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European Colloquium on Philosophy of Life Sciences – [EUPhilBio](#)

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May 18-19, 2023, Zagreb, Croatia

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Scientific Program of *EUPhilBio\_2023*

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EUPhilBio 2023



**Thursday, May 18**

*Closed Session*<sup>1</sup>

Chairs: [Petar Tomev Mitrikeski](#) & [Predrag Šustar](#)

- 09:15 – 09:30 **Contemplating EUPhilBio\_2024** – First Parley  
09:30 – 09:35 *Short pause*  
09:35 – 10:00 **Fostering EUPhilBio Summer School** – Second Parley

*Get-together & Opening the Event*

- 10:00 – 10:20 *Light refreshment*<sup>2</sup>  
10:20 – 10:25 *Opening address*<sup>3</sup>

**First Open Session: EVOLUTION**

Chair: [Dragomira Majhen](#)

- 10:30 – 11:00 *Opening Lecture* | [Eörs Szathmáry](#) (Centre for Ecological Research<sup>4</sup>)  
*The problem of open-ended evolution*<sup>5,6</sup>  
11:00 – 11:15 Discussion (Moderator: [Krunoslav Brčić-Kostić](#))  
11:15 – 11:45 [Krunoslav Brčić-Kostić](#) (Ruđer Bošković Institute)  
*Adaptation from standing genetic variation*  
11:45 – 12:00 Discussion (Moderator: [Eörs Szathmáry](#))  
12:00 – 12:15 *Short pause*  
12:15 – 12:45 [Ehud Lamm](#) (Tel Aviv University)  
*Collective knowledge and cultural evolution – An analysis of conceptual options*  
12:45 – 13:00 Discussion (Moderator: [Dario Pavić](#))  
13:00 – 13:30 **Bruno Petrušić** [Pontifical University of St. Thomas Aquinas (*Angelicum*)]  
*Philosopher's dream about evolution: Daniel Dennett*  
13:30 – 13:45 Discussion (Moderator: [Danijel Tolvajčić](#))  
13:45 – 14:25 *Light lunch*<sup>7</sup>

**Second Open Session: CODE BIOLOGY**

Chair: [Miroslav Plohl](#)

- 14:30 – 15:00 [Nikola Štambuk](#) (Ruđer Bošković Institute)  
*Standard genetic code: from IUPAC nomenclature to code biology*  
15:00 – 15:15 Discussion (Moderator: [Petar Ozretić](#))  
15:15 – 15:45 [Paško Konjevoda](#) (Ruđer Bošković Institute)  
*Relational model of the standard genetic code*  
15:45 – 16:00 Discussion (Moderator: [Krunoslav Brčić-Kostić](#))  
16:00 – 16:15 *Short pause*

See further, please.

<sup>1</sup> [The EUPilBio Core](#) only (PTM's chambers)

<sup>2</sup> Faculty café (all participants and guests)

<sup>3</sup> Opening & Closing addresses and Open sessions will take place in hall [f. Peter-Hans Kolvenbach SJ](#) (all participants and guests)

<sup>4</sup> See affiliation details below

<sup>5</sup> Duration of lectures in Open sessions: 30 min + 15 min discussion (**a muffled bell will be sounded 5 min before the lecture time expires**; exceeding the presentation time is allowed, but then the time for discussion will be shortened accordingly)

<sup>6</sup> See all abstracts below

<sup>7</sup> All **registered** participants and [EUPhilBio 2023 Crew](#) (on the roof of the building)

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## Thursday, May 18 continuation

Zoom Section: UNDERSTANDING IN BIOLOGY

Chair: [Maja Tomičić-Christmann](#)

- 16:15 – 16:45 [Arnon Levy](#) (Hebrew University of Jerusalem)  
*Revisiting the value-free ideal*
- 16:45 – 17:00 Discussion (Moderator: [Maja Tomičić-Christmann](#))
- 17:00 – 17:05 *Short get-together in the open (end of Working Day 1)*
- 17:05 – 18:30 *Free time*

### Non-Session

- 19:00 – *Casual get-together over dinner*<sup>8</sup>



## Friday, May 19

### Get-together

- 09:00 – 09:40 *Light refreshment (get-together in the open)*

### Student's Corner<sup>9</sup>

Chair: [Tomislav Šerić](#)

