used to decode the meaning and contextual significance of the biological codes in world 1 evidence. The phenomenon of DNA profiling is understood on this analysis as the application of scientific and cultural codes to decode biological codes: codes within codes.

This paper provides an analysis of forensic science as a specialized coding system designed to establish meaningful connections between world 1 codes and world 3 codes in the service of criminal justice. It is suggested that forensic science in practice is a system of codes within codes; in particular, the world 3 investigative methods themselves are created to decode the significance of world 1 evidence, which in the case of fingerprints and DNA, are themselves codes. This fractal-type analysis of forensic science is intended to extend the new field of code biology into the realm of philosophical considerations of how we use biological coding systems in the service of the uniquely human codes of science, law, and ethics. Furthermore, this paper initiates a new discussion on philosophical issues in forensic science; its fundamental assumptions, methods, and results are as deserving of philosophical analysis as any other branch of science, and perhaps even more so because of its direct effect on our legal system and thus on our society.

Dinucleotide circular codes

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Abstract

Circular codes have gained considerable attention in the last few years. In fact they seem to be highly involved in detecting and maintaining the normal reading frame in protein coding sequences. The discovery [2] of an universal code X_0 across species suggested many theoretical and experimental questions. It was empirically found both in eukaryotes and in prokaryotes and a recent analysis [3] showed that on average, X_0 has the best covering capability. Moreover, this code had the additional nice properties of being circular, self-complementary, maximal and C^3 , i.e. X_0 in frame one and frame two is still circular. There are exactly 216 such codes and it was shown in [1] that these 216 maximal self-complementary C^3 -codes can be divided into 27 equivalence classes defined by a particular set L of transformations.

In this talk we discuss in analogy to the above maximal dinucleotide circular codes. There exist 24 such codes and these have been completely classified in [4]. However, we take two different points of view and show the same classification using group theory and geometry. Moreover, the weaker dinucleotide 1-circular and 2-circular codes are described. Using the set L of transformations from [1] we also explain an interesting partitioning of the 24 maximal dinucleotide circular codes into 3 classes that has been mentioned in [4] and establish a connection between the self-complementary maximal C^3 -codes and the maximal dinucleotide circular codes.

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Codes and interpretation in perception

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Abstract

In this talk I present work in progress on the role of interpretation vs. codes in perception, where perception is understood in terms of coherent (unified) subjective experience. I follow Jakob von Uexküll (1956, cf. 2010) in assuming that all organisms except plants and fungi have such coherent, unified subjective experience (i.e. Umwelt experience). My starting point is the tripartite Umwelt model (Tønnessen 2011), according to which any Umwelt has two aspects (core and mediated) and some have three (including conceptual). In Tønnessen, forthcoming, I outline the workings of the Umwelt in terms of these three aspects in more detail. We can generally conceive of six types, or categories, of acts, and these can be located within the three different aspects of the Umwelt:

<i>Core Umwelt</i>	Automated acts of perception Automated mental acts
<i>Mediated Umwelt</i>	Wilful acts of perception Wilful mental acts
<i>Conceptual Umwelt</i>	Habitual acts of perception Habitual mental acts

By *automated*, I mean the exact and physiologically based matching of something with something else, by *wilful* I mean the agenda- and interest-driven matching of something with something else, and by *habitual* I mean the learned matching of something with something else. Whereas *conscious animals* carry out all six types of acts, non-conscious creatures, in so far as they perceive, only carry out two, namely automated and wilful acts of perception. Habitual, i.e. conceptual acts are reserved for conscious creatures, but even bacteria can carry out wilful acts of perception, i.e. make choices based on interpretation. In general terms automated acts can be said to be code-based, whereas both wilful and habitual acts are interpretation-based. An implication of this claim is that the core Umwelt is generally code-based, and that the mediated Umwelt and the conceptual Umwelt are interpretation-based. If this is correct, the interpretive threshold is not located where animals *with* a nervous system meet creatures *without* a nervous system, nor where the biotic meets the abiotic. Instead, the interpretive threshold must be located where core experience meets mediated experience (and since these aspects often intermingle, the dividing line is not in plain sight).

Questions for further investigation include the following: Can coding in automated acts of perception and in automated mental acts be understood within the framework of code biology (Barbieri, de Beule and Hofmeyr 2014)? Particularly, can they be understood as organic codes? While I have only begun reflecting on the notion of code itself, I will relate codes in perception as presented here to the notions of a *neural* code and of *ecological* codes.

