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IUPAC nucleotide ambiguity codes specify molecular descriptors for amino acid statistical potential and relative solvent accessibility

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The computational design and prediction of protein structures from the primary amino acid sequence are largely solved—with satisfactory precision [1]. This article addresses similar problems from another angle, using simple and fast algorithms based on the physico-chemical properties of amino acids encoded by the Cayley table of the Klein 4-group and Relational Model of the Standard GeneticCode (SGC) [2–5]. SGC table is a specific biological code array, characterized by a two-dimensional arrangement of 20 aminoacidsand 3 stop codons for the protein synthesis, that are specified by a total of 64 base triplets. Štambuk etal. [3] recently demonstrated that algorithms based on IUPAC ambiguity codes for incomplete nucleic acid specification extract accurate nucleo base information about different properties of the aminoacids and proteins, that corresponds to a known 3D crystal structure in the Protein Data Bank (PDB). IUPAC nucleotide ambiguity codes could be applied to [3–5]: 1. Encoding descriptive information on aminoacids and proteins (e.g., about relative solvent accessibility, polarity, atom depth, etc.), and 2. 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). We first present how to use this method of nucleotide and aminoacid encoding in order to extract valuable information on different properties of the biological systems. We then present several examples, with statistical and machine learning procedures that enable the use of IUPAC codes and related truth functions for the experimental measurements, validation and simplification of complex system modeling in CodeBiology. It is concluded that the algorithms based on IUPAC codes, logical operators, truth table andRelational Model [3–5] enable the investigations of codepoiesis and ambiguity reduction—two essential Code Biology terms defined by Marcello Barbieri [6–8].

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Individuation of Personhood in European Modernity:
comparative study of the two cultural codes

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The paper critically reevaluates philosophical debates on *individuation of personhood* (*individuatione personae*) from Pre-Modern to Modern times (Gilles Deleuze, Gilbert Simondon, Evald Ilyenkov). While the idea of universal personhood is ingrained in the notion of Abrahamic God – a singular Personal authority creating and maintaining the World, its individuation supervened in the apparition of Christ. The initial upsurge of early modernizing trends within the Christian civilization domain in the times of Renaissance was marked by a new variety of personhood – the humanized and individuated one, multiplied in numerous assorted human beings. This development was soon converted intotwo specific ideal types of encoding. Cultural encrypting of modernizing humans in Western Europe tended to rely on *"descending individuation"* (attributing affinities of the universal authority down to individual humans), while a similar processes in the Orthodox Christian domain inclined to count on *"ascending individuation"* (individual efforts to advance towards the universal authority). The ideal type of descending individuation of human personhood was promoted further in a variety of human social and cultural practices first within Reformation and Counter-Reformation as well as later in the stages of individuation of first of morality and then individualized secularization of politics, economy and all ways of everyday life. The ideal type of ascending individuation of human personhood distinctly appeared as the Old-Believers social resistance to Early Romanov's repressions orchestrated by imposition of the imported descending individuation standards. This led to a protracted variance of conflicting cultural coding – ascending and descending ones. In milder configurations similar variance of cultural coding gradually emerged also in Western Europe and global modernizing world producing multiple modernization and plurality of cultural codes. This is partially also due to numerous alternative civilization impacts. Though both types of individuation of personhood have their common root in all European Christian and post-Christian Modernity, and thus construct its fundamental cultural coding, historically they had different level of social influence in Post-Catholic and post-Orthodox world. The ascending type of individuation became the determining factor of social integration and political culture in the framework of the Russian Orthodox paradigm, as well as the descending type played the same fundamental role for social integrity of Western Catholic and Protestant world. So, the cultural code of European Modernity contains two variations – "ascending" and "descending"- forms of individualization of personhood. Both have strong and socially dangerous aspects. Thought they can be seen as opposition to each other, the report concludes by suggesting to overcome possible conflict through the social synergy of the two types of individuation of personhood.

The Tree of Representation
Bridging the Gap between Brain and Mind

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This is the *code theory of mind*, the idea that there has been a *universal neural code* at the origin of mind as there has been a universal genetic code at the origin of life.   *Barbieri, 2015*

The biological development of mapping and its direct consequence –images and minds—is an insufficiently heralded transition in evolution.   *Damasio 2012, 143*

We must be prepared...to assume the existence…not only of a second unconscious, but of a third, fourth, perhaps of an unlimited number of states of consciousness, all unknown to us and to one another.   *Freud, 1915,170*

This presentation traces epigenetic steps in the evolution of re-presentation examining when, how, and even *why,* this neural advance would have begun, in light of what evidence there is from pre-history, neuroscience, and contemporary developmental studies. Psychoanalytic research in particular informs of the vicissitudes in the development of this function. Through our portal into the dream's primary process meaning-making forms we infer how from sensorimotor embodied registrations other coding mechanisms would have evolved layer by layer adding new semiotic vehicles each with its own distinct signifying vocabulary. This most fundamental of human cerebral faculties, that begets mind, requires a broad interdisciplinary palette to integrate into a Barbierian evolutionary framework, its many psycho-cognitive accomplishments correlating with changing forms of internalization, mnemonic processes, and kinds of meaning-making. From paleo-anthropology we learn of its manifest embryonic beginnings; from iconography, implications for interpreting the signifying level of its images; from neuroscience the mapping of evolving functional circuitry connecting the old brain stem with the newer cortex. Continuing my quest in finding continuities between body and mind this exploration concludes with the meta-codes for our tree of representation.

Biological information and the genetic code

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In our time, information is becoming increasingly important in all human activities. Information is a fundamental concept, so it cannot be reduced to something more fundamental. Understanding and meaning of information is not the same in science, technology, art and everyday life. It is especially important to know and develop biological information. A living organism is a special state of matter, composed of connected ordered systems that function as a single unit. One of such systems is the biological information system, which is composed of subsystems with respectively the following main three functions: source, transmission and realization of information.DNA and RNA are the basic sources and carriers of biological information that is transmitted from one generation to the next.DNA and RNA contain information that governs the development and functioning of a living organism. The genetic code determines which codons in the messenger RNA encode one of the 20 amino acids and a stop signal in the process of protein synthesis. In this talk, I will give an overview and my understanding of biological information and genetic code modeling.

