Tenth International Conference in Code Biology

La Spezia (Italy) 11 – 15 June 2024

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Open-ended evolution achieved by repurposing of codes

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Open-ended evolution can produce “endless forms most beautiful”. We are now beginning to appreciate the ways that allow the often minor changes in the genetic makeup to drastically alter the form and/or functioning of an organism. Open-ended evolution is not about the vastness of the genotype space, that space is too large to traverse. Open-ended evolution is more about how an organism can use what it already has in a different way. So, while a rigid mapping can solve one evolutionary problem, a Code of Life could potentially solve many.From the evolutionary perspective, the arbitrariness of a code is key: by the change of the adapter the mapping can also change. While the realms thus connected might not change, the exact mapping does. If the coding changes, then the same input can lead to a different output or a different input can produce the same output. We observe, for example in development of multicellular organisms, that the key molecules and genes involved change very little through evolution, but the resulting forms produced do. This is achieved by often subtle differences in the targeting, tissue specificity, timing, etc. of the mapping. Consequently, here I make two propositions: (1) We need to search for codes of life in the origin of life (past or the be more precise before the genetic code) as it is codes that might have allowed the required increase in complexity that allowed the emergence of modern cells. (2) I propose that the series of stages in the evolution of a code of life is extended. Codes emerge (beginning), their ambiguity is reduced (evolution) and the mapping is optimized. The next step is conservation for a given purpose, but the potential for ambiguity is not eliminated. Then the code could later be used for other purposes. This phase might be called repurposing.

Square of Opposition based Modelling in Code Biology: From Biological Codes to Codes of Culture

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The Square of Opposition is a diagram for the representation of four basic categorical propositions. Its origin can be traced back to Aristotle's tractate "On Interpretation", and it has been used and described by some of the most distinguished scholars in the history of philosophical logic. During the last decade a considerable progress was made in the application of the Square of Opposition to propositional logic and Data science. Štambuk et al. [1, 2] used Square of Opposition and Semiotic Square based analyses in the Code Biology investigations to gain insight into the code ambiguity and codepoiesis concepts by Marcello Barbieri [3]. Pfeifer and coworkers constructed "probabilistic versions of the square and of the hexagon of opposition" [4], and implemented "the new paradigm psychology of reasoning characterized by using probability theory as a rationality framework for human reasoning" [5]. These results enabled the use of the same methodology for the analyses of biological and culture codes in Code Biology. The investigation of genetic code susing the Square of Opposition method represents a typical biological encoding problem. The models based on Square of Opposition and IUPAC ambiguity codes for nucleotides enable: 1. Encoding and decoding of a descriptive information of nucleotides, amino acids and proteins, and 2. Biological systems modelling with the tools ranging from standard bioinformatics methods to classic evolutionary models [1, 2]. We also introduce the application of Square of Opposition diagram to a culture code of religosity, i.e. assesment of intrinsic and extrinsicic religious motivation. This particular example was selected since religion is an essential element of the human culture, and research has confirmed that individuals' religion is linked to their cultural beliefs and background [6]. Religiosity was examined with Hoge Intrinsic Religious Motivation Scale because this is a standard psychological instrument that measures different ways of being religious, and it is applicable to a wide range of religious groups. New scoring system based on the Square of Opposition was applied. Machine learning analysis of the responses enabled us to extract 6 variables and 7 rules relevant for >97% accurate discrimination of the examinees on the basis of religious beliefs.

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The evolution of the Lunigiana territory as an example of the universality of the biological codes and of their hierarchical organization.

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In the past century the theory of evolution has maintained a central position in the scientific debate. In this millennium the growing awareness about the health conditions of the Earth, has oriented the scientific debate and the research toward the assessment, conservation and monitoring of the biodiversity and on the climatic changes as consequences of direct human responsibility. In summary, the passage of time has been transformed in sequences of temporal segments like epochs, era, age, that have a dramatic consequences on the ecological complexity. A general reset of processes seem to occur at some temporal expirations, and in this presentation I will call "seasons" such discontinuities. We observe seasons in the rock stratigraphy, in the growth of tree rings, in deep sea strata organization, in the economics, in the pandemic events, and so on. It seems reasonable to explain such seasons in terms of variation in physical condition of our planet and as a consequence in various coding processes. This presupposes the universality of the coding mechanisms and supports a general theory on codes. I will limit my presentation to few axioms: Codes operate at every biological, ecological, and cultural scale. Codes create nested systems in which a hierarchy of events is associated to codes. In particular it is evident the emergence of clocks regulating the coding events at the highest level of this hierarchy. To illustrate this perspective - that is integrative and not substitutive of other perspectives like the biological and ecological evolution and the competition theories - I'll use as an example the contribution of the coding processes in the recent ecological evolution of the small region of "the Lunigiana" by tracing back its "code history".

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The Algorithm; Mind of a Virtual Era
Our Code of Codes

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> *Our first step in understanding any mental phenomenon must be to delimit its existence in historical time. When did it first occur?* *J. Jaynes, 1996, 340*

> *We need first to understand that the human form—including human desire and all its external representations – may be changing radically, and thus must be re-visioned …*
> *five hundred years of humanism may be coming to an end as humanism transforms itself into something we must helplessly call posthumanism.* *I. Habib, 1977, 212*

This presentation takes the Barbierian (2015) idea that new coding forms mark the advent of new eras and brings it up to date examining the code that has reconfigured human life and is defining a new era - the algorithm. As soon as something implicit intrudes consciousness human thought undergoes a radical change. The introduction of any new tool or code brings a shift in cognition; every micro-step layering new semiotic forms within each macroevolutionary-stage has buttressed a new semantic leap. Our mechanization of everyday life and the tech-systems we interact with are impacting communication, cultural norms and values, market-aesthetics, and economics, in societies at large. Undergirded by a survey of the significance of tools in human evolution, this presentation arrives at what is already a well-entrenched new era: the digital, screen-mediated age. Revolutionized by the algorithm, introduced by computers, the 'Anthropocene' is dominated by the addictive quality of instant contact, unlimited information, virtual gaming, and titillating service-forms, all at our finger tips. Aside from the interpersonal impact on the new humans growing up with devices in hand, how does this disembodied, digital code-form through which we mediate our interactions condition human cognition? How does its seductive efficiency interfere with how we relate, feel, assign meanings, think? Rooted in macro-evolutionary and psychoanalytic principles, I examine the algorithm itself and take a sweeping interdisciplinary approach to the developmental, psychosocial, and cognitive implications for the human mind/brain as it interacts with its technological extension.