- 09:45 – 10:05 [Toma Gruica](#)<sup>10</sup> (University of Graz)  
*Seeing red: the phenomenology of color and the biological basis of artistic experience*
- 10:05 – 10:15 Discussion (Moderator: [Jan Defrančeski](#))
- 10:15 – 10:35 [Filip Sente](#)<sup>11</sup> (University of Zagreb)  
*Quantitation of fundamental attribute of life through xenobot classification*
- 10:35 – 10:45 Discussion (Moderator: [Branimir Antun Puntarić](#))

### Third Open Session: UNDERSTANDING IN BIOLOGY

Chair: [Darko Polšek](#)

- 10:45 – 11:15 [Petar Tomev Mitrikeski](#) (University of Zagreb)  
*Applying the elegance paradigm to rank recombination models*
- 11:15 – 11:30 Discussion (Moderator: [Krunoslav Brčić-Kostić](#))
- 11:30 – 12:00 [Tomislav Stojanov](#) (University of Nottingham)  
*On Croatian eels and Serbian snakes: natural science taxonomies vs. sociolinguistic typologies*
- 12:00 – 12:15 Discussion (Moderator: [Ines Skelac](#))
- 12:15 – 12:30 *Short pause*
- 12:30 – 13:00 [Predrag Šustar](#) (University of Rijeka)  
*Explanation and understanding in biology: the case of scientific metaphors*
- 13:00 – 13:15 Discussion (Moderator: [Ehud Lamm](#))
- 13:15 – 14:00 *Light lunch*<sup>12</sup>

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See further, please.

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<sup>8</sup> [PUB MEDVEDGRAD ILICA](#) (all participants interested in casual socializing; dinner and beverages at one's own expense)

<sup>9</sup> Duration of lectures in Student's Section: 20 min + 10 min discussion

<sup>10</sup> Doctoral student of Professor [Sonja Rinofner-Kreidl](#)

<sup>11</sup> PTM's research group

<sup>12</sup> All registered participants and EUPhilBio\_2023 Crew (on the roof of the building)

**Friday, May 19 continuation**

*Fourth Open Session: COMPLEXITY*

Chair: [Denis Sunko](#)

14:00 – 14:30	<a href="#">Hrvoj Vančik</a> (University of Zagreb) <i>Complexity, systems, and function</i>
14:30 – 14:45	Discussion (Moderator: <i>Denis Sunko</i> )
14:45 – 15:15	<i>Closing Lecture</i>   <a href="#">Franz Klein</a> (University of Vienna) <i>Structure versus function, seeing is believing</i>
15:15 – 15:30	Discussion (Moderator: <a href="#">Anamaria Brozović</a> )
15:30 – 15:35	<i>Closing address</i>
15:35 – 16:00	<i>Short get-together in the open (end of Working Day 2)</i>
<i>Panel discussion, Chair: Petar Tomev Mitrikeski</i>	
16:00 – 17:00	No-agenda discussion <sup>13</sup>

See further, please.

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<sup>13</sup> Possible extension till 17.30 h if necessary

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## Abstracts

Research Professor **Eörs Szathmáry**

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Opening Lecture | *The problem of open-ended evolution*

Topic | *EVOLUTION*

Charles Darwin closed the first edition of *The Origin* with one of the best-known passages of all biology, beautifully summarizing the two basic pillars of his theory: descent with modification and the power of natural selection to 'produce higher animals' and 'endless forms most beautiful' from a 'simple beginning'. Many still feel uncertain about whether the production of higher animals would indeed (even indirectly) follow, simply because a quantitative theory of macroevolutionary change is in its infancy. Despite major advances in evolutionary theories, some aspects of evolution remain neglected: whether evolution would come to a halt without abiotic change; is unbounded and open-ended; or is progressive and something beyond fitness is maximized. I shall discuss some models of ecology and evolution and argue that ecological change, resulting in Red Queen dynamics, facilitates (but does not ensure) innovation. I distinguish three forms of open-endedness. In weak open-endedness, novel phenotypes can occur indefinitely. Strong open-endedness requires the continual appearance of evolutionary novelties and/or innovations. Ultimate open-endedness entails an indefinite increase in complexity, which requires unlimited heredity. Open-ended innovation needs exaptations that generate novel niches. This can result in new traits and new rules as the dynamics unfolds, suggesting that evolution is not fully algorithmic.