Creativity and evolution from the perspective of Code Biology

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The aim of this paper is to advance the idea that aesthetic phenomena, including the creative process, should be read from an evolutionary perspective as understood in the field of Code Biology. The basic concept we start from is that creativity - of which the creation of a work of art is only one possible outcome of the whole process - has far deeper roots than the purely symbolic and culturally orientated one, i.e. it is based on the primordial and evolutionarily developed relationship that humans have between their bodies and their sorrounding environment. Starting from these premises, it would be unproductive to study the origin of creativity in a purely symbolic and interpretative sense - i.e. exclusively in terms of a process of semiosis - as this would imply that creativity is an aesthetic process that is already culturally orientated and limited to the production of works of art; a theory that has been questioned by many biologists, anthropologists and psychobiologists, starting from the fact that creativity is a process that is common to at least all humans and most probably to other animal species. So the idea we want to advance here is that the creative process has far deeper origins than the symbolic ones and that these origins can be found in the concept of evolution as proposed by the founder of Code Biology, Marcello Barbieri. That is, evolution would not be limited to the process of copying (evolution by natural selection) - as claimed by the Modern Synthesis theory of evolution - but would include a further and most fundamentals process of coding (evolution by natural conventions), where copying has to do with information and coding with meaning and is the only process that makes absolute novelty possible. The creation of models of the world that can be defined as "aesthetic" through the creative process would therefore not be the result of autopoiesis, but of codepoiesis, with the symbolic production of artworks being only the final stage of a larger process.

The Ontological Status of Cultural Codes:
Social Constructions or Natural Kinds?

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There can be no doubt that biological codes exist at an indefinite number of levels. Emerging from neural and psychological codes in humans are an enormous number of codes that exist between individuals, at the social level. Linguistic codes, non-verbal communication codes, religious codes, driving codes, dress codes, codes of conduct, honor codes and myriad others can be found in codes all around the world, binding some groups and separating them from others. Philosophically, this drives the question of whether cultural codes are real and objective, what philosophers might call natural kinds, or whether they are instead social constructions. Think for a moment about the cultural code of personal space, for instance. Across different cultures, people maintain different physical distances during social interactions. The anthropologist Edward Hall demonstrated over decades that remarkably consistent patterns can be found within cultural groups, although the patterns vary significantly between cultures. Languages as well develop organically, and change as cultures do, but does that mean that they don't constitute natural kinds that emerge and disappear over time, as other entities and activities that we consider natural kinds have? Richard Boyd considers biological species to be paradigmatic natural kind clusters, where the clustering is due to a homeostatic mechanism. In these cases, mechanisms can be identified that cause the properties to cluster by ensuring that deviations from the cluster have a low chance of persisting. The philosopher John Searle takes a middle ground here, distinguishing between intrinsic properties of objects and processes, and those whose function can't be achieved solely in virtue of physics and chemistry, but requires continued human cooperation. Money is his famous example—nothing about paper or credit cards is inherently valuable; it is human cooperation that imposes function and status on them. The things that make such things operate in society are what Searle calls 'constitutive rules'. So, like Wittgenstein, Searle believes that by creating constitutive rules, humans are creating new realities. Humans add new functions and statuses to phenomena, within cultures that evolve through adaptation and natural selection, in a manner analogous to the way in which species evolve. Why is this important? One reason is that if we take cultural codes to be natural kinds, based on something like objective essences, there might be no good reason for giving up on bad coding. For example, the political coding involving rulers, including the concept of the divine right of kings, which was understood as a natural kind for centuries (as was the concept of the divine, period) provided certain individuals with the right to oppress others without redress. Most recently, we can see a cultural evolution away from the idea that there are 2 and only 2 sexes, and the idea that gender is identical with sex. Despite the fact thatgeneticists decades ago put that falsehood to rest, the social facts of the matter, and the coding that created those social facts, held firm. In contrast, though, many philosophers have asserted that gender is something more performative than essential, and that is certainly not based on the genetic sex or intersex of humans. Seeing the coding around this issue as social construction has opened a path to greater freedoms and safety for those who express a gender other than the one that doctors assigned them at birth.

The Extended Metabolic Code

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There is increasing evidence that many small metabolites produced by subsequent reactions of standard metabolic pathways have highly divergent cellular functions. Because short sequences of reactions can contribute to very different functions depending on which step of the reaction sequence is altered, there is no obvious link between metabolic pathways and the associated cellular functions. Current studies in metabolomics assume that changes in intermediary metabolite concentrations may reflect functional differences, but only indirectly. Indeed these changes are viewed as mere surrogates for metabolic fluxes that are rerouted to produce different endpoint metabolites under different conditions. Gordon Tomkins (1975) proposed a "metabolic code" to describe the signaling function of modified forms of metabolic end products (such as cyclic AMP relative to AMP) or their specialized derivatives (such as many amino acid catabolites acting as neurotransmitters). The question of whether all metabolites within the central metabolism may have signaling roles in addition to regulating their own production or disposal has not been addressed. While representing an extension of the previous hypothesis, it has very different implications. Indeed, endpoint-specialized metabolites are intended to provide signaling by accumulating in large amounts, since their sole function is to act as signals. In contrast, metabolites of the inner metabolic network mediate the transformation of chemical structures into each other, and it is not obvious that their physiological levels can change to the extent that they can embody a signal (unless they are segregated into specialized vesicles, like the amino acids that act as neurotransmitters). A growing list of metabolic pathways appears to participate in the extended code, including the biosynthesis of serine, the biosynthesis of creatine, the terminal catabolism of lysine, the catabolism of urea cycle-related arginine and ornithine, some still poorly defined functions of respiratory chain complexes I-III, and metabolic interactions, post-translational modifications of proteins and epigenetic DNA modifications by a wealth of mono- and dicarboxylic organic acids, notably the Krebs cycle intermediate alpha-ketoglutarate with its derivatives, L-2-hydroxyglutarate and D-2-hydroxyglutarate. A formal identification of this code is lacking, as it has not yet been asked whether or which targets of the regulatory metabolites represent specific adaptors. The identification of the adaptors will also answer the question of whether this is a comprehensive code or a group of related codes. This is in contrast to the restricted metabolic code for specialized signaling metabolites of 1975, in which similarly specialized adaptors have been partly identified. The extended metabolic code could be helpfully compared with the codes that likely govern low complexity sequences in proteins and RNAs, with possible implications for the mechanisms of origin of new codes. In summary, far from reducing metabolism to biological fuels and their end products, there appear to be mechanisms of arbitrary coding that directly connect the whole core energy metabolism to a wide range of regulatory functions, affecting from cell behavior to cell fate, across tissues and embryonic development.