Key words: macro-evolutionary code-power, psycho-social and cognitive developmental implications.

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What is the Extended Mechanism?

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Barbieri's semantic biology (originally Barbieri 1985) provides an extension of the standard biological ontology, through a new theoretical entity: the code. A specific feature of Barbieri's semantic turn in biology is the use of mechanistic explanations of living systems. This approach, although criticized by part of the biosemiotics community, allows to work with meaning as the *new observable* of biology. The relationship between meaning and code is expressed by Barbieri as follows: "(...) meaning is an entity which is related to another entity by a code." (Barbieri 2015, 26). Barbieri refers to the mechanistic model of meaning as *extended mechanism*. Our previous investigation resulted in the finding that the von Neumann probe (and the Turing machine) can serve as a "minimal sufficient model of Barbieri's extended mechanism" (Jurková and Zámečník 2023, 5). To further conceptually analyse the *extended mechanism*, we now use Wiener's concept of a *self-propagating machine* (Wiener 2019). In contrast to von Neumann, Wiener emphasizes that a machine is "an agency for accomplishing certain definite purposes" (Wiener 2019, 245) and self-propagation "is the creation of a replica capable of the same functions" (Ibid). We suggest that when Wiener views the machine in terms of an *operative procedure* that enables machine self-propagation, he is implicitly referring to the role of code as thematized in Barbieri's *extended mechanism* (Wiener 2019, 249). The goals of our paper include:

(a) an attempt to link von Neumann's and Wiener's conceptions of the self-propagating machine
(b) the task of providing code biology with the conceptual resources of a new mechanism
(c) in particular, the task of providing a conceptual analysis of Barbieri's *extended mechanism*.

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From physical to biological information and the genetic code

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According to the modern scientific developments, the information is getting to be a fundamental notion like space, time and matter. These four fundamental concepts are substantially interconnected and represent the basic ingredients of the universe. Being fundamental, there is no complete definition of the information. According to our intuition, we distinguish between what is and what is not information. In the present contribution, I consider information as a very special state of the matter with a definite meaning which affects the evolution of the universe as a whole or its parts. Depending on complexity of the system one can speak about physical, biological and other information. By physical information, first of all, I mean definite values of fundamental physical constants (c - the speed of light in vacuum, h - the Planck constant, and G - the universal gravitational constant). These constants are valid in every space, at every time and for every kind of matter. Physical information also includes basic properties of elementary particles (mass, electric charge, spin,...). Physical information should mean everything that was given at the beginning of the universe and does not change over time. Biological information (bioinformation) is a very special state of the biological system, which was given at the beginning of life or became during evolution. A basic example of a biological information system is DNA, which is a special long sequence of pairs of nucleotides. A part of DNA codes proteins, while the other one should be related to the regulation functions. The DNA contains special sequences of codons to which certain sequences of aminoacids correspond. The special connection between 64 codons (elements of mRNA) and 20 amino acids (building blocks of proteins) with the stop signal is known as the genetic code. In this talk, I will speak about physical and biological information as well as about some modeling of the genetic code.

Code Biology and abduction in the creative process

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The main aim of the presentation is to explore how the logical process of abduction is fundamental to the creative process that leads to the constitution of the work of art. The starting point is that of Code Biology, where abduction is not a generic logical function, but a vital process that enables humans and the other animals to make interpretations of signals in their surrounding environment, with three processes required for interpretation: coding, decoding and abduction (Barbieri 2015). The abductive process would thus be the basis of what in Code Biology is called Second Cognitive System, where chains of neural networks would allow a series of discrete memories to be unified and then 'jump to a conclusion'. Abductive logic is a 'logic of guessing' (Peirce 1906) and as such is both fundamental to survival and the logical system most likely to lead to errors of interpretation. We would like to argue here that the abductive process also underlies creativity, especially aesthetic creativity, where two fundamental elements are at play. The first element is the necessary relationship between a conservative part - the memory - and a dynamic part - the non-deterministic way in which memories are connected in abduction. The second element of the analysis is that abduction is a pre-linguistic creation process and as such belongs to the unconscious part of creativity. To summarise, we argue that abduction is not only a vital process, but also fundamental to the creative process, both for art and for scientific discovery. In conclusion, some examples are given, especially from the field of design, where the question of the necessity of the abductive process for creativity is a matter of great debate (Kroll and Kosela 2017).

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Social Codes and Some Huge Social Problems: The Problem May Be in the Solution

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The U.S. and other countries that share social and some linguistic coding with it are currently facing some problems of enormous proportions, in terms of healthcare expense, lost productivity, and damage to personal quality of life. Obesity, for example, has been a growing problem around the world; worldwide obesity tripled between 1975 and 2016. In the U.S., not the most obese country by far, over 2/3 of the population are overweight and obese. Perhaps more alarmingly, around the world in 2019, an estimated 38.2 million children under the age of 5 years were overweight or obese. In another example, the world is experiencing a global pandemic of substance abuse disorders that are killing millions—over 110,000 people die in the U.S. alone from drug overdoses. The number of deaths due to accident and disease related to alcohol alone double that number, and statistics regarding death and disease related to other drug use are simply too difficult for reliable numbers to be generated. Finally in the U.S. there is a well-recognized public health issue associated with gun violence. Our children have to be trained in active shooter drills from the time they are in pre-kindergarten, due to the fact that there have been approximately 80 school shootings per year in recent years. Additionally, 654 mass shootings were recorded across the US in 2023 alone, and 45000 gun-related deaths were reported in total for that year. Some proximate causes of these devastating public health failures are easily cited: overweight and obesity are caused by an imbalance between energy input and energy expenditures. Ubiquitous availability of hyperpalatable food, together with urbanization and technological changes in work have increasingly allowed this imbalance to arise. The explosion of drug overdoses, caused proximally by depression of the human respiratory system, is traceable in recent years to the production and distribution of exponentially more potent and easily available substances. And gun violence in the US is a function of the more than 400 million guns found in the country—more than twice as many its closest runners-up (Yemin, Serbia, and Uruguay). But these kinds of “causal” explanations do not get at the real problems underlying these issues, nor at why recently proposed approaches for solving them not only will not be effective but may in fact exacerbate the problems. These responses all fail to acknowledge the powerful role that social and linguistic coding have played in the development of the health issues discussed here, as well as how well-meaning attempts at addressing them have redirected attention from the machinations that allowed them to develop, toward alternative social coding that will not only allow them to persist but may in fact make them worse. I am talking here about the re-coding of obesity as not a matter of personal control and the shameless promotion and lack of regulation of the food industry together with a dearth of health education, but as a metabolic problem addressable by pharmacology; and the re-coding of addiction not as a matter of exploitative behavior by big pharma, draconian reactive behavior by lawmakers, and lack of supportive social systems, but as a matter of weakness of will, indulgence, and criminality; and re-coding of the gun violence as the very definition of freedom and “the American Way”, rather than as libertine endorsement of the proliferation of weapons of increasingly massive destructive abilities. Adequately addressing these problems will require serious and reflective thinking about how to effectively use the power of social coding to get at important causal mechanisms that can have profound consequences in shaping the lives of entire populations.

