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BOOK OF ABSTRACTS

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Dream Codes IV
Cradle of Meanings, Origins of Thought
The Dream as Research Vehicle

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Freud's trailblazing 1900 Dream book lifted the dream out of the soothsayer's hands situating it in the realm of legitimate scientific scrutiny. In fact, the dream in psychoanalysis is a prime specimen and empirical window into human unconscious mental processes, where meanings and cognition take shape.

Not only is the dream in clinical psychoanalysis an MRI of the dreamer's psychic structure, predominant current preoccupations and subjective formulations of these, but it also reveals formal configurations that provide hypotheses for research into the evolutionary progression of human language and mentation. By unveiling its two-tiered semiotic structure; decoding its pictographic grammar; identifying its four constitutive actions as the "mind's work," and establishing a dictionary for primary process forms of unconscious meanings, Freud provided an interpretive vocabulary for the dream's compositional expressions while also pointing to fundamental cognitive underpinnings: the dream is "another mode of thought".

Despite these clearly implied cognitive underpinnings in Freud's topographical and later structural models of mind, this contribution from psychoanalysis has not been adequately integrated theoretically or made publicly known. The psychoanalytic use and interpretive understanding of the continuous influence of the body's sensory-affective input on mind as well as through the metaphorical underpinnings of speech has gone largely ignored. Consequently emphasis on the pervasive presence of metaphor and metonymy in the underlay of human thought and language has come from the cognitive sciences, not psychoanalysis.

This presentation continues my inquiry into the infiltration of body in mind, from within the framework of a revised bio-semiotic model of mind (Aragno1991/2016), as it addresses the convergence of psychoanalysis with cognitive science. Most specifically I will trace how meaning-forms and cognitive-modes may be seen, decoded and understood, through dreams, in both Freud's topographical and structural models, as these predate and expand upon contemporary cognitive research.

In defence of Code Biology

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Various independent discoveries have shown that many organic codes exist in living systems and this has suggested a new theoretical framework where codes appeared throughout the history of life and gave specific contributions to that history. The objections to this theory have gone through all three canonical stages: (1) the theory is wrong, (2) the theory is right but not important, and (3) the theory is right and important but it has been known for a long time.

The objection that the Code theory is ‘wrong’ comes from the idea that even the genetic code is not a real code because it does not have the arbitrariness that is essential in any code. The very first model of the genetic code was the Stereochemical Theory, an idea proposed in various forms since 1954, which states that the relationships between codons and amino acids are determined by stereochemical affinities. This theory automatically implies that the genetic code is not really a code because its rules are the inevitable result of chemical reactions. It has taken a long time and much experimental work to overturn this belief, but eventually it has been shown in laboratory experiments that any codon can be associated, in principle, to any amino acid, and therefore that there are no deterministic links between them.

The objection that the Code theory is ‘*right-but-not-important*’ comes from the argument that the genetic code is but a component of the apparatus of protein synthesis, and once we know this apparatus we know all that there is to know about its code. In reality, there are many different apparatuses of protein synthesis in living systems, and their components are highly variable in different lineages; the ribosomes, for example, have average molecular weights of 2 millions in prokaryotes and 4 millions in eukaryotes, and their actual molecular weights change from species to species. In fact, the only thing that all apparatuses of protein synthesis have in common is the genetic code, and this tells us something important. It tells us that the rules of the genetic code are the great invariants of life, the sole entities that have been conserved for billions of years while everything else has been changed.

The objection that the Code theory is ‘*right-and-important-but-it-has-been-known-for-a-long-time*’ is the claim of Biosemiotics, the synthesis of semiotics and biology which has been advocated by Thomas Sebeok and his followers even since the 1980s. In reality, what Sebeok and his followers have proposed is the Peirce’s idea that semiosis is always produced by a process of interpretation whereas the Code theory maintains that that the genetic code was the result of coding, not of interpretation, because it has been the same in all living creatures and in all environments ever since the origin of life.

As a matter of fact, it has taken a split from Biosemiotics, in 2012, to give origin to Code Biology as a new independent field of research whose purpose, explicitly written in its

Constitution, is *“the study of all codes of life, from the genetic code to the codes of culture, with the standard methods of science”*.

How the glycomic code determines the cell wall storage function in seeds

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A Glycomic Code (GC) is thought to confer chemical diversity to cell wall structure, this being one of the features responsible for differences among cells and tissues. The GC generates semantics through the formation of composites (combination of different polymers) that display different chemical and physical properties. The GC determines, for instance, whether a given cell wall or cell wall polymer could be hydrolysed by enzymes, thus influencing plant defence and storage mobilization in plant systems. The existence of codes in polysaccharide fine structures supports the GC hypothesis. This is the case of xyloglucan, one of the main hemicelluloses of plant cell walls. The fine structure of storage cell wall xyloglucan extant in legume seeds has been studied, revealing the presence of molecular blocks that are combined to giving rise to molecular properties related to polysaccharide function. Xyloglucans are formed by unit-blocks composed of 4 glucose molecules branched with three xylose units. These constitutive blocks (Glc4Xyl3 - tetramers) may be branched by galactosyl and fucosyl residues in some positions of the oligosaccharide block. The seeds of one tropical legume species (*Hymenaea courbaril*) display another oligosaccharide family based on Glc5Xyl4 (pentamers) and its galactosyl branches. It has been found that tetramers (T) and pentamers (P) are combined in one single molecule in combinations that are not random, presenting the most likely domains TTPPTT. Altogether, this led to the proposition of the hypothesis that the polysaccharide possesses two encoded domains: hydrolysable (pexons) and cellulose-binding (pointrons). Here we present further evidence that the fine structure of seed storage xyloglucans from legume species display non-random combinations of oligosaccharide blocks encoding structural domains that determine the mode of hydrolysis by Xyloglucan Endo-Glucanase (XEG) and beta-galactosidase (BG) attack to the polymer. Xyloglucans from seeds of the legume tree species from the tropical forests, *Tamarindus indica*, *Copaifera langsdorffii* and *H. courbaril*, were subjected to “restriction-mode” endo-hydrolysis with XEG to produce polymers with higher combinations of blocks. These polymers were treated with BG to find out the sequence of blocks in the molecules. Our results suggest that seed storage xyloglucans display encoded information, with domains that are more or less hydrolysable (pexons) or more or less prone to bind to cellulose or itself (pointrons). In the case of seed xyloglucans, the GC seems to be important in the determination of biological function during tree seedling establishment in tropical forests.

