Twelfth International Conference in Code Biology
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ABSTRACTS

Ecoacoustics codes from sonic soil

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Sound in ecosystems operates primarily as a *sign* rather than as physical energy, structuring processes of environmental communication and interpretation. Alongside *acoustic semiosis*, based on intentional signals, *sonic ecosemiosis*—defined as the process by which ecosystems generate biotic and abiotic sounds that are not intentionally produced but are nonetheless interpreted by organisms as meaningful information—organizes sounds into original *ecoacoustic codes* through which organisms read the soundscape. Within this framework, the ecosemiotic approach can be translated into the analysis of these codes. *Soil vibrations* and sounds play a central role because, in a substrate where visual signals are impeded, they often represent *the only vehicle of semiotic exchange*, conveying information about structure, resources, and risk. The *sonoscape* thus emerges as a dynamic semantic network, articulated into sonotopes and function-specific sonic eco-fields that modulate niches, ecological interactions, and responses to environmental disturbances.

The 'Commedia dell'Arte'
A Coded Satire of Everyday Archetypes

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This presentation belongs to the realm of cultural-aesthetic codes: Characters of the Commedia dell'Arte exploded out of Italy between the 15 and 17 hundreds readily capturing the imagination of the whole of Europe. Even today, their masked and mannered prototypes and exaggerated 'personages' are easily grasped as universal 'types' in western societies. Likewise, C.G. Jung writes, "Archetypal images," usually appearing in projections, "can be taken metaphorically, as intuitive concepts for physical phenomena. For instance, *ether*, the primordial breath or soul-substance, is a concept found all over the world, and *energy,* or magical power, is an intuitive idea equally widespread." The archetypes are 'psychic realities'…" (*Jung, 1916/1953, 95, Two Essays on Analytical Psychology).* Humans are born with few programmed instincts: rooting (orienting to the nipple), grabbing, the visual cliff and a set of emotional expressions. All other 'schemas' or 'imagoes' are acquired through perceptual-sensory social experiences after birth since signified-categories and types are re-presented via our integrating area, the cortex. There can be no pre-figured 'archetypes' prior to 'representation,' and dynamic-schematization begins in sensory-motor form, leaving mnemonic traces as 'pattern-templates' only later on. No phylogenetically stored categories, types, or archetypes, exist in the unborn human brain. Neural coding, possibly, applies to a tight-knit cognitive/ideational process condensing sensory-motor and representational aspects, observed by Freud (1900) as a "ready-made structure" producing the dream's 'core ideas.' Human "intellection," (cognition), working unconsciously, integrates mnemonic fragments with current experience from many functional areas of the brain into 'ideas,' much like a metaphoric process. Jung focused on content; Freud on cerebral processes. The satirized character types represented in the Commedia dell'Arte, each of which 'performs' according to a stylistically coded type and story-line, underscore the socio-cultural origins of all archetypes, including those of earliest childhood, the broad universal mythological templates of the Jungian cannon. Ghosts and goblins, witches and wisemen, magicians and imagoes, are all acquired categories created by the human imagination.

Code-Biology for Communicating the Climate Crisis (and Countering Denialism)

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In the contemporary era, the need for clear and effective communication on ecological and environmental issues has become increasingly urgent. The polarized debate between environmentalists and climate denialists has progressively hindered a shared understanding of what should be considered "life" as a complex system, and consequently of what can be defined as a "climate crisis" and its effects on life itself. On the one hand, climate denialists often display a strong resistance to acknowledging the existence of an ecosystem that is not anthropomorphic, frequently coupled with a rejection of the value of scientific research – an attitude that, in some cases, takes on explicit political forms. On the other hand, environmentalists sometimes respond with naïve and overly simplistic views of ecosystems, failing to account for their intrinsic complexity. Such simplifications ultimately further obstruct constructive debate and the development and implementation of eco-biologically informed policies. Within this context, the aim of this paper is to show how the principles of Code-Biology can contribute to a deeper and more accurate understanding of the ecosystem of life, thereby offering a conceptual framework capable of better informing socio-political decision-making. More specifically, we argue that the principles of Code-Biology help address a fundamental question in ecological philosophy and environmental ethics (Attfield 2018; Næss 1973): how it is possible to demonstrate – both theoretically and scientifically, as well as to effectively communicate – that all living beings can be regarded as ethical subjects, while at the same time acknowledging that human beings exhibit unique, species-specific evolutionary characteristics, such as language. In conclusion, the paper examines the twelve fundamental principles proposed by Marcello Barbieri (2025) in order to identify the moral criteria that justify the conservation of species and ecosystems, and to evaluate the most effective ways to communicate these concepts within contemporary ecological discourse.