Are there Grounded Semantics in (Model) Organisms?

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When trying to convene a sense of meaning as a biological property, we should probably want to figure out how exactly we are supposed to cash out the notion of meaning that we have in mind. Though certainly not the same, meaning and semantics ought to be seen as related, and satisfying a definition for each is a desirable theoretical step forward in trying to understand whether and how meaning is connected with explanations in biology. On the one hand, a constrained definition of semantics is indicative of a linguistic intuition about meaning. On the other, this same notion can stifle a more corresponding understanding of meaning in simple and non-linguistic organisms. In this paper, I wish to propose a reduced view of content for handling meaning while retaining a guiding notion of semanticity informing how we look at experience in non-linguistic organisms.

Forbidden Codon Combinations in Error-Detecting Circular Codes

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Circular codes, which are considered as putative remnants of primeval comma-free codes, have recently become a focal point of research. These codes constitute a secondary type of genetic code, primarily tasked with detecting and preserving the normal reading frame within protein-coding sequences. The identification of a universal code present across various species has sparked numerous theoretical and experimental inquiries. Among these, the exploration of the class of 216 maximal self-complementary C^3-codes has garnered significant attention. However, the origin of the number 216 lacks a satisfactory explanation, and the mathematical construction of these codes remains elusive. This talk introduces a new software designed to facilitate the construction of maximal self-complementary C^3-codes. The approach involves a systematic exclusion of codons, guided by two fundamental mathematical theorems. These theorems demonstrate how codons can be automatically excluded from consideration when imposing requirements such as self-complementarity, circularity, or maximality. By leveraging these theorems, our software provides a novel and efficient means to construct these intriguing circular codes, shedding light on their mathematical foundations and contributing to a deeper understanding of their biological significance.

The Innate Psychobiological Symbol Code

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Since the 1980s on, affective neuroscience, embodied metaphor theory, evolutionary psychology, and many other developments have helped us to see the mind as a thoroughly embodied entity. The recent emergence of code biology, furthermore, has shown us that the element of meaning exists in all scales of biology down to the molecular level. Code biology reveals a great many codes beyond the genetic code as integral to biological functioning and recent scholars have linked code biology to analytical psychology. In this talk, I will expand on this project by showing how developments in embodied cognition reveal yet another code that links the world of universal emotional experiences to the world of embodied visuospatial expressions--i.e., the "archetypes" of analytical psychology, with the adapter being the human body itself. Viewed in this manner, it becomes evident that the "archetypes" of analytical psychology can be easily and clearly identified via the tools of code biology, providing greater precision for research in cognitive science and successfully integrating psychoanalysis with powerful bioscience tools.

The Code View of Language: challenges and promises

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Marcello Barbieri (2020) contrasts his code view of language with Noam Chomsky's linguistic approach. For Chomsky language is an innate biological faculty, whereas for Barbieri it is a learned cultural construct. To be sure, Barbieri does not deny biology a role in human language, but neither does he approve of the extent to which Chomsky assigns to this role. Even when both agree on the existence of an intimate link between language uniqueness and brain wiring, they nevertheless differ as to what lies behind such a link; it is a slight mutation according to Chomsky's (2005: 11-12) speculation, and it is a distinctive fetal development according Barbieri's (2020: 3) conjecture. Admittedly, the contrast between the two views is so sharp that one wonders whether any attempt at reconciliation is doomed to failure. However, it is well to remember that, in a broader context, Chomsky's views also stand in sharp opposition to cognitive and functional approaches to language and mind, so sharp in fact that it involves Chomsky's wholesale rejection of modern cognitive psychology on the grounds that it is not 'biological' in the proprietorial sense (Chomsky in Cela-Conde and Marty, 1998: 21; see also Al-Mutairi, 2014: 176). It remains to be seen how Barbieri's code view of language fares with respect to current approaches in cognitive science in general and cognitive linguistics in particular. This is the main aim of this paper; to scrutinize the code view of language against the background of current cognitive and functional approaches to language and mind. Of particular interest are the notions of code and interpretation, and how they relate to the notion of meaning. Since this is a contested issue between biosemioticians and code biologists at a more fundamental level, the secondary aim of this paper is to shed some light on this important issue. The upshot of the discussion will lay out the challenges to the code view of language while highlighting its promises.

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Facial codes: From physiognomy to semiotics

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The paper examines the evolution of understanding the human face, tracing its journey from the ancient practice of physiognomy to modern semiotic analysis. Physiognomy, the art of judging character from facial features, has been a subject of intrigue and skepticism throughout history. The paper deconstructs its premises, highlighting how these early beliefs laid a foundational, albeit rudimentary, framework for interpreting facial expressions and features. Moving into the realm of semiotics, the paper discusses how this discipline offers a more nuanced and scientifically grounded approach to interpreting faces. Semiotics, the study of signs and symbols as elements of communicative behavior, provides tools to decode the 'facial codes' – the myriad of signs expressed through facial gestures and configurations. This transition marks a significant shift from a deterministic view of physiognomy to a more dynamic understanding of the face as a complex sign system. The paper delves into how facial expressions are not just passive displays of internal emotions but active communicative tools. It explores the role of cultural, social, and contextual factors in shaping facial communication, arguing that facial codes are not universal but vary across different societies and situations. This perspective is crucial in understanding the face in today’s global and multicultural world. Furthermore, the paper discusses the impact of technology on facial codes, particularly in the age of digital communication and artificial intelligence. It examines how technologies like facial recognition software and emotion detection algorithms interpret and sometimes misinterpret facial codes, raising ethical and practical concerns. In summary, the paper presents an overview of the human face's journey from being a subject of pseudoscience to a critical area of study in understanding human communication and interaction. It calls for an interdisciplinary approach, combining insights from history, psychology, cultural studies, and technology, to fully grasp the complexity and significance of facial codes in contemporary society. The face is a textbook object of inquiry for a perspective such as that of code biology, since it stands as a key intersection between two realms: rather than being something merely "natural", the face definitely is a naturalized entity. It is the site where "Nature" and "Culture" collide, intertwining biological expressions with cultural significances. This perspective broadens the discourse on facial codes, considering the face as a complex construct where biological and cultural semiotics converge to create a dynamic and multifaceted medium of human expression and communication.