Circular Cut Codes in Genetic Information

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In this talk we present an analysis of the dinucleotide occurences in the 3 possible codon sites: site 1 - 2, site 2 - 3 and also site 1 - 3 based on a computation of the codon usage of large sets of bacterial, archaeal and eukaryotic genomes. The same method used to identify the trinucleotide circular, self-complementary code X in genes of bacteria, archaea, eukaryotes, plasmids and viruses was used in the present work to identify two circular dinucleotide codes in codon sites 1-2 and 2-3. Surprisingly, these dinucleotide codes are shifted versions of each other. Moreover, it turns out that the dinucleotide code in codon site 1-3 is self-complementary and contained in the projection of X onto the first and third bases, i.e. cutting the middle base in each codon of X. These maximal dinucleotide circular codes also appear to be universally identifiable in the genome regardless of the species, which raises, among other things, the question of their role in the evolution of the genetic code. We prove several results showing that the circularity and self-complementarity of trinucleotide codes is induced by the circularity and self-complementarity of its dinucleotide cut codes. Finally, we present several approaches of how parts of the genetic code could have evolved from the cut codes during evolution.

Organic Meaning: A Critical Analysis

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This paper attempts to indicate and deal with an apparent tension in Marcello Barbieri's position on 'biological meaning.' On the one hand, and according to Barbieri (2024: 1), "the rule that a codon corresponds to an amino acid is equivalent to saying that that amino acid is the *organic meaning* of that codon." On the other, Barbieri (2024: 141) invokes the Fregean notion of 'sense' to suggestthe following: "Proteins do not have other meanings and this means that the signs of the genetic code (the codons) have sense but not reference, i.e., they have internal meanings but not external ones." The apparent tension here is between reducing 'organic meaning' to referent and reducing it to sense. I focus on both sides of this tension and reveal their consequences. Of particular interest here 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.

Jungian Archetypes as Biological Assembly Artifacts

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Carl Jung's concept of archetypes as universal patterns of the human psyche resonates deeply with contemporary explorations in biology, particularly the work of Marcello Barbieri. Jung proposed that archetypes are innate, collectively inherited forms that shape human behavior and cultural expression. They emerge from a shared biological foundation – or collective unconscious – providing a framework for understanding common psychological and symbolic structures across time and space. Barbieri's research in code biology introduces the idea that life is governed not only by biochemical reactions but also by codified systems (natural conventions) or biological codes that guide the assembly and organization of life at the molecular, cellular, and organismal levels. These codes serve as instructions for constructing and maintaining biological forms and functions, similar to how archetypes shape psychological and cultural constructs. Recent advances in neuroscience reveal the presence of neural codes – patterns of neuronal activity that encode, transmit, and process information within the brain. These codes enable the emergence of cognition, perception, and memory, serving as the biological substratum for archetypal phenomena. By exploring the connection between neural codes and Jungian archetypes, we can clarify how archetypes manifest as structured neural activation patterns, bridging the divide between abstract symbolic forms and their neurobiological correlates. This presentation explores the synergy between Jung's archetypes, Barbieri's biological assembly artifacts, and the neural codes that underlie mental processes. We can conceptualize archetypes as the codes of the psyche, that is, biological conventions embodied in the form of neural codes that govern cognitive life. By interpreting archetypes this way, we position them within a broader semiotic paradigm, where the underlying principles of coded information unify biology, neuroscience, and psychology. This interdisciplinary perspective highlights the unity between the concepts of mind and body, bridging the gap among symbolic representation, neural processes, and material organization. It opens new pathways for understanding how universal patterns in nature and human experience come together into coherent, self-organizing systems, transforming our understanding of life as a interplay of material, neural, and symbolic realities.

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Dreams as a Code Language

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Since Freud, several psychologists have attempted to create a manual containing the correct rules for deciphering and translating the unconscious psychic material. However, while we have not yet fully understood the dream language of the unconscious, this does not mean that we are far from identifying some of its rules, functions, and structures, especially with the advances in the field of dream neuroscience and the advent of Code Biology. Since Code Biology, the study of coding processes in living systems, offers a framework for understanding how neural and symbolic patterns might coalesce to generate the structured narratives of dreams. Firstly, it is essential to understand that dreams, beyond being a universal process in human experience, are not an epiphenomenon but a crucial functional mechanism (Walker, 2017), underscoring their study's importance. Several authors have demonstrated that dreaming plays fundamental roles, such as emotional integration and mood regulation (Cartwright et al., 2003; Walker, 2009; Stickgold & Walker, 2013; Rasch & Born, 2013), cognitive development and learning (McNamara, 2023; Winkelman, 2017; Vallat & Ruby, 2019), as well as memory consolidation (Gais & Born, 2004; Diekelmann & Born, 2010). In addition to its functionalities, dreams follow a set of rules, as they depend on interactions between specific brain modules, especially during the REM phase. The specialization of these modules, often associated with emotional circuits in the limbic system, combined with the characteristic activation of REM sleep, forms the necessary circuitry for transducing raw emotions and memories into highly symbolic and sensory narratives. This process occurs even in the presence of atonia, which prevents the body from moving during dreams, underscoring an intriguing aspect of embodiment in the dream state: even in the absence of overt physical engagement, the brain's mechanisms for processing emotions and memories rely on neural structures deeply connected to the body's affective states.This phenomenon may also be correlated with the generation of archetypal images or representations (Vedor, 2023), as cognition and affective imagery are thought to be organized by underlying archetypal codes (Major, 2021;Alcaro, Carta &Panksepp, 2017; Goodwyn, 2024). Deeply embedded in the psyche, these codes may act as fundamental organizing principles, shaping dream narratives' symbolic structure and affective resonance. These archetypal codes, potentially encoded in the form of neurognosis (Vedor, 2023), provide the scaffolding through which symbolic imagery and affective narratives are constructed. Moreover, these REM-phase dreams, which activate circuits associated with the limbic system, often have a prospective, bizarre, extravagant, and symbolically dense nature (Hobson, 2009; McNamara, 2023), echoing ideas defended by Carl Jung. However, Solms (2018) identified a less typical class of dreams associated with the expression of desire and pleasure, as proposed by Freud. These dreams, occurring during the NREM phase, are distinguished by the activation of the prefrontal cortex, which is deactivated in the REM modality. This discovery demonstrates that the activation and deactivation of specific brain modules create the grammatical structure necessary to develop the symbolic language of dreams.