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Therapeutic Code-Switching and the Translation of Distress

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This paper analyzes a critically under-examined dimension of code-switching: the linguistic and conceptual translation work that patients must perform within mental health and addiction treatment systems to render their experiences legible and worthy of care. I define therapeutic code-switching here as the strategic modulation of self-presentation, symptom narratives, and emotional expression required to align with clinical frameworks, diagnostic categories, and institutional expectations that often diverge fundamentally from patients lived experiences of distress. Drawing on medical anthropology, critical psychiatry, and patient narrative analysis, we examine who bears the burden of this translation—disproportionately individuals from marginalized communities whose cultural idioms of distress, trauma responses, and coping mechanisms fail to map neatly onto Western psychiatric nosology. The analysis explores circumstances that compel such switching, including intake assessments where benefit eligibility hinges on symptom performance, therapy sessions structured around evidence-based protocols that presuppose particular emotional vocabularies, and peer support environments where recovery narratives must conform to programmatic frameworks. Profound consequences accompany this required code-switching. While successful translation can secure access to services and validate suffering within medical frameworks, it simultaneously demands that patients suppress alternative understandings of their experiences, perform emotional labor while in crisis, and risk clinical invisibility if their presentations deviate from expected patterns. The paper examines how Indigenous patients must translate spiritual crises into anxiety disorders, how chronic pain patients must reframe suffering as "drug-seeking" to access medication, and how neurodivergent individuals must mask authentic communication styles to appear "engaged" in treatment. I argue that therapeutic code-switching operates as a gatekeeping mechanism that privileges linguistic facility and cultural capital, effectively penalizing those least able to perform the required translations while experiencing severe distress or cognitive impairment from substance use. The analysis concludes by questioning whether person-centered care can exist within systems that demand wholesale linguistic assimilation rather than developing institutional capacity for multilingual, culturally responsive frameworks of understanding mental health and addiction.

Five types of performative codes

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John Austin recognized five major types of performative functions of language that suggest similar functions at the basis of life. The three main ones can be described as 1) the expression of a pre-existing and unconditional power, 2) the pronouncement of a verdict that leads to one decision rather than another, and 3) the promise of a future realization. The other groups (fourth and fifth) are, according to Austin himself, less easy to define, but to me they might implement some standard gender connotations as often expected from individuals of either sex in many cultures. Leaving aside gender issues for simplicity's sake, in biology there is a clear link between type 1 and the most immediate physical-chemical functions performed by molecular structures of any kind, as long modeled in biochemistry and molecular biology. Furthermore, it is easy to see a correspondence between type 3 and the notion of commitment during embryonic development or in other collaborative and symbiotic relationships between living beings – even if, unlike type 1, the mechanisms involved in biological commitment are far from clear. Type 2 bears at least some resemblance to what is often referred to as cell fate choice, and it is surprising that while, according to Austin, types 2 and 3 are largely distinct in language, the equivalent processes tend to be confused in biology. Overall, it is reassuring that such a limited number of essential notions can perhaps encompass the entire modus operandi of living organisms. On the other hand, it is clear that, for code biology, the only obvious point of contact is Austin's type 1. In fact, from a functional point of view, a biological code, while implementing arbitrary logic, acts like a machine and functions like any ordered set of enzymatic reactions. This is both an advantage and a limitation. In fact, the relationship between code biology and the notions of commitment and cell fate choice is an underexplored field, and it should require a much greater shift away from traditional biochemistry than has been attempted so far.

Construction of Dinucleotide Circular Codes Based on Nucleotide Probabilities

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The construction of a circular code through a biological process, particularly a primitive one in the absence of the protein world, has remained an open problem since the discovery of a maximal C3 self-complementary trinucleotide circular code in genes in 1996 by Arquès and Michel in 1996. Circular codes are defined by their ability to recover the correct reading frame of genes at any position. While a class of 216 such trinucleotide codes has been identified, the KL method (defined by Koch and Lehman in 1997), based on nucleotide probability products, generates only a restricted subclass of 88 C3-codes. Revisiting this probabilistic framework 25 years later, we demonstrate that various classes of dinucleotide circular codes can be generated using a nucleotide probability product model. We introduce the concept of transitive dinucleotide codes and prove new theorems characterizing their circularity and comma-free properties. Using codon usage from bacteria, archaea, and eukaryotes, 2 "universal" maximal dinucleotide circular codes are observed: D1,2 = {AT, CA, CT, GA, GC, GT } in the codon site 1− 2 and D2,3 in the codon site 2− 3 which can be deduced from D1,2 by 1-letter cyclical permutation or identically by reversing permutation. Unexpectedly, we then show that, under the independence assumption, the dinucleotide code E1,2 through the probabilistic construction from nucleotide frequencies in the codon sites 1 and 2, is a maximal dinucleotide circular code and is equal to the observed dinucleotide code: E1,2 = D1,2. These findings support a theoretical model in which dinucleotide circular codes may have originated from statistical properties of primitive nucleotide distributions, providing insights into the possible emergence of the genetic code.