Sherlock Holmes Doesn’t Play Dice: The mathematics of novel possibilities in uncertain information transmission.

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While biological codes are still in the making, they exhibit two paramount features: (1) The correspondence between input and output information is not one-to-one, and (2) Novel meanings can be attached to novel outputs. My presentation suggests that Evidence Theory (ET), also known as Belief Functions Theory or Dempster-Shafer Theory, is well-suited to represent the above features.

ET is a mathematical framework for uncertain reasoning that has a judge listening for testimonies or a detective looking for cues as its reference problem, rather than a gambler throwing dice. Since testimonies can partially overlap while they still differ in other respects, ET does not impose that possibilities are mutually exclusive but rather represents them as sets that may be in any relation of inclusion or intersection with one another. Partial overlap should address concern (1) above.

Novel testimonies can bring novel meanings to previously disregarded clues, as it tipycally happens in detective stories. ET can accept novel meanings because its possibility set does not imply the complementation operator, which invariably forces the definition of a "residual event" that reduces any open world to a closed one. This should address point (2) above.

ET does not specify what reasons may generate novel meanings. However, its open-world version posits that contradictory evidence triggers the search for novel possibilities. Whether this is a plausible mechanism for at least certain biological codes, is an open research question.

The cortex as a 'model builder' or 'archetype maker'

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Neuroscientific research has made significant strides in uncovering the ways underlying perception. In the realm of cognitive neuroscience, the brain's crucial role in deriving meaning from limited, noisy, and ambiguous sensory information through inferences and abstractions is emphasized. Perceptions result from elaborate brain processes or codifications triggered by sensations. This leads us to realize that perception and memory, while distinct processes are inherently intertwined. Perception involves contrasting sensory features with stored representations, thus highlighting the interplay between these two cognitive processes. Instances of visual associative agnosia, where patients with specific lesions struggle to associate a percept with its meaning despite having normal vision, further underscore this connection. The idea that our perceptions and thoughts are based on models we make of the external world traces back to the early days of scientific reasoning, particularly Aristotle's ideas. Hermann von Helmholtz further supported this notion, arguing that perception arises from representations formed from unconscious inferences. As Piaget pointed out, human cognition coalesces in the form of 'mental schemas.' Schema is a denomination created by Jean Piaget to explain the mental maturation of children and, in general, the mental progression of any individual. Schemas are ways of seeing the world that organize past experiences and assign a pattern to understanding future experiences. But not everything is emergent (emergence, a term from systems theory, describes properties that only arise due to the interaction between the individual parts of a system). Code biology helps us better understand that some factors are 'a priori', i.e., hardwired or codified in a phylogenetic memory, as Carl Jung once proposed. So, cognitive processes rely on memories, associative connections, neuronal codes, schemas, and archetypes - words that convey the representation of the environment based on predictive coding principles. Acting as a 'model builder' and 'archetype maker,' the cortex plays a pivotal role in translating external events into mental models. By possessing a representation of the surrounding world, the brain can make predictions about behavioral outcomes, guiding decision-making in a complex environment.

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In the Beginning was the Deed

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In my recent article "Revisiting Carl Jung's Archetype Theory: A Psychobiological Approach" [1], I introduced some conceptual ideas about embodiment and enaction but couldn't elaborate appropriately. The main idea was to evidence the dynamism our body takes between its structural innate categories of mind (archetypes-as-such or structural archetypes) and our environment. In psychology and cognitive science, embodiment suggests that the mind is not only located in the brain but is distributed throughout the body and is deeply influenced by the body's interactions with the world [2]. In the context of archetypes, embodiment could suggest that these deeply rooted structures are not static or solely biologically determined but are dynamically shaped and activated through our embodied experiences. For instance, how we physically navigate and interact with our environment might influence how archetypal patterns are expressed in our behavior and psychological experiences. The idea of enaction encapsulates two points: (1) perception consists of perceptually guided action, and (2) cognitive structures emerge from the recurrent sensorimotor patterns that enable action to be perceptually guided [3]. In this definition of enaction, perception appears as a mechanism emerging from an organism's response to its environment. While this view acknowledges sensorimotor patterns stemming from these interactions, it often overlooks the unique limitations and specific traits inherent to each species. In this conference, I aim to elucidate the complex nature of human subjectivity, arguing that it is not only a product of our interactions with the environment but also deeply rooted in our innate predispositions. I propose a mechanism I term 'enacting archetype.' This concept posits that our engagement with the environment has the potential to activate specific archetypal patterns, thereby influencing universal behavioral patterns and shaping human experiences. For this process to unfold, the individual must possess inherent neural or cognitive structures responsive to environmental stimuli. This perspective challenges the constructivist viewpoint prevalent in enactivism, which predominantly emphasizes the role of the individual in actively shaping their own reality. While acknowledging the significant role of individual agency and creativity, my approach seeks to balance this with an appreciation of our species' more static and universal aspects. It suggests a more integrative epistemology that recognizes the interplay between the creative capacities of humans and the enduring, innate elements of our psychological species. To support this idea, I'll discuss relevant research, such as a study on individual males who identify themselves as females or have a female identity [4]. Post-mortem analysis showed these individuals had a brain structure; the bed nucleus of the stria terminalis was short, like typically found in females, regardless of hormonal treatment. This finding, consistent even in a control group who hadn't undergone hormonal therapy, suggests a biological basis for gender identity, highlighting the interplay between innate neural structures and personal identity.