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Merging Biology with Humanities:
Code Biology, Biosemiotics and Eidetic Biology

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One of the characteristic features of contemporary science is the emergence and development of frontier disciplines that link the fields of science, social science and the humanities. Philosophy of science has not paid enough attention to this topic (Kellert 2008 may be an exception). The origins of some of these frontier disciplines seem to be historically traceable to the 1970s and 1980s. Important examples for us are the birth of semantic biology by Marcello Barbieri (especially Barbieri 1985) and eidetic biology by Zdeněk Neubauer (e.g. Neubauer 2002, Kováč and Neubauer 2019). Barbieri's semantic biology and later code biology retained the link to the original biological background, which he expanded (adding a new meaning/code to the traditional concepts of biology – energy and information). While Neubauer's theory remained biological only nominally, it was transformed into a new philosophy of life/living. Neubauer's case is interesting at the same time also because his long intellectual career inspired a whole branch of biosemiotics – Barbieri calls it hermeneutic (e.g.Markoš 2002, cf. Barbieri 2015). Thus, the circumstances of the emergence of frontier disciplines between biology and the humanities also enter into answering the key question concerning the relationship between biosemiotics and code biology. Biosemiotics as a new philosophy of the living; and code biology, which still seeks a close alliance with mainstream biology (cf. Zámečník 2023). The aim (1) of this paper is to trace some of the causes that led to the merging of biology and humanities in the aforementioned period of the 1970s and 1980s (and which also resulted in the phenomenon of *new age science*, cf. Hanegraaff 1997). Using Barbieri (1985) and Neubauer (2002) as examples, the narrower aim is then (2) to trace the diametrically opposed trajectories along which the frontier disciplines can take; and (3) to elucidate the origins of these differences (following the texts Zámečník 2021, 2019). (Translated with the support of DeepL.com)

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The Mechanisms of Evolution

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One of the main concepts of Code Biology is the idea that evolution took place by two distinct mechanisms, by natural selection and by natural conventions. Natural selection is the long term result of the copying of the genes and is based on chemistry and information. Natural conventions are based on chemistry, information and meaning, where meaning is the result of semantic processes, and in particular of codes. Today we have ample experimental evidence that hundreds of codes exist in living systems and it is a fact therefore that the evolution of codes was an integral part of the evolution of life. Here it is shown that not only the evolution of codes but also the conservation of codes requires meaning and is therefore the result of natural conventions.

The Glycomic Code Degradation is a Biodiversity Driver

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One of the main drivers of biodiversity life cycle adjustment is the Glycomic Code, the code within the extracellular matrices of living beings that determines function, simultaneously avoids degradation, and keeps cells alive. Plants comprise 60% of Earth's biomass, most in the extracellular matrices. Alternatively, without biomass degradation, life would be impossible on Earth as the planet would quickly become wholly covered by kilometers of dry leaves, stems and branches, dead microorganism cells, and the bodies of animals. Thus, if degradation were too easy, the survival of plants and other organisms would be difficult or nearly impossible. Due to the Glycomic Code, degradation cannot be performed by a single organism but by cooperating ones that are individually capable of breaking parts of the code. Because plants and other photosynthetic organisms are the first step in any food chain, life's stability is determined by the timing of the planet's carbon cycle. Such timing has probably been adjusted during evolution so that degradation of dead biomass can send C back to the atmosphere so that the concentration of CO_2 is balanced in the range that photosynthesis can occur along with biological development and reproduction. The Glycomic Code is one of the key factors in the stabilization of biodiversity.

Ecolinguistics, codes and the Möbius loop

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Eco linguistics aims at responding to Haugen's (1972) question: "how does a language interact with its environment?" Although a focus on "language" offers no answer, the question opens-up a challenge to linguistics. Some asked how discourse favors ecosystemic neglect, degradation and, above all, toxic decisions that fuel climate change. Seeking a positive agenda, ecolinguists slowly abandoned the notion of "language" to develop a normative approach to life sustaining relations (Döring et al., in press). It became clear that a language and its environment interact as people perform practices, tell stories and use how communities and emplaced bodies channel energy. Haugen's question leads enquiry to languaging: as integrated with practices and agency, a lived *now-here* can be used to achieve intended and unintended effects. In languaging as in life, stability balances with a flux of novelty. Languaging, practices and agency constitute a Möbius loop. As living systems adapt at varying rates, they find and sustain interdependencies that allow and set off viability. Organic codes and simplex tricks gave rise to nervous systems that favor anticipatory activity and learning. Neural coding responds to niche construction and how adaptors bring knowhow to bodiment. Humans themselves self-construct as adaptors who use practices and languaging. As communities of bodies, they stabilize practices as parties monitor, re-render and refine the use of skills. Individuals orient to icons, rituals, alphabets and number systems etc. as cultural codes sustain custom, routine and habits. In Gahrn-Andersen's (in press) terms, we use praxeological codes. Yet, in cases like 'willing' moves by a cyborg cockroach, parties bring self-directed action to epistemic engineering (Cowley & Gahrn-Andersen, 2023). They establish neural techniques that override old habits (and beliefs) by drawing on languaging. As a result of coming to coordinate practices, we alter knowing, agency and even the observed. As a result, we assemble, systematize, reject or lose, epistemic markers of what is (or counts as) warranted. Just as the looping draws on the workings (and constraints) of code, they carry implications for practices. First, epistemology must consider how practices enable coming to know. Second, much pivots on how groups or gatherings make explicit use of ecosocial knowledge in order to achieve normative concerns. Third, within every *now-here*, the bioecological flux of languaging brings awareness and some sense of the possible. Thus, the epistemological conception of mind gives way to recognition that living uses a Möbius loop to discern "quality" and, by harnessing directedness, uses the results to change the possible.

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What expands the primary codes of human communication/cognition to broader complexes of cultural affordances?
Why do our cultural affordances still essentially work as codes?