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Arms and the mollusc: Encoding biomineralization

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More than half a billion years ago in the Cambrian, there began an evolutionary arms race between molluscs and their predators, in which molluscs developed armour in the form of a biomineral exoskeleton — a shell — to avoid being eaten by predators that were developing jaws and other novel means of devouring them. The mollusc fabricates multiple layers of shell, each of a particular microstructure of a composite between an inorganic and an organic phase, which are the end result of over five hundred million years of co-evolution with increasingly deadly predators. Molluscan biomineralization is an excellent case in which to study how a biological process produces a complex structure, because the shell is constructed as an extracellular structure in which all construction materials are passed out of the cells to self-assemble outside the cell wall. We take what is known of the development of multilayer composite armour in the form of nacre (mother of pearl) and the other strong microstructures with which molluscs construct their shells, together with what is known of the evolution of these structures in geological time. We put alongside this knowledge the most recent data for the biomineralization genome — the conchome — and the biomineral proteome. We bring together all these data to begin to disentangle how much of the structure is owing to self-organization and how much to genetic programming, in order to make a first guess at the genomic assembly complexity; at answering the question: how much information is necessary to encode biomineralization?

Mezo-scale dynamics of the semantic space

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Culturomics, the analysis of frequency changes of discrete semantic units of human language over historical time, has shed light on many intriguing social and cultural phenomena in the recent years. Here we propose a step towards a more comprehensive theory of semantic dynamics by defining different types of semantic interactions between these units (i.e., words, or more preferably, lemmas) based on their co-occurrence statistics obtained from large text corpora. In particular, we focus on two types of interactions: one is of cooperative nature, analogous to syntagmatic relations between words, and the other is a competitive one similar to paradigmatic relations. In order to understand global mechanisms governing semantic changes, we regard densely interacting clusters of units as basic building blocks of the semantic space. This allows us to focus on structural properties of these clusters, such as their size, coherence, or susceptibility to external disturbances. Furthermore, by using clustering algorithms that permits the death, birth, merge and split of the clusters, we are able to determine the types of interactions that are indeed realized between clusters in the function of their inner structure. This modeling scheme also has the practical advantage of being insensitive to actual wordforms, making cross-linguistic comparisons and universal, language-free modeling possible.

Discrepant codes of social identity

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Two competing theories deal with the pattern of social identity in contemporary Western society. According to constructivism identity is matter of negotiation between actors who are in need to reduce uncertainty and look after a place in the world devoid of meaning.

Essentialism is the view that for identity there is set of physical, biological and cultural attributes of the actors which are necessary to be recognised by in-group as well as out-group members. The paper hypothesises that the contradiction between the two theories is apparent. The paper will analyse the text of the memoirs titled “Maskerado. Dancing around Death in Nazi Hungary” written by Tivadar Soros about his adventures in Budapest during the German occupation between March 19,1944 – January 18, 1945, and the subsequent Soviet Occupation. By analysing the relevant episodes taken from the text the paper will show that in order to survive how Soros did skilfully manipulate the codes of his identity interacting with in-group and out-group members in the hostile political environment.

Analyzing Molecular Codes in Metabolic Networks

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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 possess 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. In this contribution we investigate metabolic networks with respect to the molecular codes they contain. Due to the networks' size, our exact algorithms are not sufficiently efficient. Therefore we introduce a novel heuristic search algorithm that can be applied to networks of arbitrary size. The basic idea is to sample small, closed, and connected sub-networks sufficiently large to contain a molecular code; and then to apply our exact algorithm on the sub-network. When applying the new method to models of bacterial central metabolism we found several molecular codes. That is, the relation between some metabolites can be "switched" by the presence of other metabolite. However the meaning of this observation remains unclear. We will discuss it from different perspectives and in particular what it means that the reactions of the metabolic network are catalyzed by enzymes.

The poetics of cell attachment

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Cell-matrix adhesion complexes (CMACs) are responsible for cellular attachment to the extracellular matrix (ECM), they are mainly composed by integrins, α/β heterodimers that bind selectively different ECM components through their extracellular domains acting as receptors. Upon ECM binding the cytoplasmic tails of integrins will interact with a wide range of recruited factors that regulate integrin clustering in the cell membrane; and also activate signaling pathways that will provide a physical linkage between activated integrins and the microfilament system to be remodeled during cell migration. Ultimately CMACs work as functional protein networks controlling cell migration through the continual rearrangement of both ECM adhesion, and Actin polymerization. In the present work we shall examine some attempts to conceptualize “cell migration” in the recent specialized literature; they introduce the notions of hierarchic organization into levels i.e. molecular, sub-cellular and cellular and describe an informational flow of increasing complexity versus decreasing number of entities, between these levels. We shall discuss the particular example of endothelial cells engagement into angiogenesis (the making of new blood vessels in adult vertebrates), an activity that requires intense CMACs’ remodeling, to argue that cell migration is also organized into semiotic dimensions. Beyond the syntactic level – illustrated in that case as the specific recognition of discrete ECM motifs by integrin heterodimers – we shall reach the semantic and pragmatic levels by bringing into light the dynamics of some “word games”, e.g. Lewis Carroll’s doublets; and magic squares. In such poetic games the synthetic transformations subjected by the words have to deal with semantic rules, but are ultimately dictated by meaning, as concrete pragmatic constrains. We postulate that figures of language and structural features which are characteristic of poetic writing have direct correlates in the cell/cell and cell/matrix recognition processes.

Ecoacoustic codes and Ecological complexity

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The discovery of many organic codes at the cellular and multicellular levels has led to the new research field of Code biology and has suggested a new approach to the problems of evolution. In ecology, however, the application of the code approach has remained a controversial and difficult issue, mainly because codes in ecology do not have a direct physical substrate as they have in biology. The presence of ecological codes can however be studied by simulations and functional models. We define ecoacoustic events (represented by geophonic, biophonic, and technophonic sounds and their combinations) all the inclusive portions of the soundscape where we recognize distinct roles and/or meanings. Their identification allows us to decode the ecosemiotic complexity of the soundscape, and for this we have developed a model called Ecoacoustic Event Detection and Identification (EEDI) based on the combination of three ecoacoustic indices. EEDI simulates the presence of a community of acoustic events that represent the basis for an acoustic code hypothesis.