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Why Narratives? The Evolutionary Necessity of Narrations In Natural and Social World

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Both in social and in natural world, systems preserve and develop themselves through various forms of inter-action (energy transfers, exchanges of cues and random signals, focused conversational cooperation etc.). Given this fact, it is not immediately clear why narratives - the messages which cannot be used in face-to-face communication - are necessary at all. Indeed, despite the phono-centric nature of human writing, we can hardly employ it in conversation without recoding the written text "back" to its oral form. In a similar vein, the genetic information contained in DNA polymers cannot be used for building proteins without their transcription (recoding) into mRNA messages (molecules).

Building upon the general code theory, proposed by Marcello Barbieri for social and biological systems, the project seeks to derive the evolutionary necessity of narratives in nature and society from the specifics of digital code, which, in contrast to the analogue representation, can afford invariance to its environment (Barbieri 2003, 5). This, in turn, allows for the functional differentiation between preservation and exchange of cultural, genetic and other information (von Neumann, 1945, 4; Luhmann 1987, 7; Paivio 1990, 58; Hahn 2000, 241, 244, 249, 251). In culture, this independence of narratives from the surrounding context has been an object of sustained reflexion: for instance, the significance of Bible and other sacred texts has been repeatedly derived from their (ostensible) permanence and validity in all imaginable contexts (Goldberg 1987; Boisliveau2011; Watson 2018). The longevity of genome exceeding our imagination of time and history is another example which also has some important social repercussions (Vavouri, Semple & Lehner 2008). The ideas of the talk will be illustrated with the recourse to the grand political narratives of culture, religion and nature.

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The spiderweb of error-detecting codes in the genetic information

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Nature possesses inherent mechanisms for error detection and correction during the translation of genetic information, as demonstrated by the discovery of a highly self-complementary circular C^3-code called X_0 in various organisms such as bacteria, eukaryotes, plasmids, and viruses (Arquès and Michel, 1996; Michel, 2015, 2017). Since then, extensive research has focused on circular codes, which are believed to be remnants of ancient comma-free codes. These codes can be regarded as an additional genetic code specifically optimized for detecting and preserving the proper reading frame in protein-coding sequences. A total of 216 maximal self-complementary C^3-codes have been identified and a study by Fimmel et al. in 2014 revealed a group operation on this set that classified these codes into 27 equivalence classes with eight codes in each class. However, a general construction principle for the 216 maximal self-complementary C^3-codes is not known nor a complete understanding of how nature uses the code X_0. In this talk we show that all 216 maximal self-complementary C^3-codes can be derived from X_0 using a natural algorithm that is compatible with the above group operation. Two new graphs representing the set of all 216 maximal self-complementary C^3-codes as well as the set of 27 equivalence classes of such codes are studied. It is proved that the first one is bipartite while the other one has hamiltonian cycles of length 27. This implies a set of 27 codes,each one representing one equivalence class, that can be ordered as a sequence C_1, …., C_27 such that for each i the intersection of C_i and C_{i+1} is as large as possible, i.e. of size 18. A statistical analysis by Giannerini et al. in 2021 supports the fact that these special codes outperform other codes within their respective equivalence classes.

Verses, Nerves, Veins and Arabesques - the morphogenesis of patterns that make sense

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Structuralist thinkers from a wide variety of backgrounds such as Literary theory, Philosophy and Biology, have been challenging the rigid opposition usually made between Physis and Techné, nature and culture. One interesting example is Paul Valéry, the French poet and polymath who has proposed the existence of a "general morphology" in which the works of mind echoes the morphogenetic processes at place in nature, he claims that the po(i)etic creation of artifacts follows similar principles to those at work in the hemato(poietic) creation of blood or in the galacto(poietic) generation of milk. Code Biology is another example, by posing codepoiesis as the general mechanism that reunites and concatenates the origin(s) of life, mind and culture, this biological view shows that organic, neural and cultural formative acts share an artifactual nature. I intend to consolidate relevant contributions made indistinctly by scientists, poets and philosophers to this strand of structuralist thought exemplified above by briefly examining the (morpho)genesis of a variety of "semiotic nets". These nets, or symbolic systems, here understood as patterned topological structures that actualize and are actualized by poietic codes. The patterning of Nervous and vascular systems in vertebrates will be discussed in concert with the creation of some forms in poetry and graphic arts which are constrained by fixed and arbitrary metric parameters to produce recognizable patterns without losing unpredictability and creative potential. My presentation will be organized around the following pivotal concepts and topics: 1) Templum, trail to formation - growth factors and sonnets; 2) Templum, threshold for transformation– catalysis and rhymed verses; 3) Templum, space creation of meaningful forms - neural/vascular tropism, arabesques and themes. As a corollary, if we accept that the poetic craft is a physiological process, humanity could eventually find a place in nature that is contiguous to and not isolated from other living creatures, and adopt the neologism "physiomorfism"
(Vercruysse, 2022)[1] as the general mechanism in all levels of organic formation, it should come as a natural alternative to the prevailing anthropomorphic views about life, matter and imagination.

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The Novelties of Code Biology

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Modern Biology has emerged from a century-old battle against vitalism, and its major argument is the idea that "*life is based on the laws of physics and chemistry*". Code Biology is different from vitalism because it is firmly based on experimental discoveries whereas vitalism claimed that life cannot be reduced to the results of our experiments. At the same time, Code Biology is different from Modern Biology because it does not accept that the idea that "*life is based on the laws of physics and chemistry*". The conclusion of Code Biology is that "*life obeys the laws of physics and chemistry but is based on the arbitrary rules of its codes*". This is the first novelty: the idea that life is the result of '*arbitrary rules*'. The second novelty comes from the fact that the copying of the genes and the coding of proteins are two different mechanisms of life, which is why Code Biology concluded that there are two different mechanisms in evolution, one based on copying and the other on coding. Code Biology, in other words, has added the mechanism of coding to the mechanism of copying, and in this sense it can be compared with the novelty that took place in physics when electromagnetism was added to gravitation and it became clear that there are two universal forces in the universe and not just one. This is the second novelty of Code Biology, the idea that evolution took place by two distinct mechanisms, by copying and by coding, by natural selection and by natural conventions. The third novelty comes from the fact that coding, interpretation and language are three different types of natural conventions because they are based on three different types of arbitrary rules.