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Univ. Prof. Dr. **Franz Klein**

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Closing Lecture | *Structure versus function, seeing is believing*

Topic | *COMPLEXITY*

Bodies and to a large part the capacity of the mind of living beings are genetically encoded in the genome. The genome, however, is a biophysical object, organized in the form of chromosomes. Owing to this physical existence, the chromosomes have very biological needs, such as the need to duplicate and the need to interact with the bodies they encode. Recently it became clear that they also have a specific architecture, even outside of mitosis. These results identify chromosomes as self-organizing matter. I will discuss novel results from the field and primarily from our lab to address the questions: What is the secret of chromosomal self-organization? What is the connection between chromosome structure (visible and invisible) and its function? When does it make sense to ascribe function to a structure?



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Dr. **Krinoslav Brčić-Kostić**

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Lecture | *Adaptation from standing genetic variation*

Topic | *EVOLUTION*

A change of environment triggers an adaptation from standing genetic variation when it causes an already segregating non-adaptive allele to become advantageous. Previous studies of adaptation from standing genetic variation were focused on equilibrium populations (mutation-drift equilibrium and mutation-selection-drift equilibrium) which is special and simple condition. Since environmental change can occur at any time, including prior to the establishment of equilibrium, my talk will also include a general case when population is not necessarily in equilibrium. The idea connected with the non-equilibrium situation is to introduce the rate of change of selection regime  $r$  (reciprocal of time when selection regime changes). I will present theoretical and simulation studies of adaptation from standing genetic variation which include distribution of allele frequencies, average fixation probability and molecular evolution. The average fixation probability decreases as the distribution of allele frequencies deviates from equilibrium distribution. However, the fixation probability from standing variation in a non-equilibrium population is higher than

from new mutation for  $N_e s \leq 10^5$ . This is consistent with the empirical evidence that adaptation from standing variation predominates in populations with smaller  $N_e$ . Also, adaptation from standing genetic variation accelerates molecular evolution.

**Dr. Ehud Lamm**

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Lecture | *Collective knowledge and cultural evolution – An analysis of conceptual options*

Topic | *EVOLUTION*

Collective knowledge has long interested scholars interested in human culture. Related ideas have also appeared in the study of non-human animals, specifically in work on cultural evolution in animals. Here, we focus on how collective knowledge is conceptualized within the field of cultural evolution. Specifically, we review important notions from the literature and compare them with the newly introduced notion of Distributed Adaptation (Lamm & Kolodny 2022; Lamm, Finkel & Kolodny, 2023). The notion of Distributed Adaptation (DA) emphasizes scenarios in which adaptively relevant information cannot be reduced to information possessed by a single individual.

In this paper we first analyze the notions of cumulative cultural evolution, the collective brain (Muthukrishna & Henrich, 2016), collective intelligence (Migliano & Vinicius, 2021), recent work on collective knowledge (Whiten et al., 2021), as well as their similarities and differences with the notions of Extended mind (Clark & Chalmers, 1998), and scaffolded mind (Sterelny, 2010). We then discuss the relation of the notion of Distributed Adaptation to these existing notions. We conclude by carefully comparing DA with niche construction theory. We will argue that NC theory is primarily a theory of process while DAs attempt to characterize a specific kind of evolutionary outcomes. Thus, the process/outcome distinction helps identify a crucial difference in the evolutionary questions captured by the two approaches.

*References*

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- Lamm, E., Finkel, M., & Kolodny, O. (2023). [Human major transitions from the perspective of distributed adaptations](#). *Philosophical Transactions of the Royal Society B: Biological Sciences*, 378, 20210401.
- Lamm, E., & Kolodny, O. (2022). [Distributed adaptations: can a species be adapted while no single individual carries the adaptation?](#) *Frontiers in Ecology and Evolution*, 10, 791104.
- Migliano, A. B., & Vinicius, L. (2022). [The origins of human cumulative culture: from the foraging niche to collective intelligence](#). *Philosophical Transactions of the Royal Society B: Biological Sciences*, 377, 20200317.
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**Dr. Bruno Petrušić**

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Lecture | *Philosopher's dream about evolution: Daniel Dennett*