EEDI is articulated in three successive steps:

- 1) Processing acoustics files by adopting the Acoustic Complexity Indices (ACIf and ACIt).
- 2) Combining ACIf with its temporal evenness (ACIf_e) and the frequency evenness of ACIt (ACIt_e) in an Euclidean space, which we call Ecoacoustics Event Space (EES), after the assumption that the value of ACIf and ACIt found in a temporal interval (e.g., one minute) may have a different temporal e frequency distribution inside the sampled time. For instance, heavy rains are characterized by high values of ACIf, ACIf_e and ACIt_e, while background isolated calls of birds generally are characterized by low values of ACIf and ACIf_e but by moderate of high values of ACIt_e (f.i. the alarming call of a European robin (*Erithacus rubecula*)). The application of empirical thresholds to the metrics can restrict the identification process to events of interest.
- 3) Labelling when possible every typology of events and searching for significant correlations between the labelled events and a library of classified acoustic signatures (ACIt) to complete the identification process of the acoustic components inside each event.

There is significant evidences that when a soundscape is analyzed by EEDI, recurrent patterns emerge assuming that species, at least for acoustic issues, interact with discrete recurrent phenomenological entities. This is the premise of an ecological-code-oriented interacting environment and mechanisms.

Strong comma-free codes and their role in the formation of comma-free ones

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It is common knowledge that Crick et al. proposed the notion of comma-free codes to simultaneously solve the problem of amino acid coding and that of frame maintenance. It is also well-known that so far there has been no evidence found of comma-free codes used in nature. At the same time, there are some grounds to believe that the modern circular codes detected in nature might have originated from ancient comma-free ones. For instance, the so-called primeval RNY-code that is thought to be one possible ancestor code is comma-free even in every possible reading frame (CF3-property).

Based on a recent approach using graph theory to study circular codes (Fimmel et al., 2016), a new subclass of comma-free codes, called strong comma-free codes, is identified. These codes detect a frameshift during the translation process immediately after a reading window of at most two nucleotides, i.e. they have even stronger error-detecting properties than “general” comma-free codes. According to our results, strong comma-free codes can be seen as evolutionary predecessors of comma-free codes. For instance, the primeval (self-complementary!) RNY-code mentioned above is of size 16 and can be formed as a union of two strong comma-free codes of size 8, complementary to each other. This fact might indicate that during the evolutionary process the RNY code was created from a more ancient strong comma-free code by complementation. One more interesting biological fact about strong comma-free codes is that each amino acid in a standard genetic code is coded by at least one strong comma-free code.

Revisiting the Ribotype

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In 1981 Marcello Barbieri introduced the concept of the ribotype as comprising all RNAs and ribonucleoproteins of any organic system [1]. He also introduced the term ribosoid to indicate a molecule made of RNA or RNA and peptides; this allowed an alternative description of the ribotype as the collection of all ribosoids of an organic system. The ribotype has an ontological status on par with that of the genotype and phenotype, so that the ribotype theory substitutes the genotype-phenotype duality with the genotype-ribotype-phenotype triad, in which the ribotype translates genotype into phenotype. Whereas Barbieri was quite clear about what constitutes the ribotype, others have equated the ribotype with the ribosome itself [2,3], or described the ribosome as the “interpreter” between DNA and protein [4] or as a Von Neumann universal constructor [2] that can produce copies of itself. All these other statements are highly problematic, if not wrong.

I intend clearing up this matter by using a category theoretical model of the cell couched in terms of sets and mappings. The model is based on a description of whole cell biochemistry in terms of three sets of efficient causes that form a hierarchical cycle, which is closed to efficient causation [5]. Enzyme-catalysed covalent catalysis (efficient cause 1) leads to the production of non-functional polypeptides that are activated to functional enzymes and transporters by the supramolecular processes of folding and chaperone-assisted self-assembly, made possible by an intracellular milieu (efficient cause 2) with the appropriate properties (pH, ionic strength, electrolyte composition, chaperones). In turn, the correct intracellular milieu is maintained by processes such as membrane transport of electrolytes, metabolism and macromolecular crowding (efficient cause 3) that is already accounted for by efficient causes 1 and 2. Decomposing the mappings representing the three efficient causes into their constituent processes creates a diagram of mappings in which a number of concepts become explicit: the exact nature of the ribotype and its relation to genotype and phenotype, the role of coding, Rosen’s metabolism-repair relation, and the role of the ribosome within a set of relationships that is analogous to a Von Neumann universal constructor.

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The “code of the codes”: a classification and evaluation of approaches to the origins of the genetic code

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The origin of the genetic code and translation is a “notoriously difficult problem”. In this survey we present a classification of hypotheses and we critically assess them. The relevant dimensions are: assignment of amino acids to triplets before or during the origin of translation, with or without coding stereochemistry, with and without selection for the reduction of transcriptional and translational errors.

A host of experiments that could (in)validate some of the models is suggested. We focus especially on the coding coenzyme handle (CCH) hypothesis. The CCH suggests that amino acids attached to RNA handles enhanced catalytic activities of ribozymes. Alternatively, amino acids without handles or with a handle consisting of a single adenine, like in contemporary coenzymes could have been employed. All three scenarios can be tested in *in vitro* compartmentalized systems. Randomized RNA is encapsulated in water droplets with enzymes for their replication and a substrate. The droplets are selected for conversion of the substrate. In order to assess the enhancement by the cofactor we should add either (a) single amino acid; (b) amino acid attached to a small triplet bearing handle; (c) amino acid attached to an adenine; and (d) nothing for control. Experimental support for the CCH requires that the ribozyme evolved in option (b) outperforms the others, or at least the same efficiency is reached faster in evolution.