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The paper elaborates a major finding of code biology and communication studies about actual plurality of codes that provide multiple coding for actual biological and human communication/cognition. As for December 2022 the code biology data base by Robert Prinz included 237 individual codes, some of them actually being multiple (complex) ones. There are more to be discovered and included to this data base. Most likely is that human social, communicative and cognitive codes are even more numerous. Actual instrumental and operational setups for human interaction include devises for autocatalyzing, copying, habituating and 'memorizing' that are simpler than codes and propensities for evaluating, selecting, foreseeing, imagining, comparing and conventionalizing that are far more subtle that ordinary codes. When a person looks for an umbrella term for all those setups and their constituents s/he is typically inclined to call the human codes or cultural codes. Why is that possible and highly probable? A plausible explanation is that all constituent devises are just modifications of their common eigenform. In the interminable eigenform succession or array codes are close to midway crux extension. The central location of codes and humans in the Observable Universe between its 10^{-20} quantum-mechanical depth and 10^{24} width (Rees 1999, see Figure 1.1 on p. 8) corresponds with the vision of agentive work that shapes the universe (Deacon 2011). The evolution of the universe emerges with elementary quantum-mechanical distinction of inside and outside at the moment of primary quanta as modeled with Albert quantum-mechanical automation (Albert 1983; Albert 1987). The elementary quantum enclosure embodies the initial eigenform that evolves as recursion. Its more elaborate version is recursion and recursion with inversive switch (Ilyin 2020; Ilyin 2023). Further series of emerging eigenforms model successions of poieses yielding coping, habituating, coding, evaluating, selecting, foreseeing, imagining, cognizing and languaging. The most evolutionary eigenforms of anthropogenic autopoiesis are sophisticated complexes of devises that are habitually are called culture codes.

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Evolutionary Symmetries of the Genetic Code and their Implications for Natural Computing

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The genetic code, viewed as the simplest abstract description of the complex process of translation, is characterized by various symmetries. These symmetries are not mere mathematical peculiarities but are deeply intertwined with the molecular mechanisms governing gene expression and the faithful decoding of genetic information. The emergence and evolutionary path of these molecular mechanisms are intrinsically linked to the origin and evolution of the standard genetic code in the progenotic stages of life, indicating that certain symmetries can be evolutionarily very distant. Despite the considerable uncertainty and complexity surrounding primordial evolution, it can be considered as a consensus view that the genetic code has evolved from a rudimentary, imprecise form to its current advanced, highly accurate state. This evolution, encompassing the transcription and translation machinery and the organization of genetic information itself, could have left traces in the transition of symmetry from the dinucleotide to the trinucleotide (codon) level. While dinucleotides determine the most prominent symmetry of the genetic code in the form of bipartition associated with its degeneracy (redundancy), codons are essential for the precise specification of all proteinogenic amino acids. This code redundancy is crucial not only for minimizing translational errors but also for enabling other "regulatory codes". Within certain protein-coding regions, synonymous codon preference is often influenced by factors beyond protein structure, such as transcription factor binding. This overlap of the genetic code and other regulatory codes related to transcription, chromatin organization, mRNA splicing, cotranslational folding, etc., is considered to be partly manifested in constrained codon choice, more precisely defined through codon and codon-pair usage bias, phenomena directly linked to dinucleotide bias. Remarkably, this hierarchical organization of the genetic code and its numerous symmetries are describable through arithmetic regularities in nucleon numbers of its constituents. Given that some of these symmetries likely originated in different evolutionary epochs, nucleon number balancing may represent a fundamental, underlying mechanism influencing the organization of living matter. We further propose that these phenomena are relevant to natural computing.

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Algorithms for code biology – from truth table to relational model

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We present recently developed algorithms for coding, decoding and encoding procedures in Code Biology [1,2]. The aim of the presentation is to show that the algorithms based on logical operators and truth table are applicable to:

1. Relational model (RM) approach to managing data—using a structure and language consistent with first-order logic;
2. Use of mathematical and logical operators and truth table elements as a toolkit for statistical and machine learning methods in data analysis;
3. Encoding of operators by means of the Standard Genetic Code (SGC) table and other genetic code tables;
4. Extractionof (bio)informatic genotype and phenotype descriptors that are relevant for biological system analysis – including structure, function, interaction and evolution.

According to Marcello Barbieri: "Code Biology studies all codes of life, from the genetic code to the codes of culture"[3]. We show "how and why" the algorithms based on Boolean functions, truth table elements and relational models may be used to prepare data, evaluate models and validate results in Code Biology [1,2]. Modeling and manipulating with uncertain and imprecise information is discussed considering algorithms based on probabilistic square of opposition, semiotics quare and Klein four-group encoding.

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Mapping Knowledge Domains and Research Trajectories
in Code Biology Through Scientometric Analysis

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Code biology has emerged as a promising framework for understanding life's fundamental organizational principles by integrating insights from biology, philosophy, and systems science. Through a comprehensive scientometric analysis of the field's literature, we present its intellectual landscape and developmental trajectory. Our study reveals 24 distinct thematic clusters that span from theoretical foundations—including the philosophical underpinnings of biological codes—to specialized domains such as neural coding mechanisms and information processing in brain networks. Scientometric approach provides unique insights into code biology's complex landscape that traditional literature reviews might miss, revealing both explicit connections and hidden patterns between research domains. Such approach also exposes how the field's fragmented nature has hindered the development of comprehensive theories about how biological codes interact across scales, resulting in isolated knowledge niche that limit our understanding of coding systems' role in life's complexity. Using natural language processing techniques, we tracked the temporal evolution of research themes, mapped their geographical distribution, and identified emerging collaborative networks. This analysis demonstrates how peripheral concepts developed into core theoretical frameworks, leading to productive cross-disciplinary collaborations. Our investigation also reveals significant research gaps, particularly in understanding how biological codes operate hierarchically and shape the emergent properties of living systems. Our findings provide the first systematic overview of code biology's knowledge architecture, demonstrating its potential to bridge reductionist and holistic approaches in biological research. We identify key research directions, including decoding the grammar and code structure of neural signaling, understanding code-driven evolutionary transitions, and examining the relationship between biological and artificial codes. Beyond serving as a roadmap for researchers, this work emphasizes the need for standardized methodologies and definitions to study biological codes across multiple scales of organization—from molecular interactions to ecosystem and cultural dynamics.

Codepoiesis Approach to the Exaptation of Molecular Architecture in Simple Cells: A Biophysics and Biosemiotic Framework for Basal Cognition Processes

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Assembly theory currently offers a promising framework to connect the construction of subcellular "objects" with evolutionary processes. A critical question is whether, within this theory, biophysical patterns impose proscriptive constraints that limit developmental capacities. In other words, these patterns may permit interactions as long as they do not violate survival thresholds, thereby enabling satisfactory modifications to be incorporated. This process reflects a biomolecular and subcellular form of exaptation.