Modeling: Moments and Manifestations, Affordances and Outcomes

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The paper addresses the grand debate on coding and interpretation (2004 – 2012) as well as further explorations on the two paradigms of biosemiotics and code biology. Its primary foci are their correspondences and particularly attempts to reconcile both approaches. Both schools of scholarship promote their specific ways of modeling meaning-making in biological and social processes and interactions. Both interpret such processes as intellectual entities or reify them into so to say rei or things. The focus moves away from modeling (or coding, forming etc.) to models, information units and al kind of other ‘objects’. Processes of interacting, living and understanding are reduced to its momentary displays and exhibitions. The paper analyses word for word a key formulation by Marcello Barbieri on mechanism and models, scientific method and modeling, “Mechanism, in short, is virtually equivalent to scientific method. The difference is that the *hypotheses* of the scientific method are replaced by *models*, i.e. descriptions of fully functional working systems. Mechanism, in other words, is *scientific modeling*” (Barbieri 2014, p.241). Another case of analysis is a key claim by Kalevi Kull, “Indeed, the strictly random decision is not, strictly speaking, a choice, because the device which generates randomness (e.g. the coin) does not “see” the elements involved as simultaneous “options” to be chosen from. Instead it merely performs its actions blindly, under the full determination of its physics and/or programming” (Kull 2023, p. 82). Textual analysis allows discriminating similarities and differences (virtual or actual, partial or complete) between processes of modeling and choosing, their specific manifestations and moments, affordances and outcomes. The author believes that such practices of textual scrutiny as well as similar re-readings and re-interpretation of key claims made by proponents of both code biology and hermeneutic biosemiotics may pave ways to reciprocated understanding of mutual insights in investigating processes of formatting (=information), interacting (=interaction), copying, coding, living (=life) and finally free human understanding (=cognition) and scientific investigating (=research).

Relational Model of all GeneticCodes

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The genetic code represents a set of rules used by cells to translate the information encoded within the genetic material into proteins. Translation takes place on the ribosome which reads the mRNA codon triplet and uses transfer RNA (tRNA) molecules to provide appropriate amino acids for the protein synthesis. The genetic code is highly similar between different organisms, however, a total of 33 genetic codes can be set independently for nucleus, mitochondria, plastids and hydrogenosomes. The most common way to display the rules of all genetic codes is the Standard Genetic Code (SGC) table and its 32 variants [1]. This lecture describes an approach to the genetic code based on Relational data Model (RM), introduced to Code Biology in 2021 by Paško Konjevoda and Nikola Štambuk[2]. RM proposes distributed storage of the data into a collection of tables, which are called relations. Basic elements of the SGC table are rows (called records or tuples), and columns (called fields or attributes). The SGC table, according to the RM, represents the so called unnormalized form of a table, and it can be decomposed or divided into 4 tables, using a set of rules called normal forms. Tables produced in this way are called normalized forms [2]. The rows and columns of single tables are defined by the first and second base, and individual tables are specified by the third codon base. The result of this model is an approach to managing genetic code data, represented in terms of tuples and grouped into relations, with table structure and language consistent with: 1. first-order (predicate) logic, 2. Klein four-group and Cayley's table, and 3. sixteen truth functions defined by IUPAC ambiguity codes for incomplete nucleic acid specification [3]. The Relational Model is a suitable method to display the rules of the Standard Genetic Code (SGC) and its 32 variants. The applications of RM to Code Biology enable: 1. investigations of code ambiguity and codepoiesis during the evolution of the genetic codes according to Marcello Barbieri's concepts [4], and 2. simple and accurate bioinformatics and phylogenetics studies in Code Biology.

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The Dual Code Continuum: Bridging Cellular Composition to Cognitive Functions in Brain Organization

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Brain organization is a complex interplay of anatomical and functional activation signatures, intricately woven into the emergence of brain circuits. These circuits, characterized by cytoarchitectonic structures, evolve through integration at various molecular biological scales, giving rise to a distinctive cellular composition. This cellular diversity is a product of intricate gene regulatory programs, giving rise to specific electrophysiological signatures. The prevailing theories of consciousness, Integrated Information Theory, and Global Neuronal Workspaces, posit that whether viewed as an integrated or global network, the brain necessitates the encoding of diverse electrophysiological signatures, commonly known as neural codes. This suggests that the underlying code governing brain functions comprises two interconnected layers or codes. The first layer arises from the cellular composition that solidifies a brain circuit, culminating in a unique electrophysiological signature. The second layer forges connections between electrophysiological signatures and cognitive functions, manifesting as a series of neuronal codes. While the differentiation code and meta-code have been proposed as hypotheses for the first layer, the second layer has seen the establishment of various neuronal codes. This study focuses on postulating the interplay between these two levels, drawing insights from evidence presented by the BRAIN Initiative Cell Census Network consortium and ongoing debates on consciousness theories. The hypothesis presented herein offers a roadmap for understanding the coupling of these layers, providing guidance to unravel the fundamental principles governing the continuum of codes. This continuum extends beyond mere neuronal codes, encompassing higher-order codes, including cultural codes, contributing to a more comprehensive understanding of code biology.

Codepoiesis approach to the exaptation molecular architecture in simple cells: A biophysics and biosemiotic framework for basal cognition processes

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Currently, assembly theory offers the opportunity to connect the execution of the construction of subcellular “objects” with evolution. It is urgent to know if, in this theory, biophysical patterns establish proscriptive conditions of constrictions in their development capacity. That is, they allow any interaction that is not prohibited or exceeds the survival threshold, forming satisfactory modifications established for their incorporation. This is a kind of biomolecular and subcellular exaptation. The assemblage space that Sharma and his colleagues describe is a plausible model for establishing semiotic landscapes of agency that allow for meaningful connections. It means there can be an Umwelt where the “semiophysical” and “semiochemical” field of perception is based on constructing biomolecular objects with code and biomolecular semantics, into which I intend to delve deeper. The effective response is found in oscillations, synchrony rhythms, and noise discriminations. It would be essential to establish a connection between the communication of chemical oscillators through bioelectrical and, quite possibly, biophotonic patterning for the assembly, recycling, and polymerization of protein organelles and the generation of codes through adapters and agents. I will develop a theoretical framework of the mechanotransductive implications in the protein assembly of actin filaments and microtubules for coherence/decoherence activity in chemical and bioelectric oscillators. I will study the implication in quantum biology of these activities as the foundation of communication, i.e. if quantum rheology and bioelectrodynamics are implicated to the sol/gel colloidal behavior of the cytoplasmic environment of these organelles. These protophenomenological glimpses probably develop one kind of model of assembly code with tubulins, actins, and second-order messengers; one kind of codepoiesis that plays exaptation with adaptation. I promote a preliminary draft of a new paradigm in the branch of biosemiotics and reach a status of a pluralistic epistemology, which will study structural relationships, not only via multilevel - like the New Mechanistic Philosophy - but also via “organism/agency - environment/ecosystem.” Greater homeostatic balance develops in a dynamic ecosystem when structural stability is maximized. In this way, there is a greater recognition of the processual and physiological capacities of the organism/agency where the organism coexists and recognizes the possibilities of its persistence in the sentience/basal cognition and vivaciousness, subjectivity, and subjecthood of the organism.