Associative learning and epigenetic inheritance of a neural code: Theoretical and code biological problems

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One of the key questions of code biology concerns the emergence of new organic codes during evolution. In this presentation, we propose that an important aspect of this problem can be approached in the light of recent studies in neuroepigenetics, on the one hand, and its history and theory in the field of evolutionary physiology of associative learning, on the other. Recently, these two areas have begun to converge, with first direct evidence now indicating the possibility of transgenerational epigenetic inheritance of conditional associations in the mammalian nervous system (Dias et al 2014; Szyf 2014). This may serve as an interesting example of evolutionary code-making, where the molecular mechanisms underlying arbitrary associations between stimuli are found to involve lasting changes in gene expression that may be transmitted epigenetically across generations (Dias et al 2014; Szyf 2014), and which, given recent findings and analysis, may become further stabilized and assimilated into the genome over subsequent evolution (Noble et al 2014). Here, we show how this would offer an interesting and so far overlooked confirmation of earlier research carried out in the field of evolutionary physiology, primarily by one of I.P. Pavlov's leading students, P.K. Anokhin, and his colleagues (Anokhin 1974), but also eminent physiologists of the time, several of whom offered arguments for the possibility of inborn reflexes representing evolutionarily later, specialized and reduced forms of conditional reflexes, from which they may be derived (Ukhtomsky A.A., Biryukov D.A., Kogan A.B., et al), with interesting, seemingly intermediate cases between the two found in nature (Anokhin 1974: 17-24). It is proposed that these early investigations were, possibly prematurely, discarded under the growing dominance of modern synthesis (cf. Suvorov et al 1991), notwithstanding the ecological, developmental, and theoretical arguments in their favor. The latter may deserve renewed attention given the current re-emergence of physiology and neo-Lamarckian modes of inheritance to the center stage of evolutionary biology (Noble et al 2014), and directly compatible empirical findings (Dias et al 2014). Incorporating these aspects may confirm some basic claims of the code biological interpretation of life, in particular, by showing how associative rules may become historically established to form stable, if not irreversibly assimilated, neural codes. While admittedly provisional, this may offer a new window for understanding the morphofunctional evolution of the nervous system, and specify the role of associative learning as a possible driving factor of metazoan evolution (Ginsburg et al 2010), similarly as this has been shown for microorganisms (Mitchell et al 2009), and may be relevant even for plants (Gagliano et al 2016).

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How prokaryotes “encode” their environment

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An important issue related to code biology concerns the cell's informational relationships with the environment. As an open self-producing system, a great variety of inputs and outputs are necessary for the living cell, not only consisting of matter and energy flows but also involving information flows. Whether those information flows may configure genuine “codes” either globally or regarding important environmental constellations of stimuli is at the stake. The analysis herein will involve two basic aspects. On the one side, the structure of the prokaryotic signalling system itself, with all its variety of environmental signals and component pathways (what has been called the 1-2-3 Component Systems), including the role of a few second messengers which have been pointed out in bacteria too. And in the other side, the gene transcription system as depending not only on signalling inputs but also on a diversity of factors: from metabolic outputs, to sigma factors, to house-keeping systems, to channels and transporters, etc. In spite of this remarkable degree of complexity, actually the gene expression system of bacteria is highly systematic in its hierarchic organization and has been compared to computer operating systems. So, there is room to explore the organized and systematic convergence of stimuli from different signalling paths “encoding” integrated aspects of the environment. The specific life cycle of the bacterium will be the essential factor motivating the classes of convergence to be found. After inspecting the most relevant 1CS, 2CS, and 3CS and the putative second messengers, as well as the strategic role played by sigma factors, and taking into account the life cycle of different bacteria (though we will mostly focus on the molecular apparatuses of *E. coli K-12* strain), we will conclude with a nuanced positive response. Amidst the continuum of energy, matter, and information flows, there seems to be evidence for robust signalling codes, mostly established around the arrangement of life-cycle stages and large metabolic changes, in the relationships with conspecifics (quorum sensing, colonies, biofilms), in the multispecies relationships within microbial ecosystems (commensalism, cooperation, predation), and in the interaction of parasitic bacteria with the physiological milieu of the host (virulence switching). Along that way of thinking, we are actually extending Tomkins' “metabolic code theory,” as outlined for the origins of prokaryotic symbolic communication more than four decades ago (1975), now enlarging it towards a bunch of new functional realms. The extent to which different definitions of coding, more rigorous or less, may intervene in the characterization of the coding spectrum of prokaryotic signalling will be discussed finally.

Hidden meanings of the past: Decoding the Chernel

Mónika Mátay

During the past decades historians posed radical, self-reflective questions about their own academic activities and also their relationship with ever existing reality. Among others, Alan Munslow questioned to what extent history, as a discipline, can accurately recover and represent the past through the form of narrative? Along heated debates on the role of the historian and language as a transmitter between the past reality and the present, it also became uncertain to what extent the narrative can be adequate for historical explanation? Amidst the historiographical turmoil of the late 20th and early 21st century, the traditional positivist construction of historical facts became target of harsh criticism.

All of these debates warn us against simplifying the historian's task when he/she is involved in reconstructing or rather decoding the past and explores hidden and unknown signs and meanings. Since the past is a changing present, and interpretations of the past are subjective and highly dependent on the decoder, decoding can never be objective and a procedure that is finished. Just the opposite is the case! Considering all of these circumstances, in my lecture I shall make an attempt to learn about the buildings and the people who ever inhabited them at our street, Chernel, and most importantly, our house, the Sigray palace. Although the history of the street originates in the Middle Ages, it only became a more significant part of Kőszeg during the first decades of the 18th century due to aristocratic and noble families who moved there. The beautiful palaces hide many stories about love, betrayal, imprisonment, loneliness, spying and even fortune telling. While putting the individual stories into wider political, social, and cultural context, I shall demonstrate the procedure of the decoding itself and also my specific questions which provoked the answers.

Arithmetic regularities inside the standard genetic code as potential relics of a physicochemical mechanism involved in direct codon/amino acid interactions

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Revealing of arithmetic regularities inside the standard genetic code (SGC) [1] was supported in various ways [2,3]. These regularities are distinguished by at least five unusual features and characteristics: 1) relevant nucleon sums, obtained for the most prominent divisions of SGC, are divisible by the decimal number 37; 2) SGC degeneracy pattern, in the form of Rumer's division on the fourfold and twofold degenerate codon halves and their associated amino acids [4], most consistently reflects the 37 divisibility; 3) arithmetical regularities are almost exclusively related to sets of molecules, not individual molecules or molecule pairs of amino acid and its cognate codon; 4) to some degree, arithmetical regularities are valid both for free molecules and molecule residues; and 5) SGC consistently reflects the 37 divisibility compared to nonstandard genetic codes, since most of the changes in nonstandard codes have resulted negatively in terms of the nucleon regularities (e.g. *only* SGC fulfils exact correlation between the code degeneracy and the 37 divisibility). A deeper insight in some mathematical properties of the number 37 (its relation to cyclic structures and regular multiplying [1,3], self-similar nested structures, decimal scaling, and discrete space [3]), reveals their compatibility with some concepts of the complex systems theory (e.g. interlocking feedback loops, critical transitions, distributed networks, and top-down causation), and thus potentially provides clues for understanding the mentioned features and characteristics of the arithmetical nature of SGC.