The "assemblage space" described by Sharma and colleagues presents a plausible model for establishing semiotic landscapes of agency that facilitate meaningful connections. Such connections imply the existence of an Umwelt in which the "semiophysical" and "semiochemical" fields of perception are grounded in constructing biomolecular objects with both code and biomolecular semantics. This concept forms the basis of our exploration. Effective responses in this framework manifest as oscillations, rhythmic synchronies, and the discrimination of noise. It is vital to establish a link between chemical oscillator communication and bioelectrical—and potentially biophotonic—patterning for protein organelle assembly, recycling, polymerization, and the generation of codes via molecular adapters and agents. We aim to develop a theoretical framework to investigate the mechanotransductive implications of protein assembly, focusing on actin filaments and microtubules, and their role in coherence and decoherence activities within chemical and bioelectric oscillators. This study will also explore the quantum biological implications of these processes as the foundation of intracellular communication. Specifically, we seek to understand whether quantum rheology and bioelectrodynamics influence the sol-gel colloidal behavior of the cytoplasmic environment surrounding these organelles. These protophenomenological insights may lay the groundwork for a model of assembly coding involving tubulins, actins, and second-order messengers. This "codepoiesis" integrates exaptation with adaptation processes. Our proposal introduces a preliminary paradigm within biosemiotics, advancing a pluralistic epistemology. This paradigm emphasizes structural relationships, not only through multilevel analysis—as in the New Mechanistic Philosophy—but also by examining the interplay between "organism/agency" and "environment/ecosystem." In dynamic ecosystems, greater homeostatic balance is achieved when structural stability is maximized. This balance highlights the processual and physiological capacities of organisms/agencies, fostering coexistence and enabling recognition of the conditions for persistence. Such recognition extends to sentience, basal cognition, vivaciousness, subjectivity, and the subjecthood of organisms.

Code evolvability and extendibility:
The difficult extension of the genic code to 22amino acids versus the high plasticity of the transcription regulatory code

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The genetic code is an unambiguous and virtually universal code. Unambiguous means that each codon codes for only one amino acid or a stop signal. Universal means that the translation table is the same for all organisms and, consequently, also for all cell types in a multicellular organism. It is believed that the genetic was frozen early in evolution. Consequential subsequent modifications of the code have not occurred later in evolution, presumably because of the pleiotropic effects that such changes would have on virtually all proteins of an organisms. Exceptions proof the rule. The minor variations observed in the alternative genetic codes discovered so far primarily occur in organelle genomes coding only for a few proteins and mostly involve substitutions between chemically similar amino acids. Nevertheless, evolution managed to add two amino acids to the code, selenocysteine and pyrrolysine. These amino acids are considered true additions to the code because they are inserted into proteins during translation, by a process guided by cryptic signals with the messenger RNA sequence. Much less is known about the transcriptional regulatory code. The inputs are transcription regulatory DNA sequences, the outputs are transcription rates of target genes. This code has not been cracked so far, as we are largely unable to predict output from input. Nevertheless, we do know some general features of the code from experiments. The code is definitely not universal, not even withing the same organisms. It has been shown that the same transcription regulatory sequence drives transcription of the same target genes in some cell types but not in others. We also have some knowledge of the highly complex decoding machinery. The first step of the decoding process involves transcription factors (TFs) binding to degenerate DNA sequence motifs. TFs are the primary adaptors of the transcription regulatory code, and sequence motifs its elementary inputs. DNA motifs may occur in overlapping fashion, in which case the same DNA sequences could potentially be bound by alternative adapters. All this leads to high ambiguity of the code. The cell type specificity of the code can be explained by cell type-specific expression of different subsets of genes. Code extension is documented by a massif expansion of TF repertoires correlated with organismic complexity. In my talk, I will present more details on the extensions of the genetic code. I will argue that the addition of selenocysteine and pyrrolysine to the code involved complicated workarounds and *ad hoc* solutions, which make further extensions unlikely. The reason why biological evolution cannot simply reassign codons to new amino acids is presumably the lack of an evolutionary path towards this goal via viable intermediates. By contrast, code expansion by means of synthetic biology technology appears entirely feasible after the successful chemical synthesis of an entire microbial genome. I hope to be able to stimulate a discussion on the desirability and dangers of technological advances in this direction. I will also present more details on the transcriptional regulatory code in support of a grand claim that three characteristics of the transcription regulatory code, namely evolvability, ambiguity and tissue-specificity, have enabled the evolution of the first multicellular organism with cellular specialization, and driven the evolution towards organisms of ever higher complexity since then.

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A Million Codes Away – Steps Towards Code Cladistics

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In this conference contribution the roadmap from the *Code List* (Prinz, 2022) published by the International Society of Code Biology towards an integrated online *Code Database* and a subsequent systematic classification of codes will be discussed. Codes are involved in basic cellular functions, like metabolism or inheritance (Prinz, 2023a). Such codes often can be found piggybacked with regulatory codes embedding the conduct of life processes in dynamically changing environments. Comparative code research can be based on various aspects shared by or distinguishing different kinds of codes, including mechanisms of involved components, number of instances, or pattern of mapping. In the literature, codes are described with certain terminology: Codes involving chemical modification of molecules and resulting modification patterns, e.g., phosphorylation, are often reported in conjunction with *roles* like readers and writers. Whereas such roles can differ between codes, components maybe shared by many codes. Also, the nature of involved components (e.g., analog vs. digital, discrete vs. continuous) can be used to characterize codes. Accounting for various aspects will enable a deep understanding of the web of codes that builds the fundament of cellular life. An ever-increasing list of organic, neuronal, psychological and mental codes emerges (Goodwyn, 2024; Prinz, 2023a) - among them a variety of "*non-Barbierian*" (adaptorless) codes have been published recently (Gordon & Gordon, 2019; Igamberdiev & Gordon, 2023) (Heng & Heng, 2021; Heng & Heng, 2023; Paredes et al., 2021) calling for a systematic classification. A comprehensive knowledge of all codes across biological kingdoms, domains, and levels of hierarchy will enable a better understanding of evolution (Prinz, 2023b), health and disease (Heng, 2025; Heng & Heng, 2022; Kasperski & Heng, 2024).

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The Unconscious and the Process of Falling in Love:
An Integrative Perspective from Analytical Psychology, Code Biology, and Affective Neuroscience

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This presentation explores the role of the unconscious in the process of falling in love, based on the Jungian perspective. This perspective views the unconscious as a repository of archetypes – phylogenetic memories that influence human behavior. When we fall in love, we access these deeply rooted patterns, experiencing echoes of ancestral emotions. Love isoften seen as a universal experience because it has been a fundamental part of human life for millennia. By combining this understanding with Code Biology, which views organic codes as carriers of encoded meanings, and affective neuroscience, which investigates how emotions are stored and expressed in the brain, we aim to provide a comprehensive framework for understanding romantic attraction. The research suggests that the unconscious mind, serving as the center of emotional processing, interacts with the conscious mind and environmental stimuli to activate archetypes – essentially biological behavioral programs – that guide interpersonal attraction. Emotions and feelings, which are central to neuroscientific inquiry, position love as the quintessential human emotion. It represents the culmination of various phases, each regulated by evolutionarily conserved and integrated neural substrates. Scientific findings highlight the positive effects of love on mental and physical health, emphasizing the roles of oxytocin, vasopressin, neuropeptides, and neurotrophins in these processes.