Topic | *EVOLUTION*

Daniel Dennett is a contemporary American philosopher. His philosophy of biology attracted a lot of attention, which Dennett himself directed through the New Atheism movement. His philosophical interpretation of biological evolution - which he sees as a universal acid that can explain everything, with metaphors that are visually and intellectually appealing to the average reader, represents a kind of naturalistic dream of a materialist philosopher. Therefore, in my presentation, I will present this philosopher's dream about evolution and critically analyze it in order to prove that it is only a dream - not a philosophical reality. And this dream relies heavily on scientific positivism, which, although based in methodological naturalism, is nevertheless unjustified because it considers an exclusively scientific approach to be the only correct one. And this represents an unjustified reductionism about which, ironically, Dennett

himself writes a lot. In this philosophical dream, the Tree of Life and the Space of Design are spoken of as metaphors for the totality of reality, which can be fully explained exclusively by evolutionary mechanisms. Therefore, my lecture will have three parts: in the first part, I will briefly present Dennett's view on evolution; then I will critically analyze his dream about evolution and in the end, I will valorize what is true and correct in that dream, and reject what is only a dream and as such incorrect and untrue.

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| References | <ul style="list-style-type: none"><li>Dennett, D.C. (1996). <a href="#">Darwin's dangerous idea: Evolution and the meanings of life</a>. Simon &amp; Schuster.</li></ul> |
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**Nikola Štambuk, M.D., Ph.D.**

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Lecture | *Standard genetic code: from IUPAC nomenclature to code biology*

Topic | *CODE BIOLOGY*

The Standard Genetic Code (SGC) table translates the biological information from genotype to phenotype, and represents the genetic coding algorithm that shows the relations between the biological information of the mRNA and the protein (Štambuk & Konjevoda, 2020; Štambuk *et al.*, 2018). 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 (Štambuk & Konjevoda, 2020). It has been demonstrated that IUPAC-based encoding of codon and amino acid sequences could be used for the representation of nucleobases with the probabilistic Square of Opposition, and Klein four-group representation (Štambuk & Konjevoda, 2020; Konjevoda & Štambuk, 2021). In accordance to that fact—the structural, functional and evolutionary patterns of protein sequences may be modelled using codon based amino acid information instead of using information based on amino acid physicochemical properties (Štambuk & Konjevoda, 2020; Štambuk *et al.*, 2018; Konjevoda & Štambuk, 2021). Underlying coding theory principles and application of IUPAC ambiguity codes will be discussed. A particular attention will be paid to the interpretation of results in the context of the Code Biology concept by Marcello Barbieri (Barbieri, 2015).

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| References | <ul style="list-style-type: none"><li>Štambuk, N., &amp; Konjevoda, P. (2020). <a href="#">Determining amino acid scores of the genetic code table: Complementarity, structure, function and evolution</a>. <i>Biosystems</i>, 187, 104026.</li><li>Štambuk, N., <i>et al.</i> (2018). <a href="#">Genetic coding algorithm for sense and antisense peptide interactions</a>. <i>Biosystems</i>, 164, 199-216.</li><li>Konjevoda, P., &amp; Štambuk, N. (2021). <a href="#">Relational model of the standard genetic code</a>. <i>Biosystems</i>, 210, 104529.</li><li>Barbieri, M. (2015). <a href="#">Code Biology – A New Science of Life</a>. Springer, Cham.</li></ul> |
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**Paško Konjevoda, M.D., Ph.D.**

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Lecture | *Relational model of the standard genetic code*

Topic | *CODE BIOLOGY*

The genetic code is a set of rules used by ribosomes to translate a linear sequence of triplets in messenger RNA into proteins. In a computer science terminology, the use of these rules is called encoding. The Standard Genetic Code (SGC) table is the most commonly way to describe encoding rules. It has pseudo-2D structure due to subrows defined by the third base of triplets. An alternative approach is proposed, based on the relational data model by Edgar F. Codd (Codd, 1970). The relational model (RM) is based on a distributed storage of data into a collection of tables that can be connected by shared communality. Basic elements of the table are rows, and columns, and RM tables have pure 2D structure. The SGC table, according to the relational data model, represents the so called unnormalized form of a table. Using normalization rules, it is possible to subdivide the SGC table into four tables. The rows and columns of single tables are defined by the first and second base and individual tables are specified by the third codon base. The biological interpretation of the RM is surprisingly simple and straightforward: the genetic code with 64 triplets evolved by functional fusion of several simpler codes based on 16 doubles as a consequence of an extreme form of lateral gene transfer, that is, cell fusion. The RM explains that the final step in the development of the SGC was the adoption of coding function by the third base, which makes an informational/functional unit with the first



base, despite the different physical location in a triplet. This enabled the synthesis of specific proteins without ambiguity. tRNA system still reflects the 16 doublets code system, which strongly supports Relational Model of the Standard Genetic Code.