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The Statistical Collective AI and the recurring Archetypal Patterns

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If archetypes are understood as structurally recurring patterns within human symbolic production, they should be detectable across sufficiently large corpora of cultural expression — and potentially reproducible by systems trained on such corpora. This paper examines whether large language models (LLMs) can generate outputs consistent with archetypal organization and how such capacities may be interpreted within the code–mediator–artifact (CMA) framework. Major's (2021, 2025) triadic model of codified form — code, mediator, artifact — grounded in Marcello Barbieri's Code Biology (2018), provides the structural lens for this inquiry. Rather than asserting strong equivalence between artificial and biological systems, we explore whether LLM architectures can be meaningfully described in CMA terms. While LLMs operate through large-scale statistical compression over artifacts produced within historically codified symbolic systems, they do not generate codifications endogenously in the biological sense. Instead, they process and recombine artifacts shaped by existing codes. A bounded analogy between next-token prediction and Jungian word association is considered at the level of associative artifact production, insofar as both processes reveal organized patterns through sequential response. We distinguish three claims: (1) LLMs can generate outputs consistent with archetypal patterns; (2) they do not instantiate unconscious processes; and (3) their role in facilitating users' access to their own unconscious material remains an open empirical question. To explore this third possibility, we developed a structured prompt designed to reduce default validation behaviors (RLHF) in favor of analytical confrontation. An autoethnographic proof-of-concept across three sessions with a single intellectualized participant examined exposed reasoning traces (chain-of-thought), providing a window into AI-mediated reflective processes and a more rigorous basis for assessing intellectual collusion. The traces reveal multi-hypothesis deliberation, cross-validation, and self-correction not visible in standard transcripts, while also exposing systematic bias toward over-pathologizing reasoning. Drawing on mentalization theory (Fonagy et al., 2002) and on analyses of archetypal organization as coherence-restoring structures, we hypothesize that any therapeutic effect operates through reflective distance and externalized symbolic scaffolding rather than interpretive authority. In this sense, the LLM may function as a "therapeutic artifact" against which psychological processes become visible, without thereby instantiating unconscious structures.

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Defining Code: Structural Criteria and Boundary Conditions in Code Biology

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The concept of "code" occupies a central place in contemporary biology, neuroscience, semiotics, and increasingly in discussions of artificial intelligence. Yet its use across domains is often analogical rather than structurally precise. This paper clarifies what qualifies as a genuine code within the framework of Code Biology. Drawing on the code–mediator–artifact (CMA) model, we argue that a code cannot be reduced to statistical regularity, algorithmic instruction, or functional mapping. A genuine code requires: (1) two relatively independent domains, (2) a contingent rule of correspondence between them, and (3) a mediational architecture capable of implementing and stabilizing that correspondence across contexts. Without these criteria, we risk conflating large-scale pattern detection with codification. These structural conditions are examined across three domains: genetic translation, neural and symbolic organization (including *archetypal* mediation), and contemporary artificial systems. While biological systems implement codified correspondences through dedicated mediators, artificial systems such as large language models (LLMs) primarily operate through large-scale artifact compression. The analysis, therefore, focuses on identifying the boundary conditions under which artificial architectures might satisfy — or fail to satisfy — the criteria of codification. By distinguishing between statistical recurrence, algorithmic execution, and codified correspondence, the paper aims to refine the conceptual scope of Code Biology and clarify its applicability across biological, neural, and artificial domains. Rather than collapsing distinctions between natural and artificial systems, the goal is to specify precisely where structural analogies hold and where they break down.

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Redundancies in Communication: Codes, Messages, Messengers

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The talk deals with redundancy at various levels of communication, investigating its ambivalent role in the self-maintenance of communicative systems. The following levels are considered:

1 internal code redundancy (DNA, human language, checksums and parity checks in telecommunication);
2 redundant codes within a single interactional environment (neural and muscle networks enabling locomotion, primary and secondary sex traits, parallelism of colour and position in traffic lights);
3 redundant messages relying upon the same or different codes (periodical reminders, multiple spermatozoa simultaneously sent to ovary), and
4 redundant messengers concurrently emitting the similarly or differently coded messages with the same meaning (two-person rule in launching nuclear weapons, duumvirate of brain and central nervous system in vertebrates, and overlapping agencies in empires and dictatorships).

It is shown that while redundancy greatly increases the robustness of communication, it also detrimentally affects its efficiency. Furthermore, the uncontrolled redundancy may not only hinder communication by exceeding the throughput capacity of the respective channels but also trigger runaway semantic inflation which would effectively nullify the security added by the spare elements of communicative process. The concluding part of the talk is devoted to the findings of the two small-scale empirical studies, showcasing the interplay of redundancy and uncertainty in poetic discourse and totalitarian communication.

Twelfth International Conference in Code Biology – Guimarães (Portugal), 2-6 June 2026

Between strong and weak autonomy of non-causal explanations: the case of semantic explanation in code biology

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The paper will follow up on the ongoing debate in the philosophy of science about the relation between certain non-causal (Zach and Zámečník 2024, Reutlinger 2018, Lange 2017) scientific explanations and mechanistic explanations (Glennan 2017, 2016). Most arguments in favour of the irreducibility of non-causal explanations are based on some pragmatic criterion (Kostić 2023, Kostić 2018) and are supported by scientific practice (e.g., in neuroscience Kostić and Khalifa 2022, in linguistics Zámečník 2023). The first goal of this paper will be to argue in favour of the autonomy of certain types of non-causal explanations, especially topological explanations (Kostić and Khalifa 2022). We will consider weak and strong variants of autonomy: (1) autonomy in the weak sense means the irreducibility of non-causal constitutive elements of scientific explanations (Craver Povich 2017, Morrison 2015, Zámečník 2018), (2) autonomy in the strong sense means the irreducibility of (some) non-causal scientific explanations (Kostić and Khalifa 2022, Kostić 2023). The paper will show why it is much easier to defend autonomy in the weak sense and what obstacles prevent the consolidation of the position of autonomy in the strong sense. The main goal of the paper will be to show, using the example of semantic explanation in code biology (Barbieri 2015, 2003, Zámečník and Jurková 2025, Zámečník 2021), that the strong form of autonomy is difficult to defend even in the case of mechanistic explanations.