The gene regulatory code of multicellular organisms

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Gene regulatory sequences determine the subset of genes that are expressed in a given cell type at a given time and under given conditions, as well as the rate at which these genes are transcribed. These sequences encode the developmental program of a higher organism, its anatomy, and its physiology including advanced functions such as adaptive immunity and cognitive capabilities of the brain. The first layer of the cascade of decoding processes, which ultimately relategnomic information into such complex phenotypes, translates gene regulatory DNA sequences into transcription rates. I call this layer the "gene regulatory code". Gene regulatory sequences are hierarchically organized in genomic regulatory bocks, which are arrays of regulatory genomic regions interspersed with other types of DNA. Regulatory genomic regions contain as elementary units DNA motifs, which are binding sites to transcription factors (TFs). There are obvious parallels with the genetic code. Genes correspond to genomic regulatory blocks, exons to regulatory regions and DNA motifs to triplet codons. Moreover, TFs play a similar adapter role like t-RNAs. However, the analogy stops here. Two well-known molecular components of the decoding machinery of the genetic code, the ribosome and aminoacyl tRNA synthetases have no counterparts in the gene regulatory code. Moreover, the DNA motifs have no unique molecular translation targets comparable to amino acids. Rather they emit activating of repressive signals to a hypothetical second integrative layer of the decoding machinery. Four key differences between the gene regulatory code and the genetic code deserve special attention:
(i) Sequential reading versus random access: During protein synthesis, the ribosome reads and translates nucleotide sequence triplets sequentially, one by one. The output is a colinear amino acid sequence. No ribosome-like scanning device is known for the gene regulatory code. DNA motifs are randomly accessed by diffusion and the question whether the order in which different DNA motifs occur within a regulatory genomic region remains a matter of debate.
(ii) Quantitative meaning. The global output from the gene regulatory code is a transcription rate, hence a number. So is the primary output a DNA motif,its affinityto a TF. This quantity has meaning in that higher affinity sends a stronger signal to the integrative layer of the decoding machinery.
(iii) Degeneracy and ambiguity: DNA motifs are highly degenerate.As a consequence, thousands of different DNA sequences may bind to the same TF. Conversely, the same DNA sequence may bind to multiple TFs. Developing these deductions further, one reaches the conclusion that DNA motifs for different TFs may also be arranged in overlapping fashion within a regulatory genomic region.
(iv) Organism and tissue specificity. The gene regulatory code is not universal and appears to evolve surprisingly fast. Experimental evidence shows that the same DNA sequence is interpreted differently, even between closely related organisms. Changes of the code presumably result from changes in the global TF repertoire, as well as from changes inthe DNA sequence specificity of individual TFs. Importantly, the code also changes between different cell types of the same species as each cell type has its own subset of expressed TFs.
In my talk, I will summarize the experimental evidence supporting the key characteristics of the gene regulatory code outlined above. I will further illustrate the coding principles with examples and explain how the code biology paradigm helps formulate meaningful questions and design novel experimental strategies to unravel molecular decoding mechanism. Finally, I will discuss the implication of code characteristics on the evolutionary plasticity of multicellular organisms.

To code or not to code?

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This conference contribution discusses the diversity of biological codes and calls for the foundation of an open working group on code systematics and terminology. Recent years have witnessed a tremendous increase in the number of published biological codes across all disciplines. Most of them turned out to be based on adaptors as described by Marcello Barbieri that perform a mapping between two independent sets of (macro)molecules, yet others are described as adaptorless (Prinz, 2023). Among the various "*non-Barbierian*" codes are e.g., the so-called *differentiation codes*, that are involved in pattern formation of the developing embryo (Gordon & Gordon, 2019; Igamberdiev & Gordon, 2023), or determine the karyotype of a species (Heng & Heng, 2021; Heng & Heng, 2023). Others, link mappings between entire processes to the concept of code (Paredes et al., 2021). Theoretical code concepts are concerned with determining the origin of the genetic code (El Soufi & Michel, 2014; Fimmel & Strüngmann, 2019, 2023; Michel, 2021; Thompson et al., 2021). To tackle the ever-growing number and diversity of biological codes, a systematic approach is needed that will allow comparisons among codes and across disciplines. For this purpose, an open working group is to be founded that will analyse and discuss published codes, and develop common and generalized definitions of codes and criteria how they should be published. "To be or not to be (a real code)?" often remains an unanswered question while reading the claims of a respective publication due to the lack of clear defining criteria. A concept on how to organize a working group on codes and development of a position paper on unambiguous code criteria for publication will be presented.

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Biological organism as multimodal supertext

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The discovery of hundreds of codes (Prinz, 2022) inherent in biological organisms (animals, plants, fungi, microbes) raises the question of the status of the organism. The organism is not only a self-reading text with a printing machine printing it, but a unity of other type: a multimodal text created using a large number of different codes. So, some fragments of organisms can be considered as translations (a certain nucleotide sequence and the features of the phenotype encoded by it), others as comments (symbionts filling the ecological niches created by the organism), third as derivative texts-paraphrases (descendants that retain the connection with ancestors). Thus the organism turns out to a certain unity of the original multimodal text, its translations and comments to it. The categorization of such unity is very difficult (Chebanov, 2022). Organism comparable to text in a semiotic sense (verbal, graphic, pictorial, architectural, musical text), more precisely with a multimodal supertext, with all its translations, comments, imitations, adaptations (illustrations, film adaptations, dramatic productions, music based on its plot), i.e. supertext as a cultural phenomenon. Since awareness of a cultural phenomenon as part of modern (actual) culture causes difficulties, such a cultural phenomenon is more easily isolated when it is on the edge or beyond the boundaries of modern culture. Then the cultural phenomenon is recognized as a cultural monument, in particular a literary monument. The integral partsof such a monument are its translations, comments on it, adaptations by other semiotic means, etc. Such cultural phenomenon is comparable to a biological organism with hundreds of codes. The comparison of an organism with a cultural phenomenon allows us to outline the problems of studying a biological organism as a semiotic object:

- The identification of a list of codes involved in a given organism. The question is not only how to list these codes, but whether such a list exists in principle or whether a new environmental situation or a new endosymbiont will lead to a change in the set of codes.
- The description of the codes of a population of one species is incomplete in principle; the description of the codes presented in the biocenosis that includes the corresponding population can claim some completeness. As a result, it can be argued that the interpretation of a living organism as a supertext, manifested as an analogue of a cultural phenomenon, both quite adequately represents its status and opens up a broad perspective for its study.