References

- Codd, E. F. (1970). [A relational model of data for large shared data banks](#). *Communications of the ACM*, 13, 377-387.



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Associate Professor **Arnon Levy**

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Lecture | *Reviving the value-free ideal*

Topic | UNDERSTANDING IN BIOLOGY

Work on the role of values in science has grown and diversified dramatically in the 21st century. But there is a near-consensus on one basic point, namely the value-ladenness – that is, ladenness with social, moral and political values – of all aspects of the scientific process, including “core” aspects like the bearing of evidence on hypotheses. My goal in this talk is to buck this trend and argue for a somewhat old-fashioned view about the relation between science and values: science-based decision making is best carried out by separating factual assessments from value judgments. I will make the case by taking a new look at the debate over inductive risk, proposing a framing of Richard Jeffrey’s classic view (Jeffrey 1956). I argue that Jeffrey’s key contribution was a critical one. And I suggest that the critique is best supplemented by treating the separation of facts from values as a cogent division of labor.

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Lecture | *Applying the elegance paradigm to rank recombination models*

Topic | UNDERSTANDING IN BIOLOGY

Homologous recombination between a non-replicative plasmid and the chromosome can integrate the plasmid molecule into the genome (*gene targeting*). This process can also integrate more than one plasmid molecule leading to *multiple, tandem plasmid integration* (MTPI) and rendering the phenomenon evolutionary relevant owing to its capacity to alter the genome. Two alternative models try to explain the MTPI mechanism(s): the (i) *sequential model* (Orr-Weaver & Szostak, 1983) predicts repeated integration of several independent molecules, while the (ii) *multimer model* (Plessis & Dujon, 1993) envisions single integration of a super-plasmid molecule. However, the sequential model appeared a better overall explanation when a third model (the *simultaneous model*) was used as a theoretical tool to discriminate between the existing alternatives (Mitrikeski et al, 2014). Moreover, this unveiled a way to experimentally test all existing models including the simultaneous one. Due to a predicted possibility that two plasmid molecules recombine with the chromosome concurrently, the simultaneous model unified the two prior models demonstrating that an experimentally yet non-corroborated model can be used to evaluate empirically supported mutually excluding options. Additionally, this posted an inspiring possibility to analyze recombination models on the base of their *elegance*. Here, the parameter elegance was used to rank recombination models by quantifying their clarity, cleverness, correctness, explanatory power, parsimony, and beauty as suggested earlier (Casadevall & Fang, 2018).

References

- Casadevall, A., & Fang, F.C. (2018). [Elegant science](#). *mBio*, 9, e00043-18.
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- Orr-Weaver, T.L., & Szostak, J.W. (1983). [Multiple, tandem plasmid integration in \*Saccharomyces cerevisiae\*](#). *Molecular and Cellular Biology*, 3, 747-749.
- Plessis, A., & Dujon, B. (1993). [Multiple tandem integrations of transforming DNA sequences in yeast chromosomes suggest a mechanism for integrative transformation by homologous recombination](#). *Gene*, 134, 41-50.

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See further, please.



**Dr. Tomislav Stojanov**

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Lecture | *On Croatian eels and Serbian snakes: natural science taxonomies vs. sociolinguistic typologies*

Topic | UNDERSTANDING IN BIOLOGY

At first glance, linguistics and biology seem unrelated and distant enough, but, interestingly, linguists like to peek over biologists' shoulder when pondering about languages. One of the reasons for these interdisciplinary links lies in linguists' inability in establishing more robust language classifications, so biology has been perceived as an inspiring methodological source. Language classification criteria, according to which languages, dialects and language varieties are classified, are one of the central, most debatable and oldest (socio)linguistic questions (Van Rooy, 2020). For instance, in order to describe speakers' language self-identification as a 'weak' sociolinguistic criterion, compared to 'strong' linguistic (genetic and typological) criteria, Ammon (1989: 31) claimed that "[n]o serious biologist would, for instance, consider an eel to be a snake because people rate it as such."

However, these interdisciplinary analogies between biology and linguistics, despite their seemingly convincing and strong rhetorical impressions, have a serious underlying problem: species and languages are entities from very different levels of abstraction.