The *dual* degeneracy pattern of SGC could be a result of its hierarchical organization as a nested code which was determined by dual scaling constants [3]. A nucleon tuning of SGC on the level of molecular *sets*, including those determined by the code degeneracy, is compatible with the view that a chaotic situation in the primitive cell would have rendered ambiguous codon assignments common [5]. This possibility that groups of related amino acids were encoded by groups of similar codons (the merging of semantically coherent groups) also provides the basis that the concepts of ambiguity, degeneracy, and load minimization can be considered in the common framework [6]. Continuity and some scaling property of arithmetical regularities at both the free molecule and molecule residue level could reflect an existence of some relatively universal and complex physicochemical mechanism involved in direct codon/amino acid (group) interactions [3]. This mechanism would act *non-locally* as a background (shadow) information system (a top-down causation in the terms of hidden dynamical variables) [7] or as a global regulation through extended critical transitions (avoiding of hidden variables) [8]. Also, such mechanisms could be environmentally facilitated, what supports a mineral-mediated origin of SGC [9]. The *uniqueness* of SGC in regard to its fidelity to the 37 divisibility supports the hypothesis that the selective driving

forces acting during the emergence (ancient phase) and evolution (modern phase) of the genetic code are different [10], what probably most strongly suggests the mediation role of mentioned global (background) mechanism in emergence of SGC.

The phenomenon of arithmetic regularities inside SGC is probably the best defined case of top-down and bottom-up causation intertwining, and its further exploration could enrich our knowledge not only about biology, but physics as well.

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Angelorum Laus / Traces of Angelic Singing in plainsong and Renaissance motet

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The notion that angels sing has been part of our concept of music since the Middle Ages, which is derived from the much older concept of the Music of the Spheres. This fully empirical approach to the subject is led by the numerous singing experience of the researcher who is an expert in early vocal music. The idea that there must be a „hidden consensus through time and space”, a special compositorial code for angelic singing was surfacing from time to time in exceptional musical forms and solutions that seemed always to come up at the mention of the angels.

A coding perspective of adaptive immunity

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The adaptive immune system of vertebrates has long been recognized to be a cognitive system, capable of learning and complex decision-making. We argue that the way information is coded in the immune system is a key factor in this capacity.

The classic unit of vertebrate adaptive immunity is the T or B lymphocyte that bears a unique cell surface receptor capable of binding (“recognizing”) short protein motifs. The identity (information content) of each cell is determined by the specificity of its receptor, the type of (immune) effector function it has been programmed to perform, and the anatomical site(s) that it has access to. Both T and B cell receptors are highly diverse; they are generated by a stochastic somatic mechanism during the maturation of the lymphocytes, and are then stably inherited through the division of mature cells. The process of “clonal selection” can both eliminate and greatly amplify lymphocyte clones based on the specificity (and, ultimately, usefulness) of their receptor: this process has been at the centre of thinking about how information is being stored and manipulated in vertebrate adaptive immunity, and narrow (highly selective) targeting is broadly regarded as a key advantage of this system over mechanisms of “innate” immunity.

We argue that, while narrow specificity indeed contributes quantitatively to the high information density of the immune system, there is also a qualitative dimension, arising from associative coding, that is crucial for the cognitive capacity of vertebrate adaptive immunity. In light of the latest empirical findings, we discuss complementary mechanisms and possible pathways of associative coding in the system, and draw parallels with structural motifs and learning processes in the nervous system. Finally, we present a comparative survey of various systems of adaptive immunity, explaining how and why the cognitive capacity afforded by associative coding appears to be restricted to the lymphocyte based immune system of vertebrates.

Time and space as biological constructions

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Whatever we can say, we say in rhythms of symbols – e.g., words, spoken or written, and mathematical symbols. Physicists and engineers extend our capabilities for symbol handling by building symbol-handling machinery, notably digital computers and digital communications systems such as the Global Positioning System (GPS) and the Internet. Symbols acquire meaning in the context of agents that recognize them, as when you recognize a mark that I have written on paper. Although largely overlooked in physics, what a mark symbolizes to us or to other agents is unpredictable on the basis of measurement and calculation.

Without admitting any explicit notion of an agent, the language of quantum theory implies a role for an unpredictable symbol-handling agent. In developing concepts of time and space and in the implementation of coordinates, physicists as agents relate evidence from the workbench expressed in symbols to explanations on the blackboard, also expressed in symbols. While evidence rules out many candidate explanations, we proved that whatever evidence may be on hand still fits an infinite variety of inequivalent explanations. Thus, a physicist's choice of an explanation requires a guess that reaches beyond what can be measured or calculated. This inevitable unpredictability in symbol handling demonstrably affects the material world with which people and other organisms interact. So far, this unpredictability in the role of symbol-handling agents is rarely acknowledged in physics, with its focus on particles and fields.

To accept agents and symbols into the discipline of physics is to see mechanisms, especially clocks, not in isolation but as adjustable tools built and used by agents. We model a symbol-handling agent in terms of mechanisms, beginning with Turing machine as a conceptual expression of computation. We modify the Turing machine to communicate symbols with other such machines. Implicit in the concept of a Turing machine is a single clock. To communicate, an agent must deal not only with its own clock, but also with the rhythms established by the clocks of other agents with whom it communicates. Communications between clocks requires that agents must mesh their rhythms of operation, something that takes place between two people in conversation. A simpler meshing is found in mechanized agents. We call this meshing of rhythms logical synchronization and display its features. Symbols are discrete, digital; however, maintaining logical synchronization requires something analog, idiosyncratic, and unpredictable, beyond symbols and their logical manipulations.