Sponsored by a grant 22-18-00383 (RSF).

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Code biology, genetic coding of cyclic processes, and cyclic Gray codes

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The report is related to a scientific direction that has been intensively developed in recent years under the name “code biology” [1]. It is devoted to the problem of genetic inheritance of many interconnected cyclic processes in living organisms and the analysis of which of the many types of cyclic codes most adequately corresponds to the features of genetic coding and organization of information sequences in genomic DNA. The author's results of modeling and studying the connections between the named set of cyclic processes and the hierarchical family of cyclic n-bit Gray codes are presented. The pairing of this type of cyclic codes with the molecular genetic coding system and the universal rules for the statistical organization of information sequences of single-stranded DNAs in the genomes of higher and lower organisms is shown [2, 3]. The symmetrical, dichotomous and fractal-like features of this statistical (probabilistic) organization associated with these rules are analyzed from the perspective of the Gray code family. The obtained statistical patterns of binary representations of genomic DNA are discussed in the light of P. Jordan’s statement that the laws of living organisms missed by science are the laws of probability of quantum mechanics. A binary-structured system of DNA nucleotide alphabets, consisting of alphabets of 4 nucleotides, 16 doublets, 64 triplets, is represented in the form of a family of square matrices, the rows and columns of which are numbered, respectively, with 1-bit, 2-bit and 3-bit numbers from n-bit Gray codes. This representation demonstrates the agreement of the structural features of genetic coding with the symmetrical and cyclic arrangement of amino acids and stop codons in a matrix of 64 triplets. The promise of modeling and analysis of genetic informatics structures and genetic inheritance of cyclic physiological processes based on families of n-bit Gray codes is emphasized as a new direction in code biology.

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On the Pragmatic Dimension of Genetic Coding and Performative Codons

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In code biology, it is accepted that “Genes are manufactured by molecular machines that can be referred to as copy makers and proteins by molecular machines that can be called codemakers” (Barbieri 2015, 12). Genes contain not only genetic information but also a wide range of genetic elements that control their own activity. The regulation of gene activity determines which genes will be active, when they will be active, in which cells they will be active, and how long they will remain active. It also determines the time, location, and intensity of their activity. These are the aspects of the sign, which Peirce called the Quasi-utterer and a Quasi-interpreter. When applied to genetic information, they can be called code-controllers and code-performers. Of these codes, the closest to semiotic systems are those in which discrete elements and linear organization can be distinguished. It is the characteristics that are contained in sequences of the genomic DNA. Thus, the genome also contains instructions for its actualization in the form of proteins and then cells. Regulatory codes (a) create special conditions for coding: (b) control encoding processes; c) consist of the same elements as the coding elements (nucleotide’s sequences), but they is to be read differently, as their interpretant is not some amino acids, but operations of activation or oppression (On/Of). All of them are context-sensitive, which necessitates the introduction of appropriate pragmatic coordinates: locus, time, Quasi-utterer (source) and a Quasi-interpreter (target). We begin the consideration of semiotic mechanisms of regulation in genetic coding with the simplest cases - these are the so-called nonsenses, stop-codons, and start-codons. It is more correct to call them performatives. The following features can be mentioned: 1) performative codons consist of the same elements as coding triplets; 2) performative codons, like language performatives, are homonymous with non-performatives. Their interpretation depends on the context. The external context may be more important than biochemical characteristics for the initiation and termination of translation. For example, the initial methionine may be encoded by different triplets than in the standard code. Similarly, the function of termination in the mitochondrial genome can be performed by the AGA and AGG codons. This may mean that the situation with standard performative codons is the result of evolution, because of which the degree of recognition has increased, and the degree of ambiguity has decreased. At the same time, the decisive factor was the felicitous conditions that determine the operation of initiation or termination. However, the biochemical composition may also be relevant. Thus, there is a correlation between the position of uracil in the triplet (first or second) and the function performed (initiation - termination). Such differentiation can also be seen as a result of evolution.

This research is supported by the Russian Science Foundation N° 22-18-00383 “Methodological design of extended evolutionary synthesis”.

Tenth International Conference in Code Biology – La Spezia (Italy) 11-15 June 2024

Cultural landscape and distributed languaging
A historical and linguistic encounter in Lunigiana

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In *Code Biology*, language is understood as distributed in a population rather than confined in singular brains (cf. Barbieri 2015: 140-141). A recent development in this direction is the ecological conception of language in terms of a concrete activity distributed in the biosocial environment (cf. Thibault 2021). From this point of view language is a phenomenon that takes place in a population located in an ecosystem where human agency plays a predominant role without being the sole relevant player. Despite its aim at overcoming the nature/culture dichotomy, Paul J. Thibault's theoretical proposal is mainly focused on psychological and social aspects of human ecology while it would be interesting to locate language in its wider and truer environment i.e., landscape eco-semiotically understood (cf. Farina 2021). Thibault's conception is purposedly temporary and open to integrations and, on its part, cultural landscape eco-semiotically understood includes eco-acoustic phenomena too (cf. Farina 2021: 45-54), among which human phonation fully takes part. To relate cultural landscape and language, my talk will focus on two examples concerning the economic, social, and linguistic history of Lunigiana. The historical reconstruction of how the province of Lunigiana was populated between the XII and the XIII centuries by Enrica Salvatori will be read in terms of the cultural landscape and its reflection in Ligurian linguistic history as studied by Fiorenzo Toso (cf. Ambrosi 1966-1967; Toso 1997, 2005; Salvatori 2007). Another example consists of the relations of La Spezia with Genoa and Milan during the XV century and I will discuss them in the light of Ligurian linguistic history and of the Mediterranean *longue durée* theorized by Fernand Braudel i.e., a further possible, yet macroscopic, example of a cultural landscape (cf. Braudel 1986; Toso 1997, 2005; Del Prato 2008; Fasano Guarini & Bonatti 2008).

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