Third European Advanced Seminar in the Philosophy of the Life Sciences

Ontological Issues in the Life Sciences

September 1-5, 2014

The KLI Institute,
Klosterneuburg, Austria

Participating institutions

Egenis, the Centre for the Study of Life Sciences, Exeter
European School of Molecular Medicine (SEMM), Milan
Department of Health Sciences, University of Milan
Institut d'Histoire et de Philosophie des Sciences et des Techniques,
Paris-1 Panthéon - Sorbonne
KLI Institute, Klosterneuburg/Vienna
IUFE, Faculty of Science, University of Geneva
Department of Philosophy, Faculty of Humanities, University of Geneva
Department of Logic and Philosophy of Science,
University of the Basque Country, San Sebastian

Directors

Giovanni Boniolo (Milan) & Werner Callebaut (Vienna)

FACULTÉ DES LETTRES
DÉPARTEMENT DE PHILOSOPHIE

Welcome

to the Third European Advanced School for the Philosophy of Life Sciences, which is organized by seven top-level European institutions in the philosophy and history of the life sciences. EASPLS aims at fostering research, advancement of students, and collaborations in the field of the philosophy of the biomedical sciences. Meetings are held every other year. After a preliminary meeting in Gorino Sullam (Italy) in 2008, EASPLS met in Hermance near Geneva in 2010 and 2012. The present meeting is hosted by the KLI Institute in its new setting in Klosterneuburg near Vienna.

This year's seminar topic is "Ontological Issues in the Life Sciences." The schedule mixes presentations of senior researchers, post-doctoral researchers, and PhD students from sixteen countries and three continents. The best junior papers resulting from the meeting will be published in a thematic issue of an international journal in the field. Submissions will be subject to normal peer review.

We are delighted that you are able to participate in this seminar, and we wish you a productive and enjoyable stay!

Ontological Issues in the Life Sciences

L'ontologie fait corps avec la science elle-même et ne peut en être séparée.
— Emile Meyerson

Dictionaries such as *Webster's* define ontology as the "branch of metaphysics concerned with the nature and relations of being." Western philosophy began as a quest for "the furniture of the world." Think of EMPEDOCLES' four 'roots,' which have become better known as the 'elements': Fire, Air, Water, and Earth. ARISTOTLE related each of these four elements to two of the four 'sensible qualities': hot/cold, wet/dry. If in Greek natural philosophy these entities were thought through the lens of a strong and necessary ontological commitment, the modern sciences that took shape after the

Scientific Revolution, including biology, may be seen as transforming the ancient ontological quest in terms of specialization and the use of increasingly sophisticated experimental and other empirical tools (and later also modeling), in addition to the theorizing that was—and remains—so dear to philosophers.

On this "replacement of philosophy by science" picture, it might seem that the age of philosophical ontology has gone for good—a conclusion that the logical empiricists were eager to draw about a century ago. For them, philosophy's only proper concern is the "logical analysis of the body of accepted scientific theories" (CARNAP). Representatives of the Vienna Circle's 'scientific world-conception' such as NEURATH no longer wanted to use the term 'philosophy' for their work at all, "so as to emphasize the contrast with the philosophy of (metaphysical) systems even more strongly."

However, whereas QUINE's *ontological relativism* killed whatever remained of the old dream of an aprioristic philosophical ontology that somehow 'precedes' scientific investigation, his demolition of the *analytic/synthetic* distinction, which the positivist edifice required for its foundation, re-opened, maybe somewhat paradoxically, the door for a 'scientific' metaphysics. As ALEX ROSENBERG (1985) has argued in a discussion of entelechy,

> The justification for eliminating or embracing such notions as DRIESCH's entelechy is no different in kind from that employed to assess claims about the existence of electrons, magnets, or virons. It differs from them by degree, and very great degree at that. But ridding biology of such notions is ... all a matter of applying some rule against useless metaphysics. For deciding on the existence or nonexistence of entelechies is nothing less than questioning the legitimacy of competing embryological theories altogether.

The 'new' philosophy of biology that took shape in the mid-1970s was informed by the post-positivist developments in philosophy of science (QUINE's influence being mostly indirect, through the major impact of KUHN). Among its subjects, ontological issues are legion; to mention but a few examples:

• If biological species evolve, they cannot be logical classes but must be 'individuals' of some sort.

• In a discipline such as systematics, confusion as to the significance of definitions often leads to mistakes. “Definitions apply only to words, not to the things to which they correspond” (GHISELIN).
• The ‘gene’s eye view’ vs. multi-level accounts of living systems, ‘causal democracy’ of developmental resources, etc.
• The individuality of organisms—microbiological, immunological, and other issues.
• Ecosystems as organisms, organisms as ecosystems…

Whereas philosophy has traditionally shown but disdain for the ‘application’ of scientific knowledge, many theoretical changes in the life sciences today are initiated by practical and technological applications, and many theoretical advances are pursued to answer to technical problems.