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The definitions of Information and Meaning

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It is an historical fact that information has been defined in two completely different ways. One is the definition of "*physical* information" introduced by Claude Shannon in 1948 with the idea that information is the probability of choosing a message from all its possible alternatives, and for this reason it has been described with an entropy-like formula. The second is the definition of "*biological* information" introduced by Watson and Crick in 1953 with the idea that information is what is inherited by living systems and consists in linear sequences of nucleotides. According to this second definition, biological information exists only in life and has nothing to do with physical information. The information of the genes, on the other hand, is used by the cell to produce proteins, and it is an experimental fact that the links between genes and proteins are not deterministic rules. They are arbitrary rules, more precisely they are semiotic rules where the links between genes and proteins are like those that exist between signs and meanings. The problem here is that semiosis has been defined in two very different ways. According to the classical definition of Charles Peirce, semiosis is a process that necessarily requires interpretation and this implies that protein synthesis is an interpretive process. According to the definition of Code Biology, instead, semiosis is primarily based on coding and appeared for the first time at the origin of life with the genetic code whereas the faculty of interpretation evolved in animal brains some three billion years later. Today, in conclusion, we have two different definitions of information (physical and biological) and two different definitions of meaning (one based on interpretation and one based on coding).

How Plants Write with Sugars: From Hidden Patterns in Cell Walls to Their Controlled Self-Destruction

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Plants construct their structures using a remarkable material: the cell wall, a complex network of sugars, fibres, and aromatic compounds that provides each cell with shape, strength, and protection. For a long time, these walls were viewed mainly as passive structures, with their properties depending solely on the amounts of cellulose, lignin, or other polymers they contain. Increasing research now reveals that what truly matters is not just “how much,” but “how”: the precise way sugar chains are linked, branched, and arranged in space. This concept is summarized in the idea of a Glycomic Code, which suggests that plant sugars are organized according to rules that encode biological and technological functions. One of the earliest and most compelling examples of this comes from studies on storage xyloglucans in the seeds of the tropical tree *Hymenaea* (jatobá). These sugar chains are not formed randomly; instead, they are organized into repeating structural blocks with specific patterns of side chains. Two types of units in the same polysaccharide chain were identified: “pexons,” which are regular, repeating blocks directly involved in hydrolysis, and “pointrons,” which relate to polymer–polymer interactions that maintain structure during hydrolysis. Together, these units create a structured “text” in sugar, whose organization determines how the wall stores nutrients, retains water, and can be broken down without the collapse of the polymer composite. This system clearly demonstrates that sugar polymers can carry information in their structure, supporting the idea of a Glycomic Code. However, storage walls are quite stable. They reveal the existence of structural coding but only provide a static view of how the code is constructed. They do not show how this code is actively used, changed, or deleted during life processes. To understand how this code functions dynamically in living tissues, we examine aerenchyma. Aerenchyma is a specialized oxygen-conducting tissue found in the roots and stems of many plants that grow in wet or flooded soils. In this tissue, some cells intentionally die, and their walls are remodelled in a highly controlled manner, creating air spaces that help the plant breathe. This process is not chaotic: it follows specific spatial and temporal rules, guided by metabolism, hormones, and communication between neighbouring cells. Therefore, the story of jatobá xyloglucans shows that plants “write” information into sugar structures. The study of aerenchyma provides the opportunity to observe how plants actively “read, edit, and erase” this sugar code during development, revealing that cell walls function as living, regulated systems rather than inert materials.

On the influence of adjacent codons on the selection of synonymous codons

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The distribution of neighboring nucleotides of a codon in a coding sequence is not evenly distributed [1]. This suggests that neighboring nucleotides - or equivalent neighboring codons - might influence which synonymous codon is used by nature to encode an amino acid. This paper quantifies this influence by means of machine learning methods. A one-dimensional convolutional neural network (CNN) was trained on peptides of coding sequences to predict its associated codon correctly [2]. To do this, the CNN may take up to 5 amino acids or codons up- and downstream from the neighborhood into account for the prediction. The predicted sequence was compared with the actual codons, and the accuracy of the assignments was put into context in a situation where no neighbors were taken into account for the prediction. The analysis was performed on six different species. The results show that the neighborhood has a significant influence on the correct (synonymous) codon selection. The improvement in accuracy relative to the baseline was 20% or more in *H. sapiens*. The highest impact has the first nucleotide in the next codon downstream but also distant codons influence the assignment. These findings might be of interest for optimization of mRNA codons in general as for recombinant protein synthesis etc. [3,4]. This presentation will also speculate on whether this correlated selection of synonymous codons is helpful for a better understanding of circular codes [5] in biological sequences.