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The emergence of coding specificity at the dawn of life

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Abstract

Schrödinger¹ explained that the specificity of biological inheritance required the transmission of information in some physical form, that he dubbed an “aperiodic crystal”. Then, the sequences of nucleic acid heteropolymers were enshrined as the putative source of all biological specificity by Crick² in his Central Dogma: DNA sequence information directs the construction of catalysts of exquisite specificity allowing the maintenance and operation of precisely defined metabolic, genetic control and molecular messenger networks. The emergence of genetic coding, a process of enormous complexity, was the central constitutive process of the origin of living systems from a pre-existing state of molecular disorder that lacked specificity completely. Orthodox neo-Darwinian theory cannot explain the emergence of a specific genotype-phenotype relationship as a product of natural selection, because evolution as a result of the survival of the fittest is a process that requires an already established mapping from genetic information to system traits. No genotype-phenotype relationship is pre-encoded. Investigations⁴⁻⁸ into the thermo-physical and computational self-organisation of genetic coding demonstrate how the functionality of information can co-evolve with its accumulation. The key ingredient missing from the neo-Darwinian explanation of evolution is the propensity of nature to harness and channel negentropy¹ through symmetry-breaking transitions that create bit-symbols in which information can be stored and transmitted. This is born out in phylogenomic analyses of coding enzymes – the amino acyl-tRNA synthetases. These studies provide a new insight into the origin of genetic coding and the prospect of discovering how the first organic code was associated with the nucleation of a metabolic network based on increasingly specific catalysis.

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Codes and Epigenetic Inheritance: Understanding Codes as Stabilized Stabilizers

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Abstract

From the Code Biology Glossary, a ‘code’ is “a set of rules that create a correspondence between independent worlds.” Contemporary developments in physics, psychology, and biology, however, raise the issue of whether there are in fact “independent worlds.” Specifically, it is unclear how independent worlds are capable of interacting. These interactions can be accounted for by identifying analogous developments in the forementioned fields. For example, in quantum field theory (QFT) we see a shift from a theory that takes individual particles as the basic constituents of reality to one that identifies particles as being excitations within a field. This theoretical shift suggests that *relata* are to be analyzed in terms of their relations. Similarly, both evolutionary psychology and biology make use of developmental systems theory (DST) to illustrate how both persons and species are not to be understood as enduring individuals, but are complex arrangements of interacting processes. Some extensions of the *Modern Synthesis* are consistent with these theoretical developments. For example, *epigenetic inheritance* provides a model for understanding how what is inherited undergoes modification during development; the germ line, the reconstruction of parental phenotypes, and niche construction are each capable of contributing to modification. Since inheritance plays a significant role in shaping an organism’s development, and the factors involved in allowing for inheritance to occur contribute to the organism’s development, the organism’s development is not a result of only what is inherited. In other words, development is influenced by more than a copy sequence.

There are two outcomes from considering epigenetic inheritance. First, epigenetic inheritance accommodates many of the developments from DST in suggesting that what a thing is is not simply a matter of its individuating conditions, but also the niche in which it is situated. This outcome provides insight to how we can extend evolutionary biology in a way that keeps track with contemporary developments in other fields. Second, calling into question the concept of a genome as a thing that is copied problematizes the idea that codes exist. This second outcome requires consideration from the code biologist’s perspective. I believe, however, that since epigenetic inheritance is an outcome of extending the *Modern Synthesis*, there may also be a way to accommodate the idea of a code in this extended framework.

This is what I set out to in this paper: Since a code is concerned with regulating how “worlds” correspond with one another, and correspondence is itself a dynamic interaction shaped by the features of the worlds that are interacting and the context in which they are situated when the interaction occurs, some dynamics of correspondence will need to be given. These rules did not originate from nothing, but are codified within the structure of the world that is responsible for shaping which interactions can be instantiated. This underlying structure of nature must itself be stable for reliable interactions to occur. Furthermore, once we understand the stable structure of reality being primary to its codes, codes are to be understood as stabilizing guidelines. In particular, the copying process itself modifies the codes since what is copied has the capacity to shift the structure of the world. For this reason, codes are themselves malleable during the copying process, yet provide the guidelines for how additional structures and organisms are to develop given those codes. The upshot of this discussion being that code biologists are able to accommodate contemporary developments while offering an explanation of how codes exist in nature.