In this report, our main contribution is to recognize that logically synchronized rhythms of symbols need not be seen as taking place in some externally supplied “space and time,” but

instead are the raw material out of which physicists construct time, space, and spacetime. We hypothesize that all living organisms employ logically synchronized rhythms of symbols. We invite collaboration to explore, in a variety of contexts for people and other living organisms, the construction of means of regulation of motion using rhythms of symbols that differ from those used in physics. Accompanying such initial study, we would like to see the development of mathematical expressions of logical synchronization applicable to more complex cybernetic systems than those we discuss here.

Geno-logical coding, inherited properties and algebraic biology

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The genetic code of amino acid sequences in proteins does not allow understanding and modeling inherited processes such as inborn coordinated motions of living bodies, innate principles of sensory information processing, quasi-holographic properties, etc. To be able to model these phenomena, the concept of geno-logical coding, which is connected with logical functions and Boolean algebra of logic, is put forward. The lecture describes basic pieces of evidence in favor of the existence of a geno-logical code, which exists in parallel with the known genetic code of amino acid sequences but which serves for transferring inherited processes along chains of generations. These pieces of evidence have been received due to the analysis of symmetries in structures of molecular-genetic systems. The analysis has revealed a close connection of the genetic system with dyadic groups of binary numbers and with other mathematical objects that are related with dyadic groups: Walsh functions (which are algebraic characters of dyadic groups), bit-reversal permutations, logical holography, spectral logic of systems of Boolean functions, dyadic spaces, etc. These results provide a new approach to mathematical modeling of genetic structures that uses mathematical formalisms known from technological fields of noise-immunity coding of information, binary analysis, logical holography, digital devices of artificial intellect. Some opportunities to develop algebraic-logical biology are opened.

E. Schrödinger (1944) noted: “from all we have learnt about the structure of living matter, we must be prepared to find it working in a manner that cannot be reduced to the ordinary laws of physics». For comparison, the enzymes in biological organisms work in million times more effectively than catalysts in the laboratory. What makes the enzyme in the body for 1 second, a catalyst in the laboratory can make only for 200 thousand years. We believe that such ultra-efficiency of enzymes in biological bodies is defined not only by laws of physics, but also by algebraic-logical programs of the geno-logic coding, and therefore - in accordance with Schrödinger - this ultra-efficiency cannot be reduced to the ordinary laws of physics.

As known, systems of artificial intellect cannot be constructed without usage of mathematical logic. Our algebraic-logical approach allows to consider living bodies and their parts - including the genetic systems - as intellectual substances, that communicate with each other to provide coordinated mutual functions. All physiological systems and various biological codes are inherited and become parts of the whole single organism. It seems that many of inherited biological codes interact with each other and could be modelled on the general base of mathematical formalisms of the geno-logical coding.

G. Boole created his mathematics of logic to describe the laws of thoughts: his book was titled «An Investigation of the Laws of Thoughts» (1854). Our doctrine of the geno-logic coding shows some evidences in favor that our inherited body is created on the basis of the

same laws of logic, on which our thoughts are constructed (the unity of the laws of thought and body).

The described results have been received in the frame of the so called «matrix genetics» [Petoukhov, see publications at <http://petoukhov.com/>]. Matrix genetics is based on representations of ensembles of genetic elements in forms of tensor families of mathematical matrices. It is developed to create new approaches of mathematical modeling in bioinformatics. Matrix genetics has some intersections with matrix mechanics by W. Heisenberg and matrix logic by A. Stern.

Petoukhov S.V., Petukhova E.S. Symmetries in genetic systems and the concept of geno-logical coding. - *Information*, 2017, **8**(1), 2 (online - uploaded 25 December 2016), <http://www.mdpi.com/2078-2489/8/1/2/> PDF Version: <http://www.mdpi.com/2078-2489/8/1/2/pdf>

Codes: A historian's perspective

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For a student of the humanities and social sciences the word code can refer to several concepts. It can mean patterns of behaviour both morally (ethic code, code of honour) and formally (code of conduct, dress code) but can also be used in a strictly technical sense as a form of secret communication (Da Vinci code).

This paper will focus on two further usages of the word. First, how concepts can function as codes for certain values. In spite of great analytical efforts by scholars in the humanities and social sciences to present the complexity of certain situations, personalities or ideas, their analytical concepts can be used and abused for political-ideological purposes and this way a carefully developed analytical concept becomes just a code. I shall deal with two concepts from this perspective: feudalism and progress.

The other usage is decoding the meaning of seemingly neutral words in various situations, here, among others I will present some examples of communist political rhetoric.

Finally, I will refer to a paper by Elemér Hankiss as a daring attempt at combining the approaches of numerous disciplines to decode the way perfumes shape body and soul.

When two worlds collide: A prequel to proteins, and a sequel to RNAs

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The origin of translation is still a mystery to be solved. The most supported hypothesis of modern life's prelude is the RNA world, where several main life-functions were filled by RNA-enzymes (ribozymes). Yet, in our cells, the majority of metabolism is maintained by protein enzymes. We know a lot about how present genetic information is translated into peptides. We also know an increasing amount about how the genetic code underlying translation could have evolved. But the full evolutionary path leading from the RNA world to protein utilizing cells is unclear.

There are assumptions, that present day protein enzymes could have been superior to ribozymes. Indeed, this can be true. However, mRNA – coding our modern proteins – was not yet available. Evolution has no foresight; therefore the transition cannot be explained with the distant advantages of complex protein enzymes. We really need a scenario with the proximal advantages of peptides, explaining the stages of peptide synthesis step-by-step, but most importantly: the first steps.

One way to tackle this problem is to determine the function of the first peptides, which could not be enacted by ribozymes. Only those amino acids appearing early in the genetic code should have been used: valine, alanine, aspartate and glycine. We look at amino-acid frequencies of various peptide functions examining (1) what catalytic assistance could these amino acids give to ribozymes, (2) if these oligomers could have served as scaffolds for ribozymes, and (3) if they could have facilitated transport through lipid membranes.

Based on the results, we argue that active centres containing simple amino acids could have been advantageous for an RNA-organism, principally in the case of aspartate. Furthermore, we show that transmembrane regions and ribosomal proteins have high valine, alanine and glycine frequencies, concluding that functional analogues of the aforementioned groups could have formed at the dawn of translation. The appearance of peptide synthesis was followed by a functional radiation, where amino acids and peptides helped the ancestral organisms in far-reaching tasks.