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The Genetic Code as an Operational A Priori
Xenobiology and the Rewriting of Life's Grammar

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I argue the genetic code functions as a biological a priori: an evolution-shaped, operational rule system that constrains possible lifeforms prior to any individual organism's existence. It is important to clearly distinguish between the genome (a contingent "text") and the genetic code (the necessary "grammar"), bridging evolutionary epistemology and code biology. My study refines Konrad Lorenz's naturalized transcendentalism by rigorously separating genetic coding rules from genomic sequences. Drawing on Barbieri's organic codes, Pattee's epistemic cut, and evolutionary epistemology, the genetic code is framed as a phylogenetically installed, operational a priori - historically contingent in origin but functionally necessary for biological organization. Building on this, I argue that xenobiology is the first deliberate attempt to experimentally rewrite this inherited biological a priori. By engineering alternative codon assignments, non-canonical amino acids, and orthogonal central dogmas, xenobiology shifts from modifying biological "content" to altering life's "grammar" itself. In Barbieri's terms, this creates genuinely new organic codes. This reframing carries significant philosophical and ethical weight. Intervening at the level of coding rules forces a reassessment of knowledge, agency, and the nature of the living subject. Xenobiology thus emerges as a test case for code biology - an experimental probe into the conditions for new biological grammars and new forms of life.

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Relational model of the genetic code: From IUPAC nomenclature to Code Biology application

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Standard Genetic Code (SGC) table describes the translation of RNA information into proteins. This specific biological code array is characterized by the two-dimensional arrangement of 20 amino acids specified by a three-dimensional partition of the 64 base triplets [1, 2]. This lecture presents an alternative approach to the genetic code, based on the Relational Data Model (RM). RM was introduced to Code Biology in 2021 by Konjevoda and Štambuk [1]. The model proposes distributed storage of the data into a collection of tables, which are called relations. According to RM, the SGC table represents an unnormalized form of a table, and it can be decomposed into 4 tables using normalization [1]. Normalization is a database design technique which organizes tables by reducing redundancy and dependency of data in order to avoid inconsistencies. Following this procedure, SGC is represented as a set of four monoatomic tables, consisting of 16 fields each [2]. Individual tables are specified by the third codon base (U, C, G or A), and table row (record or tuple) and column (attribute) are defined by the first and second base, respectively.

The result of RM 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 logic, 2. sixteen truth functions, and 3. Klein four-group and Cayley's table-based information coding. Two-digit nucleobase encoding of amino acids according to IUPAC nomenclature was introduced by Štambuk in 1998 [2]. The first digit represents a nucleobase ring—pYrimidine is 0, puRine is 1—and the second digit encodes its Keto (0) or a Mino (1) groups. The bit string representation of the bases is therefore {U or T = 00, C = 01, G = 10, A = 11}. Consequently, structural, functional and evolutionary patterns of protein sequences may be modeled using codon-based amino acid information instead of using information based on amino acid physicochemical properties [1, 2]. Underlying coding theory principles will be discussed from the standpoint of: 1. Molecular Recognition Theory of the protein and peptide ligand–acceptor interactions, 2. encoding descriptive information of nucleotides, amino acids and proteins (e.g., of relative solvent accessibility, hydrophobic moment, intrinsic disorder and atom depth), and 3. systems modeling—ranging from standard bioinformatic tools to classic evolutionary models, i.e. from Miyazawa-Jernigan statistical potential to Kimura three-substitution-type model, respectively. A particular attention will be paid to the interpretation of results considering the key concepts of Code Biology by Marcello Barbieri [3].

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From Mappings to Tensors in Code Biology, Meso-Levels and Meta-Codes as Structural Operators

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Classical formalizations of biological codes treat them as mappings between discrete sets, analogous to formal language codes. However, biological codes operate under conditions that resist such simplification: they translate between heterogeneous domains (molecular configurations, cellular states, phenotypic outcomes), depend on multiple contextual factors simultaneously, and are mediated by material machinery that is itself subject to modification. We propose that biological codes are more appropriately formalized as multilinear operators representable by higher-order tensors. In this framework, a code is not a function $f: X \to Y$ but a tensor $C \in X^* \otimes K_1^* \otimes \ldots \otimes K_n^* \otimes Y$ that maps inputs and contextual parameters jointly to outputs through contraction operations.
This tensorial perspective offers three key insights. First, the meso-level structures ubiquitous in biological organization—regulons, functional modules, neural assemblies—emerge as low-rank approximations of the full code tensor. These are not arbitrary simplifications but structured reductions that preserve functional regularities while reducing degrees of freedom, explaining why intermediate organizational levels exhibit greater stability than their constituent parts. Second, meta-codes—processes that modify the rules of translation rather than the translated states—are formalized as operators acting on code tensors, represented by tensors of higher order. Epigenetic modifications, neuromodulation, and developmental reprogramming become instances of the same formal operation: transformation of the translation machinery itself. Third, the continuity of codes across biological scales is captured as a chain of tensor contractions, each reducing dimensionality while preserving functional capacity and introducing emergent regularities. We present the mathematical foundations of this framework, illustrate it with a minimal worked example, and identify open problems requiring collaboration with mathematicians working in multilinear algebra and tensor theory. The tensorial formulation does not replace existing approaches to Code Biology but provides a rigorous mathematical language capable of expressing the context-dependence, hierarchical organization, and dynamic modifiability that characterize living codes.