In this presentation, striving to establish a more consistent and less controversial method of language classification, a sociolinguist seeks (again) a discussion with the biologists in order to understand how certain biologists are in their taxonomies and ontologies.

In order for biologists to better understand linguists' dilemmas, a following rhetorical question could be posed: If eels and snakes could talk, to what extent would biologists consider this self-identification criterion in determining biological species?

References

- Ammon, U. (1989). Towards a descriptive framework for the status/function (social position) of a language within a country. In U. Ammon (ed.), *Status and Function of Languages and Language Varieties*. Berlin/New York: Walter de Gruyter, pp. 21-106.
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**Professor Predrag Šustar**

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Lecture | *Explanation and understanding in biology: the case of scientific metaphors*

Topic | UNDERSTANDING IN BIOLOGY

It is undeniable that metaphors are an integral part of scientific language, but what is their role in science and why is such figurative language maintained in a specialized domain like science? The usual answers emphasize the following potential theoretical roles for scientific metaphors: (1) description; (2) explanation; (3) prediction; and most usually, (4) a heuristic role (see Stegmann 2016). Additionally, Camp (2020) proposes a more general, (5) framing role. In that regard, we will focus on their putative "explanatory" role, in particular as it relates to our understanding of some basic biological phenomena and will argue accordingly for "understanding" as a separate role for metaphors as indirect or surrogate representations in biology.

Stegmann (2016) defends an explanatory account of scientific metaphors, esp., the "coding" metaphor in molecular biology. According to him, coding schemes provide mechanism sketches that can have an explanatory role. We depart from that account for the following reasons: (1) it is not clear how the metaphor in question, as well as other metaphors (e.g., the genetic information metaphor) are related to explanatory structures; and (2) "coding" and other cognate metaphors are replaceable with other, semantically less loaded, notions such as a certain type of causal relationship.

Levy (2020) endorses Stegmann's idea and claims that metaphorical descriptions can be explanatory to the extent that they succeed in enhancing understanding. More specifically, following Camp, he claims that metaphors frame a target domain and thereby enhance our ability to think about it. According to him, this is how they explain.

We propose a reading of Camp that is not aligned with this conclusion. Camp argues that metaphors play a fruitful role in science, because they are intuitive and only partially consistent; they engage imagination, guide attention, and suggest hypotheses. These features make them useful scientific tools for the enhancement of understanding, but simultaneously distinguish them from explanations. We suggest that

metaphors can play a useful epistemic role in science, and can eventually lead to biological explanations, but cannot be equated with them. In order to emphasize that, we will point out some differences between explanation, understanding and framing in the current molecular life sciences (see Nicholson 2020).

*References*

- Camp, E. (2020). "[Imaginative frames for scientific inquiry: Metaphors, telling facts, and just-so stories.](#)" In *The Scientific Imagination*. Levy A. and Godfrey-Smith P. (eds.), Oxford University Press, pp. 304-337.
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**Hrvoj Vančik**, *Professor emeritus*

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Lecture | ***Complexity, systems, and function***

Topic | **COMPLEXITY**

Theory of complexity is in the largest part of the literature known as the theory of chaos. Since this aspect of the theory of complexity is mostly discussed within the frame of the dynamical behavior of systems, its resemblance to the general system theory invented by K. L. von Bertalanffy is obvious.

In this presentation, the systems are defined as consisting of the entities, actualities, that are positioned on the three-component "complexity space" (synchronic, diachronic, and combinatorial). In the system, these actualities are variously interconnected. As such, the system can be represented as a topological object by using the graph theory in the form how it is used in chemistry. It is argued how such graph theoretical interpretation of systems could provide a new view on the teleological problem of function to which the system should be adapted.

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*References*

- Vančik, H. (2022). [From complexity to systems.](#) *Foundations of Chemistry.*

See further, please.