The cultural linguistic code

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For over thirty years I have been researching the origins of language by means of an original and innovative method. It consists of considering oral articulations, which produce phonemic sounds, as informative gestures and expressions of a visible-expressive code that preceded the use of phonetic codes. The meaning expressed through each of these articulate gestures was identified through research-responses provided by two select sample groups of psychotics chosen because of their greater permeable accessibility to the collective unconscious. In this sense the application of phonemic sounds, that is ‘ words’, are no more than representative or substitutes of the use of pre-articulate oral-facial gestures used by pre-sapiens to express their informative intentions. Using this method I have published three books in which are analyzed precisely and systematically the inter-relationships between consonants in words of Indo-European origin –that is the roots of these words– discovering that words sharing common root-consonants do indeed express part of their current meaning in correspondence with the original meaning of the archetype. The projection into objects of these pre-articulate gestural meanings denotes them by means of mediatory metaphors and analogies, this appearing to be the reason for the variety of languages, since diverse peoples will use different metaphors for similar objects. We examined over twenty languages in relation to this generalized cultural code model, founded on biological reactivity to conditions in reality, to advantage given its extensive informative use.

Conservation of information in small organic catalysts is the key to understanding life emergence and to produce artificial life

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Thermodynamically, living beings can be described as dissipative structures, systems in disequilibrium that maintain a reproducible steady state along with combustion reactions, vortices and convection cells. Autopoietic model described life as chemical machines able to produce its own components and boundaries. However, by focusing in metabolism as the sole fundamental aspect of life, the autopoietic model failed in recognizing evolvability as another critical property of living beings, without which the impact of life on the planet would be negligible. To evolve, autopoietic systems must be able to convey information to its offspring. But what is information? Only polymers like DNA can store information? Information is a key concept linking biology, psychology and technology. Investigations on how information is apprehended by knowing subjects have made great advances since Plato until the recent advances in artificial intelligence. However, the most relevant step towards the understanding what information is came from engineering. Concerned with the problem of quantification of information, engineers defined information as a decision between possibilities. As a result, the binary unity or bit (one decision between 2 possibilities) is the smallest amount of information. Molecular biologists quickly incorporated the concept in order to describe the relations amongst monomeric sequences of DNA, RNA and proteins. However, the concept of molecular information was frequently taken as 'a useful metaphor', rather than a real feature of biopolymers. Condensing the thermodynamic and kinetic knowledge life can be defined as a dissipative structure that maintains its steady state by reproducing useful compounds as catalysts and membranes. But it is only another way to describe autopoiesis. What autopoiesis does not contemplate is that the carbon skeletons, hydrogens and heteroatoms of organic compounds can be arranged in several different ways, such that the specific arrangement of atoms from a given molecule (the useful one), constitutes information. By being able to reproduce the specific compounds, living beings produce and conserve information, a distinction from autopoiesis I stress by the term semiopoiesis. Like this, besides the biopolymers, small compounds also contain information and organocatalysts are able to conserve such information by catalyzing chemo-, regio- and enantioselective reactions. This features of organocatalysts leads two main consequences. Firstly, organocatalytic micelles may have worked as primitive repositories of the genetic information at the emergence of life, before the emergence of enzyme and ribozyme polymers. Secondly, organocatalytic micelles can be a platform to artificial life, nanorobotics and programmable materials with applications that go from artificial photosynthesis (as repairing systems to photosystems damaged by photodecomposition) to production of self-healing and self-building products (as self-healing

coatings for reactors, spacecrafts and other environments that even synthetic cellular forms of life cannot survive).

Bridging code biology and biosemiotics

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Code biology needs biosemiotics to define signs and meanings and to ground the phenomenon of coding in biological function and evolution, whereas biosemiotics needs code biology to abandon mind-centrism and recognize the existence of sign processes at the molecular level in living cells. Codes play an important role in life because they represent lower-level signaling and regulation in organisms, especially at the molecular level. Life has started from primordial molecular codes; and thus, if biosemiotics claims that life and semiosis are coextensive, then codes should be recognized as a special primitive case of semiosis, or *protosemiosis*. In my talk I explore how to bridge code biology with biosemiotics and clarify the terminology that may facilitate of a dialogue. Peirce's triadic sign relation is not relevant for protosemiosis, and thus we need to accept a broader notion of sign, as a tool used by goal-directed agents to initiate or regulate their own actions or actions of other agents. Barbieri's theory of organic codes follows the tradition of structural linguistics, where language or communication is described as a formal system with internal relationships. Such system is viewed as a stand-alone object without considering agents, who may use it or not. This structural methodology should be complemented by the *dynamic approach* where signs and their meanings emerge and change at the evolutionary and/or ontogenetic time scales. Code as a mapping of signs to their immediate meanings is not sufficient to explain these changes; it should be combined with information about the remote meanings that participate in the autopoietic closure of reproducing organisms or agents at other levels (e.g., molecular complexes, cell organelles, colonies, and consortia). For example, rules of the genetic code do not explain the pathways of genome evolution, which include the emergence of DNA methylation, binding of transcription factors, chromatin modifications, as additional sign relations. Studying the evolution of codes requires the theory of agency which is being developed in biosemiotics.

Self-complementary circular codes and their error-detecting window

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Self-complementary circular codes have been found in large populations of genes and are assumed to play an essential role in maintaining the reading frame during the translational process in the ribosome. In this talk we present recent results obtained by using a graph-theoretical approach developed in (Fimmel, Michel and Strümgmann, 2016). The directed graphs associated to circular codes are acyclic and we prove that the length and structure of a longest path in such a graph completely determines the *error-detecting window* of a maximal self-complementary circular code. By error-detecting window we mean the number of consecutive bases that have to be read (at any position) in a sequence composed of codons from our code in order to determine the correct reading frame.

Firstly, it is shown that a code X is self-complementary if and only if its graph $G(X)$ has a self-complementary set of vertices and for any vertex v the outgoing degree $d^+(v)$, i.e. the number of edges that start in v , equals the ingoing degree $d^-(c(v)^r)$ of the reversed complemented vertex $c(x)^r$, i.e. the number of edges that end in $c(x)^r$. Secondly, it is shown that the longest path in a graph of a maximal self-complementary circular code is either 4, 6, or 8 and the reading frame is therefore either 8, 13, or 14 bases.