In conclusion, this integrative perspective enhances the theoretical comprehension of falling in love and offers practical applications in therapeutic and educational contexts. By acknowledging the influence of the unconscious and archetypes in forming romantic bonds, strategies can be developed to approach relationships with greater awareness and health. Additionally, the fusion of Code Biology and affective neuroscience provides new insights into how biological codes and neural circuits underpin the intricate emotional tapestry of love.

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Algebraic gestalt-archetypes of probabilities
in genomic DNAs, cyclic Gray codes, quantum bioinformatics

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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 study of the regularities of the statistical organization of nucleotide sequences of single-stranded DNAs in genomes of higher and lower organisms, as well as their connections with cyclic Gray codes, and the problem of holistic structures (gestalts) in physiology [2, 3]. The author presents stable statistical structures of an algebraic nature, which are found in many genomic DNAs and are called algebraic gestalt-archetypes of probabilities in genomic DNAs. They are discussed as a possible basis for several genetically inherited physiological and psychophysical properties. The numerical rules of these genomic archetypes realized in nature for a representative class of genomic DNAs, whose initial data were taken by the author from the publicly available genomic data bank "GenBank", are formulated. The analysis of single-stranded genomic DNAs was carried out using the author's method of "hierarchies of multilayer statistics", representing the nucleotide sequence of DNA as a multilayer text structure, in which each n-th layer is a sequence of n-plets (that is, of monoplets, or duplets, or triplets, etc.). In each such layer, the percentages of each of the types of its n-plets are calculated, the values of which are inserted into the so-called genetic ($2^n \cdot 2^n$) Karnaugh matrices, whose columns and rows are numbered by n-bit Gray codes by analogy with Karnaugh maps from the Boolean algebra of logic. The data of the analysis of the nucleotide sequence of DNA of the human chromosome № 1, containing about 250 million nucleotides, are represented as an example. The obtained data are discussed in light of the problem of genetically inherited holistic structures in biology and the tasks of developing algebraic biology, genetic biomechanics, quantum bioinformatics, artificial intelligence, and genetic algorithms.The following aspects are also considered: the author's concept about gestalt-archetypes of probabilities in genomic DNAs of higher and lower organisms in comparison with the C.Jung concept about the archetypes of the collective unconscious in humans; structural analogies of checkers and chess with the genetic code system and multidimensional Gray codes;the role of physiological cycles and vibrations in self-organization; the fundamental problem of "stochastic and determinism" in biology.

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Code biology from the outside:
A view from languaging

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Languaging is of increasingly central concern to the language sciences (Ilyin, 2024). While views vary, languaging shapes what happens as people engage, use tools and perform practices. Thus, agency, practices and languaging coalesce in a Möbius loop. They unite a life history as wordings (and verbal patterns) integrate activity with bodiment: by definition,languaging is a *multiscaled coordinative activity in which wordings play a part*. As multi-scaledflux, its systems must co-evolve in a lineage whose practices and ontogenetic niche bring plasticity and local worlds to how people use cultural resources in *doing agency* (Cowley, 2025). The interdependencies of languaging begin in the territory of theoretical biology. How can one approach necessary life sustaining relations? The question is at odds with how, typically, "language" is formalized and said to draw on a linguistic 'competence.' Thus, while Chomsky sought universals based on symbols and computation, others suggest that older bio-modelling was extended by symbolic interpretation, recursion or embodiment. For formalists and functionalists alike "language" funnels intellect as knowledge draws on sentence-generation, interpretation or linguistic bodies. With such idealizations, attention turns away from practices, persons and agency. One conceptualizes "language"as independent of evolution and ontogeny while ignoring the coordinative activity of perceiving, speaking-hearing, thinking, feeling and acting. From a languaging perspective, formal models are cultural inventions. Multiscaled activity can only begin with how bodies bring human agency to get things moving, enact practices and instigate self-directed learning. Languaging is part of a continuous looping that prompts people to perform lived stories, adapt to circumstances and draw on brains, bodiment and practices in enlanguaged worlds (Cowley, 2024). Languaging allows communities to stabilize ways of acting by making consistent use of wordings. Practices and languages allow for the meshing of cultural and neural codes as brains self-organise to ground modes of action. In short, they attune human adaptor systems whose bodiment depends on what Barbieri (2012) calls the codes of life. In coordinative activity, happenings within practices rely on concerted wording-types in ways that can *also* be construed as signs or described formally. Hence, ecolinguists and all who pursue languaging can learn much from the interdisciplinary study of codes and adaptors in fields like biology, neurosciece, ecology, philosophy, mathematics, and computer science.

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Semiosis in Action: A Biomolecular Perspective

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By semiosis, we refer to the formation of a sign, specifically the establishment of the complex relationship between the "signified" and the "signifier." The primary scheme of such a transformation of non-semiotic units into a semiotic complex can be found in the mechanisms of genetic information where a semiotic system (the genetic code - GC) is emerged from two biochemical substances (nucleotides - amino acids).