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## Student's Abstracts

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Lecture | *Seeing red: the phenomenology of color and the biological basis of artistic experience*

### Student's Corner

The presentation analyzes the action-based ecological theory of color proposed by Evan Thompson and James J. Gibson, through an examination of the artistic contributions of Paul Cézanne, shedding light on our understanding of human anatomy. The action-based ecological theory of color, developed by Thompson and Gibson, suggests that color perception is not solely a product of the mind but is intricately tied to the actions and interactions of an embodied organism with its environment. This theory posits that our perception of color emerges through the dynamic relationship between our bodies, the objects we interact with, and the ambient light in our surroundings. By grounding color perception in embodied experience, the theory challenges traditional accounts of color that solely rely on internal mental representations. Complementing this theoretical framework, the presentation examines the art of Paul Cézanne, a prominent post-impressionist painter. Cézanne's innovative approach to representing colors and forms reveals a deep understanding of anatomy and the interplay between structure and perception. By examining the interconnections between the ABE theory of color and Cézanne's art, this presentation aims to illuminate the ways in which our perception of color and art are profoundly influenced by our biology and interaction with the world. It emphasizes the importance of considering the biological foundations of perception and the insights that art can offer in unraveling the intricate relationship between our bodies, the environment, and our understanding of ourselves.

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Lecture | *Quantitation of fundamental attribute of life through xenobot classification*

### Student's Corner

In January 2020 a paper was published describing the process of designing and producing the so-called reconfigurable organisms, made from embryonic cells of the African clawed frog (*Xenopus laevis*) (Kriegman et al, 2020). This was the beginning of a series of three papers describing the properties and capabilities of *xenobots* – biological robots, that can self-replicate, and perform useful tasks. But their existence posed a profound question: *have we created new life?* This question further led to a simple biological dilemma: *where do xenobots (and biobots in general) fall on the biological scale of life – are they life or non-life?* To try to decipher this puzzle, we compared these artificial (non-evolutionary) life forms with evolutionary-shaped biological entities. The comparison extracted two attributes of life – *evolvability* and *cellularity* – as independently capable of depriving of and granting liveness to matter.

#### References

- Kriegman, S., Blackiston, D., Levin, M. & Bongard, J. (2020). [A scalable pipeline for designing reconfigurable organisms](#). *Proceedings of the National Academy of Sciences*, 117, 1853-1859.

See further, please.

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See further, please.

## Supporting Info

### Venue

[University of Zagreb, Faculty of Philosophy and Religious Studies](#)

Jordanovac 110, HR-10000 [Zagreb, Croatia](#)

Hall: [f. Peter-Hans Kolvenbach SJ](#) (122 seats)

| Entrance: free, no registration, no fee

| *Note:* Free parking space is available at the site

### Getting to the Venue from a rally point (for lecturers only)

| *Lectures need to know (!)*

[EUPhilBio 2023 crew](#) will meet you at the rally point at 08:45 h and accompany you to the Venue on Thursday and Friday

**Rally point** | [Kaptol](#) (Cathedral square) – address: Kaptol 29a

### Currency in Croatia

Legal tender in Croatia is euro (€)

### Miscellaneous

| *Internet access*

Free Wi-Fi service is available at the premises

| *Early gatherings, breaks, and late gatherings*

**Light refreshment**

Provided for all **registered** participants and *EUPhilBio\_2023 crew*

**Short pause**

A limited supply of bottled water for all **registered** participants and *EUPhilBio\_2023 crew*

Commercial coffee machines are available at the site; the audience is encouraged to bring their source of water

**Light lunch**

Sandwich bar (provided for all **registered** participants and *EUPhilBio\_2023 crew*)

In general, special diet requests will be met if pre-announced; however, persons with special (i.e. medical) diet needs are encouraged to bring their food if necessary

**Short get-together in the open**

Beverages & a limited supply of bottled water for all **registered** participants and *EUPhilBio\_2023 crew*; the audience is encouraged to bring their source of water

**Casual get-together over dinner**

Open to all but, however, food and beverages (based on personal choice) are at one's own expense

[PUB MEDVEDGRAD ILICA](#) (all participants)

| *City of Zagreb*

In case you wanna discover the city <http://www.infozagreb.hr/&lang=en>

<https://www.zagreb.hr/en/the-mayor-of-zagreb/106869>

### Acknowledgments

[EUPhilBio](#) expresses gratitude to the **Faculty of Philosophy and Religious Studies** (chief patron and main financial and logistic supporter), and the Dean of the Faculty for supporting us. *EUPhilBio* also thanks to **Croatian university newspaper Universitas** and **Universitas Portal** for quality media coverage.

PTM would like to thank all members of [The Core](#) of *EUPhilBio* for their friendliness, professional attitude, and useful suggestions that simplified the organization of [EUPhilBio 2023](#).