[1]Fimmel E., Michel Ch. J., and Strümgmann L.: n-nucleotide circular codes in graph theory, *Phil. Trans. of Royal Soc. A*, **374**: 20150058, 2016

Deciphering Genocide – Addressing the question: □ What makes genocide possible?

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The cultural anthropological approach of genocide tries to break away from the legal terminology, and stresses the importance of a more moderate approach, as Helen Fein proposes: “Genocide is sustained purposeful action by a perpetrator to physically destroy a collectivity directly or indirectly, through interdiction of the biological and social reproduction of group members, sustained regardless of the surrender or lack of threat offered by the victim” For such an approach, as Hinton argues: ”without losing analytic specificity, more easily accounts for the fact that group boundaries are socially constructed across contexts and throughout time.”

Following the theoretical framework of anthropologist Nancy Scheper-Hughes, □genocide should be seen as part of a continuum, and that it is socially incremental and often experienced to be routine, even justified.□ Uncomfortable as it is to link nursing homes to death camps, but we must concede that an argument for the uniqueness of each genocidal event faintly and unintentionally □echoes the very exceptionalism that perpetrators invoke in defining their superiority. At the very least the genocide continuum provides a way to contextualize genocide, giving it a setting.

The Evolution and Uniqueness of Human Language

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Human language is the code upon which human culture is built. Animals may have culture, like the chimpanzees, but the complexity of this culture is dwarfed by the complexity of our own culture. The origin of human language is thus a highly fascinating and a very important question. Why did it evolve in humans and why not in any other species? Although codes that sometimes called “language” also exist in nature, most notably the honey bee “dance language”, the complexity of these codes are also dwarfed by the complexity of our own language. Here I offer an evolutionary scenario for the evolution of human language and speculate why other species did not evolve anything comparable to it.

Physical symbols systems in the brain and Fluid Construction Grammar as a biological system

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Mapping insights and frameworks from one scientific domain to another is often useful because it encourages communication between different scientific fields and acts as a conduit for the exchange of mathematical and computational tools. This talk discusses analogies between concepts and mechanisms from molecular biology and language processing. The main purpose is to find ways for understanding language as a ‘living’, dynamically evolving, self-organizing system. The analogies have been the main source of inspiration for a computational implementation of construction grammar, called Fluid Construction Grammar (FCG). The talk describes briefly the biological analogies underlying FCG and discusses the opportunities for further research that these analogies open up.

Information theory and biology: A review of recent trends

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There has recently been growing interest at borrowing both concepts and technical results from information theory for analysis in the biosciences. I will review recent efforts at incorporating notions such as entropy and uncertainty, channel capacity, noise and distortion, and mutual information into biological settings. I adopt a critical approach to recurrent claims that ‘in biology, *information flows from the environment to the genome* by the process of natural selection” and that “a population ‘measures’ the intrinsic information in the environment by differential reproduction”. I then discuss the recent attempts at suggesting that information is essentially a selectable trait and analyse additional manifestation of information, such as Kolmogorov complexity and Fisher information, and their possible relevancy in a biological framework beyond merely as metaphorical. The *information bottleneck* method will then be discussed to see whether it has fulfilled its promise of infusing meaning through its introduction of *relevant information*. Finally, I introduce a fruitful analogy from my own work between a communication channel and an inferential channel in the context of *population structure*, where the channel capacity closely corresponds to *informativeness for assignment*.

Evolutionary information

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Population genetics, a classic field that describes the genetic basis of biological evolution, has greatly benefited from the application of methods from physics' statistical mechanics. This has gained strength in the last half decade by the pseudo-independent work of several groups around the world. Although with much less strength and less attention, the same is true for information theory. Since evolutionary biology has gained so much from these fields, exposing in detail the bridge between these disciplines is timely and relevant, and constitutes the central point of my talk. I first expose the relationship between different existing approaches, with the goals of synthesizing the existing knowledge.

Second, because several of the analogies are mathematically formal (as opposed to only metaphoric), I will emphasise open paths that use both statistical mechanics and information theory. I argue that these can yield new view and new results in evolutionary biology. This is because statistical mechanics and information theory are sister fields, and, furthermore, also have a connection to the probabilistic view that evolution takes to describe gene frequencies. Thus, not only SM and IT pose different views of a problem, but also, deeper connections between these fields, such as information geometry for example, can expose different aspects of population genetics. For example, this allows seeing evolving populations as a communication channels. This will allows us assessing how much genetic information is a message passed from the parental to the offspring population.

Third, at a more metaphorical in genetics and evolution we employ and information jargon: *genetic code*, *translation*, *error*, and in some verbal theories, such as in the Major Evolutionary Transitions, *change in the mode of transmission of hereditary information* is regarded as one of the central aspects leading to such key evolutionary steps. However, there is little –if anything at all– in this jargon that links as such to formal notions of information. This is related to development: we still lack a comprehensive quantitative framework to understand the origin of traits and its relation to the major transitions. In this sense, genotype-phenotype maps can be seen as messages transmitted from genes to phenotypes through a noisy channel. To precise these analogies we can employ measures of mutual information, and thus quantify bounds the rate of information transfer to investigate evolutionary rates and the degree of complexity of genomes and organisms.

RNA-amino acid affinity and the Genetic Code

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The genetic code associates the 20 classical biological amino acids and the 64 RNA nucleotide triplets. A reasonable hypothesis is that some such linkages are governed by specific chemical interactions between the two types of molecules, amino acids and ribonucleotides. In this talk, I show that this idea is now very strongly supported by data showing that 8 kinds of amino acid binding sites selected from randomized sequence RNA are disproportionately likely to include cognate coding triplets from the “universal” biological code. Moreover, modern biological RNAs display striking examples of close association between bound amino acids and their coding triplets. Finally, newly-selected peptide binding RNAs include prominent examples with cognate triplets proximal to bound peptide side chains. It is strongly implied that early coding relied on associations between amino acids and their RNA binding sites. With these new data in hand, it is also clear that additional events intervened to construct the complete modern coding table.

See also: Yarus (2017) *Life* 7, 13.