Twelfth International Conference in Code Biology – Guimarães (Portugal), 2-6 June 2026

From Molecular Motors to Minimal Agency: Codepoiesis, Bioelectric Codes, and the Self-Organization of Coherent Semiotic Fields

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In simple cells, chemical oscillators, bioelectric gradients, and cytoskeletal networks form coupled systems that regulate movement, metabolism, and environmental responses. Molecular motors, such as actin–myosin and kinesin–dynein complexes, convert chemical energy into organized motion, creating spatial patterns and intracellular flows that carry information. Gene regulatory systems integrate these mechanical, chemical, and electrical signals, enabling adaptive, history-dependent behaviour. When these interacting processes become stabilized through code-like constraints—such as protein, bioelectric, and morphogenetic codes—the cell acquires the capacity to discriminate conditions and adjust its activity. Basal cognition thus emerges from the self-organized coordination of molecular codes within a coherent cellular field. Understanding how minimal agency and basal cognition emerge from molecular processes remains a central problem in theoretical biology and code biology. This work develops an updated codepoietic framework to explain how meaningful organization arises from the exaptation of molecular architectures in simple cells. Building on assembly theory, the project investigates how subcellular objects—protein complexes, organelles, and regulatory circuits—are constructed, reused, and stabilized under biophysical constraints that act as proscriptive filters, enabling biomolecular exaptation at the subcellular level. Assembly spaces can be interpreted as semiotic landscapes structured by interacting codes. In this context, the cell constructs a biomolecular Umwelt in which semiophysical fields—mechanical, rheological, and bioelectric dynamics—interact with semiochemical fields such as molecular signals and gradients. These coupled processes generate coherent semiotic fields characterized by oscillatory synchronies, rhythmic contractions, and noise discrimination. Molecular motors play a central role in this organization. Actin–myosin systems and kinesin–dynein transport along microtubules functions not only as mechanical devices but as code-bearing structures that transform chemical energy into organized motion and spatial information. Their coordinated activity contributes to cytoplasmic streaming, intracellular transport, and tension-based morphogenesis. Protein assemblies thus operate as dynamic coding substrates. Actin and tubulin codes interact with bioelectric and morphogenetic codes, where membrane potentials and ionic gradients establish large-scale coordination. Gene regulatory systems act as adaptive, history-dependent networks that integrate chemical, mechanical, and bioelectric inputs, enabling context-sensitive responses. Codepoiesis is understood as the capacity of living systems to generate and coordinate multiple interacting codes across scales. Through this process, exaptation and adaptation become integrated at the subcellular level, producing conditions for basal cognition and minimal agency. The project offers a unified framework linking assembly theory, molecular motors, bioelectricity, and gene regulation within a coherent semiotic model of cellular organization.

Relational model of all genetic codes
as a supercode composed of subcode tables

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Databases are an important area of computer science that deals with the efficient storage and management of data. The relational data model (RM), devised by Edger F. Codd in 1970, is the most widely used database model. In short, RM divides complex data sets into multiple simplified tables. This division into subtables is based on a theoretical concept called normalization. Normalization, applied to the standard genetic code table and its variants, yields four different subtables—U, C, G and A—specified by the third codon letter, and joined by a Primary Key (i.e. identical column C of the second codon letter) [1, 2]. Each of four subtables in RM consists of 16 fields (defined with the first two codon letters), and the first two tables—U and C—are duplicated with respect to the amino acid encoding. Sixteen fields of the tables can be fully described using first-order logic, truth functions and group theory formalism. Their genetic subcodes have a conserved core, defined by a Natural Key in a relational database management system (RDBMS), that closely resembles Rumer's transformation [2].

In a relational model, a genetic sequence and corresponding protein structure with consequent evolutionary changes are defined by four subcodes, encoded by means of IUPAC nomenclature and truth functions. Conventional triplet code is thus a supercode—originating from the functional fusion of four subcode tables that allow the use of an appropriate adaptor molecule, i.e. tRNA, without ambiguity. The relational model is in agreement with Marcello Barbieri's concepts of genetic code ambiguity reduction and codepoiesis, and enables different bioinformatic and proteogenomic investigations in Code Biology [1–3].

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From Code to Collective: A Formal Theory of Emergent Communication and Higher-Order Agency

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How individuality scales across biological organization remains a fundamental puzzle in science. This paper presents a formal, bottom-up derivation of sociality, extending a computational model of the individual agent to multi-agent systems. I begin from the premise that autonomous agents are computationally irreducible, rendering them inherently unpredictable to one another. This mutual opacity creates a fundamental "problem of predictive alignment," a form of computational uncertainty that I argue cannot be solved by behavioural modelling alone. I then formally prove that the establishment of a shared, arbitrary symbolic code is a necessary computational solution to overcome this uncertainty, enabling the coordination required for collective action. This coded communication transforms a set of isolated agents into a distributed computational network. I further prove that this network can achieve a state of collective computational irreducibility, an emergent property where the dynamics of the whole are not reducible to its parts. Finally, I demonstrate that a system exhibiting these proper ties—a collective goal, a shared code, and collective irreducibility—fulfils the formal criteria for a new, higher-order "Macro-Agent." This provides a rigorous, step-by-step derivation for the emergence of collective intelligence, offering a new computational framework for understanding the mechanisms behind the major transitions in evolution.