In molecular genetics, it has been demonstrated that the origin and functioning of the genetic code cannot be explained solely by processes of self-assembly or self-organization. Instead, it necessitates an additional level of symbolic control, as highlighted by concepts such as autogene (T. Deacon, 2011; 2021), codepoiesis (Barbieri, 2012), and biosemiosis (H. Pattee, 2012). The processes revealed in molecular genetics show that it is not signs fixed as a stable unity of the signifier and signifieds, but schemes of regular correlating these entities. Meanwile, initial analogies were drawn from the semiotics of natural language, as discussed by G. Gamow (1953) and F. Crick (1981), who viewed the GC as *a dictionary from the language of nucleotides to the language of amino acids*. However, findings in molecular genetics suggest that what we are dealing with are not stable signs, but rather schemes that regularly correlate these entities. This perspective makes it possible to rethink the very nature of semiosis. The consideration of semiotic relations and operations in genetic coding leads to a revision of the accepted linguistic understanding of the sign as a kind of substitute associated with some object by social conventions. The new perspective allows us to eliminate the conventional and socially determined characteristics of signs as *conditio sine qua non* and adopt a broader understanding of sign production as an inherent property of systems that control information processes. Such semiotics can form the basis for understanding the sign system proposed by U.Eco (1968), as it *is a system that explains itself through the unfolding of increasingly complex conventional systems*. An exemplification of such a language is the GC, it encompasses correlation schemes between nucleotides and amino acids, as well as between amino acids and proteins. It also includes operations that regulate and interact with the context (environment). The recognition of conventionality as a necessary condition can be reformulated and replaced by interaction schemes. As a first step, we need to reconsider the representation of the genetic code as a static vocabulary and recognize its dynamic character – in this case a sign as determined association between the signified and the signifier arises every time as a result of an operation performed here and now, as a codepoiesis (or semiopoiesis) in action. At the same time, the nature of semiosis at each stage of the gene expression (DNA - mRNA - tRNA) is changed. These stages can be considered as a transition from hypertext (genome as a set or sequence of texts) to a single text (gene) and sign (tRNA). A full-fledged sign as a triadic relationship (sign vehicle – sense – meaning) is represented by tRNA; it is a substantially materialized association between an anticodon and an amino acid. Additionally, in association with mRNA, tRNA acts as a second-order signifier for a complex sign: *codon of mRNA → {(tRNA anticodon + tRNA) → amino acid}*.

Titian's mythological paintings: A pictorial personal code?

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The talk attempts to introduce *pictorial personal codes* different from linguistic ones (Marconi, V. 2023. *The Flower of the Desert and a Migrant Experience: Two Examples of Personal Codes*. BioSystems, 233, 105040). Indeed, the *pictorial turn* suggests that cultural history is a struggle between words and pictures (Mitchell, W.J.T. 2015. *Image Science*. Chicago and London). Pictures differ from words but are not purely visual media (Mitchell, *ImageScience*, p. 14). The difference can be traced back to Marcello Barbieri's distinction between the *world of* perceptual *objects* and the *world of names* (*Codes and Evolution*. Cham, pp.207-217). Still, these worlds correspond to modeling systems that also employ codes. I hypothesize that pictorial personal codes do not have a second-order language or abstract system of rules behind them but still present a set of norms that can be divided into shared and individual. Much like a speaker or a writer, a painter works in a tradition and deliberates on which models are best to be creatively followed even if, differently from languaging, painting does not involve a second-order language. In painting, the second-order language is substituted by *legisigns* that are not codes: "[…] while all codes are legisigns, not all legisigns are codes: a legisign is simply a type of complex and most often familiar sign" (Jappy, *Introduction to Peircean Visual Semiotics*. London and New York, p. 48). Thus, the presence of *non-code* legisigns, i.e. signs that are types or rules without building a constant system, does not hinder the fact that pictorial personal codes are real codes since they share the normative dimension with the linguistic ones: both kinds of personal codes are made of norms constrained by legisigns, yet linguistic legisigns or symbols are organized into codes and pictorial legisigns or images are not. Moreover, I will exemplify with a case study on the Venetian painter Tiziano Vecellio that pictorial personal codes can have literary, i.e. linguistic, connotative meanings (Marconi, *The Flower of the Desert*, p. 7). Combining research results from art history, I will show that Titian developed his workshop into a modern firm and, as a legitimization, defined his original style in terms of tragic painting, namely a personal way of painting connotating a literary genre like Greek tragedy (Puttfarken, T. 2005. *Titian and Tragic Painting*. New Haven and London; Tagliaferro, G., Aikema, B., Mancini, M., Martin, A.J. 2010. *Le botteghe di Tiziano*. Florence). I will also assess the role played by a graphic code in synergy with Titian's pictorial one (Lüdemann, P. 2016. *Tiziano. Le botteghe e la grafica*. Florence). Eventually, I will draw some consequences for the social ontology of the firm from this case study to the extent that Titian's tragic painting shows how a personal code originates and spreads in a community as much as a firm is a community of community-like individuals.

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The Creation of Artificial Biological Codes
by the Pharmaceutical Industry

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I have found examples of artificial biological codes created by means of an arbitrary association, which may be compared to our concept of natural biological codes. Although these new artificial codes will not be genetically fixed, they can serve as an example of a code being learned for use during an individual's lifetime. In one case (Talwar et al., 1976), researchers developed an anti-fertility vaccine by linking the hormone Human Chorionic Gonadotropin (HCG) to a tetanus toxoid by a physical conjugate. When injected with the product, subjects develop antibody responses to the tetanus *and* the HCG. HCG is a necessary component for a successfully developing embryo. If a vaccinated subject becomes pregnant, the embryo will be spontaneously aborted. The conjugate here plays the role of an encryption apparatus. The body learns to mis-associate part of itself (HCG) with a toxic substance. This autoimmune response is a qualitatively different process than the normal process of an antibody response. Thus, we can say that learning, via a code, has taken place. With this example, we can confirm that biological systems can learn new encrypted codes, that is, new symbols, arbitrarily relating one thing to another. In this case, what is learned is irrational, from the perspective of the body, because it triggers an autoimmune response. In another case, in order to test its allergy medicines, the pharmaceutical industry has caused rodents to be allergic to things in order to use them as test subjects. To make such models, experimenters inject aluminum hydroxide (which is toxic), while at the same time exposing the rodent to, for example, egg whites. The immune system associates the egg protein with the toxin. The rodent develops an allergy to egg protein (Yasar, et al. 2016). In this example, there is no physical adapter like the conjugate above. Instead, the association appears to be made by the immune system via a process known as by-stander activation. That is, whatever proteins happen to be present in large numbers at the time of injection of the toxin tend to be identified by the immune system as related to the inflammation caused by the aluminum hydroxide toxin. Other cases of "natural" arbitrary association via by-stander activation can result in auto-immune disease as a result of an acute infection. Again in this case, the immune system mis-associates self with toxins, due to the high percentage of waste materials from the process of autophagy. It must be stressed that these false codes are not passed on to offspring and thus do not function as heritable memory in the way that other biological codes do. In addition, these "hacks" disrupt the organism's system and create illness and/or reduce reproductive fitness. Furthermore, these examples may be instructive for the health industry. Drug companies can't explain how such desired interventions (like an anti-fertility vaccine or allergy models) are possible without using the concept of biological codes. Additionally, perhaps there are other forms of chronic illnesses that are created inadvertently by such "hacks." It is worth investigating.

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