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Towards Biosemiotics Ontologies for World-Modelling in Intelligent Systems

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Recent advances in large language models (LLMs) have produced an undeniable achievement: the observation of emergent properties that surprised even their creators. These systems exhibit capabilities that were not explicitly engineered, revealing the power of scale, data, and representation learning. Yet, this same success has clarified a fundamental limitation: current LLM technology, while remarkable for pattern synthesis and linguistic competence, does not provide a pathway to general intelligence grounded in a model of the world. LLMs manipulate symbols with extraordinary fluency, but without a stable mechanism that ties those symbols to situated meaning, context, and action in physical reality. This paper argues that progressing toward intelligent systems capable of reasoning about the world requires revisiting historical knowledge-representation approaches, particularly ontologies, and rethinking them beyond their traditional static, taxonomic form. Ontologies must evolve into dynamic, context-sensitive structures that can grow, adapt, and reorganize in response to an agent's interaction with its environment. Such an evolution demands a theoretical foundation that explains how meaning emerges from perception and action rather than from symbolic description alone. An unexpected but fertile source of inspiration for this transformation lies in biosemiotics, the field that studies how living organisms construct meaning from environmental cues. Concepts such as Umwelt and semiotic scaffolding describe how organisms progressively build layered models of their world through continuous perception–interpretation–action cycles. These processes offer a conceptual blueprint for designing artificial systems that do not merely store representations of reality but develop operational world-models grounded in their own sensory and behavioural capabilities. The paper proposes that graph-oriented databases and knowledge graphs provide a practical technological substrate for prototyping such biosemiotically inspired ontologies. Their structural flexibility, relational expressiveness, and capacity for incremental growth make them suitable for implementing layered, evolving knowledge structures that emulate how meaning develops in biological systems. By integrating biosemiotic principles with dynamic ontological frameworks, it becomes possible to envision intelligent systems that move beyond symbol manipulation toward contextual, world-referenced reasoning. This perspective reframes the path toward general intelligence not as a problem of scale or data alone, but as a challenge of re-engineering how artificial systems construct and evolve meaning.

From Tissue Code to Social Code: How Horns and Antlers Became Signs of Strength

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Biological codes operate across all domains of life and have repeatedly been *co-opted* through evolution to serve new functions in diverse contexts. The molecular programs guiding keratin sheath growth and patterning in horns—for instance, relying on the Hox code—were redeployed in the evolution of antlers. Although horns and hooves share a keratin-based structure, their underlying genetic and developmental pathways differ significantly. This demonstrates that *distinct* organic *codes* can generate morphologically *similar* keratinous *structures* with divergent three-dimensional patterns. A comparable principle applies to bony tissues: antlers, though composed of bone, exhibit developmental programs more akin to those of bone cancer cells (e.g., Wnt code, Hedeghog code) than to normal bone. Within code biology, the phenomenon that different codes can direct the (almost) same output has not yet been described explicitly. From morphological and functional perspectives, horns and antlers represent evolutionary novelties that primarily serve as weapons for defence and competition, and secondarily acquired social functions like the display of health status (genetic fitness) that is important in mate selection, and to indicate social rank in herds. These structures have become communicative *signs*, illustrating how lower-level molecular codes can evolve into new *semiotic functions* when expressed in novel anatomical contexts. João Carlos Major has explicitly described such "*redeployment*" of tissue codes in the formation of extra-oral dentition on the cranial tenaculum of male *Hydrolagus colliei* (spotted ratfish), which subsequently gained a social role in mate selection. This presentation situates horns, antlers, and extra-oral teeth within a shared framework of *evolutionary innovation*, highlighting the interplay between the fields of *code biology* and *biosemiotics*. It proposes that tissues, organs, and ornaments act as mediators between *organic* and *social meaning*, positioning the body itself as an analogue interface for signalling and communicative display. Animal horns have been adapted by humans as signalling instruments, cultural artefacts, and may have contributed to cultural practices of human headdress in encoding social status or role.

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Quantum Logical Bioinformatics: Genetic Alphabet of Four Hadamard Unitary Operators, and Cyclic Groups

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This article is devoted to algebraic-operator modeling of genetic informatics systems providing the inheritance of logical structures and functional algorithms. Formalisms of quantum mechanics and quantum information science are used. The author describes the identification of algebraic-operator alphabets due to algebraic analysis of structures of molecular genetic coding, which serve as the basis for developing cyclic-spiral bioinformatics. This algebraic bioinformatics exists in parallels with established biochemical informatics, which is based on the alphabets of four nucleotides in DNA and RNA and which describes the inheritance of amino acid sequences in proteins. Algebraic bioinformatics expands the possibilities for modeling the inheritance of cyclic and spiral algorithmic structures in living organisms using the formalisms of quantum information science, unitary Hadamard operators, hypercomplex dual numbers, the screw calculus, and Fibonacci matrices. The author presents genetic algebraic-operator foundations for the inheritance and modeling of a variety of geometrically regular biological forms (mollusk shells, phyllotaxis configurations, etc.). Based on the obtained results, a paradigm of code algebraic-operator Darwinism is formulated, according to which natural selection and the inheritance of the most survival-promoting code combinations of alphabetic operators of algebraic bioinformatics play an important role in evolution. This paradigm explains the rapid evolution of organisms as follows: complex tissues are formed not so much by the emergence of new genes, but by algebraic bioinformatics operators that alter the ways existing genes are used, being linked to electromagnetic waves and resonance mechanisms. The role of bioantenna arrays in the energy-informational evolution of living organisms is discussed, including the proposed biological role of hopfion crystals, which have structural analogies with the DNA double helix, as noted by the author.

Epistemic engineering: from counterparts to codes

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Using codes, living systems are epistemically engineered. They act/perceive, make things up, build social groups, and change the surrounds. With languaging and practice, humans also add and assess knowledge claims. Neural meta-codes (Gahrn-Andersen & Prinz, 2021) are said to sustain codes of praxis (Gahrn-Andersen. 2025), functionality and valid knowledge. When humans 'will' moves by a cyborg cockroach, as epistemic engineers (Cowley & Gahrn-Andersen, 2023), they bring use of the non-organic to the living. As epistemic engineers, we can also use languaging-in-practices (as here) to sketch an argument. By hypothesis, codes shape how we perceive, act and thus co-sustain organized social life.

We know that epistemic means draw on evolution, development, learning etc. However, humans also make and steer epistemic happenings whose coherence draws on practices, techniques and languages. Co-constructed operations prompt events as operating systems function as knowing parts. Given recursive cyclicity, Watson (2025) posits that all persisting systems use autopoiesis (even a grain of sand). Cycles are sustained by meta-cycles as systems self-sustain and, at times, induce each other to self-modify. Accordingly, one can turn to how coding informs happenings, practices and systems. With metabolism and languaging, for example, coding brings nominal kinds (or empirical form) to 'objects' that enable living and practices. The resulting proteins and wordings are partly reliant on non-perceived (and non-perceivable) kinds. In the case of wordings, what Sellars calls 'counterparts' are necessary to perceptual experience (see, Seiberth, 2021). For example, a traffic light can appear *red*, *rosso*, *vermelho* (etc). Perceptual experience (and counterparts) may move a cyclist to stop, swear and/or think of "semiosis." Yet neither languages nor objective features of the world can explain the events (e.g. swearing). Rather, it seems, counterparts inform what results. By hypothesis, we use the non-perceivable – and coding -- to evaluate happenings as we organize what we do. Given recursivity, we draw on skills and techniques that, for Watson, presuppose the use of autopoietic systems. In using alphabets and digits, for example, we re-aggregate (or track) nominal kinds by using marks to draw-and-look or write-and-read. As epistemic engineers who are sustained by operations – and coding – we engage in practices as counterparts bind together the perceived, the said and the known.

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The Semiotic and Textual Features of Regulatory Codes

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Earlier we tried to demonstrate the characteristics of performative codons using the properties of the so-called nonsenses. These characteristics can be transferred to more complex regulatory codes (promoters, enhancers). Regulatory codes (a)create special conditions for coding: (b)control encoding processes; c) consist of the same elements as the coding sequences, but they are to be read differently, as their interpretant is not some amino acids, but operations of activation or oppression (On/Of). They have the following characteristics: a) sequences of nucleotides of a certain length; b) their appearance requires a special context; c) they are not decomposed into significant units like triplets, but represent a single text; d) nevertheless, they consist of heterogeneous areas, each of which has a certain function; e) they distinguish certain invariant and consensus positions assigned to a certain nucleotide. (Noteworthy: the tRNA also has similar characteristics.) In contrast to the GC and the coding sequences (genes) generated on its basis, in regulatory texts-signals it is possible to distinguish some compositionally and functionally significant segments (in relation to enhancers, distantly located motifs), but not to distinguish either vocabulary units ("words" as minimal significant units), or grammar, understood as the obligatory rules for combining lower-level elements into higher-level units. In the case of enhancers, grammaticalization followed the path of distinguishing motifs, each of which separately acts as a micro-text, but unlike nonsenses, they are not included in the general common system. In the case of promoters, grammaticalization led to a strict delimitation of their segments and the fixation of mandatory positions.

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Complexes as Codified Psychobiological Configurations: A Code Biology Approach to Analytical Psychology

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This paper proposes a reformulation of Jungian complexes within the framework of Code Biology (Barbieri, 2025). Drawing on Major's code–mediator–artifact (CMA) model (Major, 2025), we argue that complexes can be understood as stabilized psychobiological configurations resulting from codified correspondences implemented through neural, affective, and relational mediations. Rather than treating complexes as purely symbolic or interpretive phenomena, we describe them as developmentally consolidated artifacts of codification. Archetypal dispositions function as structural constraints that organize affect, imagery, and behavior through specific mediational architectures. Complexes emerge not as spontaneous narrative constructions, but as progressively stabilized configurations grounded in embodied and relational history. This approach situates Analytical Psychology within a non-mentalistic semiotic framework, in which meaning is produced through codified correspondences rather than through subjective interpretation. By integrating Analytical Psychology with Code Biology, the paper clarifies the structural status of complexes as artifacts of multi-level codification and contributes to a unified account of biological, neural, and symbolic organization.

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