This turn has been particularly evident concerning ontology. Whereas classical philosophical ontology was devoted to speculation on “what there is”—the ‘fundamental’ entities in the world—nowadays, in particular in what is called applied ontology, it deals increasingly with computerized knowledge representation and data integration. From a computational perspective, an ontology is a way of computationally modeling/ representing a particular area of knowledge, or computationally integrating/representing different areas of knowledge.

The rapidly growing field of applied ontology has recently acquired more and more relevance in the context of the sciences dealing with living beings. Bio-ontologies are proliferating in the management of many databases concerning living beings or parts of them (molecules, cells, tissues, etc.). This success is explained by the changing nature of biological research. While until some decades ago research in the life sciences was mainly observational, major advances in molecular biology and genomic technologies have led to an information overload that cannot be processed and analyzed by biological methods. Nowadays, most biological subfields are computer-aided, resorting to powerful bioinformatics tools that are required to store, organize, and index the continuously increasing mass of data. But coupling these rapidly expanding fields opened the door to the data deluge even wider: the amount of data produced exceeds

the possibility of their analysis. Bio-ontologies are a candidate to manage this information explosion by modeling and integration, since they can also bridge different levels of research on living beings connecting data, for example, from molecular biology to clinical medicine, by aligning molecular details to pathology and anatomy.

However, this picture reveals a dangerous epistemological naiveté and basic ignorance of the history of science itself. First, even if many computer scientists conceive of ontology in a simple way (without considering its history), the philosophical tradition provides many different approaches to ontological problems that can inspire new technical applications.

Second, a genuine epistemological analysis can provide theoretical support for another type of integration, knowledge integration, which is not separated from data integration but rather constitutes its counterpart. Epistemological expertise, supported by up-to-date knowledge of the science, plays a crucial role in understanding the practice of actual research. Moreover, a scientific enterprise aware of its historical and epistemological dimensions can take advantage of this level of analysis to refine and shape its methodological approach and the interpretation of those aspects of produced results that are normally neglected by scientists (the issue of theory-ladenness).

Giovanni Boniolo
Werner Callebaut

The program at a glance

	Mon, 1 Sept.	Tue, 2 Sept.	Wed, 3 Sept.	Thu, 4 Sept.	Fri, 5 Sept.
9:30		**Lowe** **Pontarotti**	 **Rogers**	**Brzović** **Räwel**	**Dupré** ***Nicoglou***
10:20		Break	Break	Break	Break
10:40	**Registration & Opening**	***Sokołowska*** Discussion **Kronfeldner** ***Schlaepfer*** Discussion	***Alves Neto*** Discussion **Nanjundiah** ***Germain*** Discussion	***Hernández-Chávez*** Discussion **Garnier** ***Dussault*** Discussion	Discussion General Discussion **Seminar Closing**
12:10	Lunch	Lunch	Lunch	Lunch	Lunch
14:00	**Boem** **Winslow** ***Berzell*** Discussion	**Racovski** **Triviño** ***Nuño de la Rosa García*** Discussion	**DiFrisco** **Tamborini** ***Brooks*** Discussion	**Fernández-Labandera Tejado** **Ratti** ***Jurjako*** Discussion	
15:20	Break	Break	Break	Break	
15:40	**Ruiz-Mirazo** ***Holm*** Discussion **Müller** *Keynote address* Discussion	**Weber** ***Binney*** Discussion **Sarto-Jackson** ***Barwich*** Discussion	**Nathan** ***Huber*** Discussion **Nicholson** ***Witteveen*** Discussion	**Mossio** ***Arnellos*** Discussion **Merlin** ***Charbonneau*** Discussion	
17:40					

Detailed program

Monday, 1 September 2014

11:00 Registration & Opening

12:10 Lunch

14:00 **Federico Boem**

"Bio-ontologies: Orienteering Tools for Biomedical Research"

14:25 **Russell Winslow**

"On the Ontology of Biological Space"

14:50 **Martin Berzell**

Commentary

15:05 Discussion

15:20 Coffee break

15:40 **Kepa Ruiz-Mirazo**

"'Synthetic Protocell Philosophy': Fabricating New Ontological Constructs, *in vitro* and *in silico*, to Establish More Solid Epistemological Bases for Biology"

16:15 **Sune Holm**

Commentary

16:30 Discussion

16:40 **Gerd B. Müller**

Keynote address

17:20 Discussion

Tuesday, 2 September 2014

09:30 **James Lowe**

"Ontological Issues in Developmental Biology: Taking Variation Seriously"

09:55 **Gaëlle Pontarotti**

"Integrating Expanding Data in Pluralistic Models of Heredity: Toward an Organizational Framework"

10:20 Coffee break

10:40 **Ewelina Sokołowska**

Commentary

10:55 Discussion

11:10 **Maria Kronfeldner**

"How Behavioral Scientists Deal with Explanatory Complexity"

11:45 **Guillaume Schlaepfer**

Commentary

12:00 Discussion

12:10 Lunch

14:00 **Thibault Racovski**

"Evolutionary Novelty, a Concept Still in Search of a Definition"

14:25 **Vanessa Triviño**

"Emergent Properties in an Evo-Devo Biological Context"

14:50 **Laura Nuño de la Rosa García**

Commentary

15:05 Discussion

15:20 Coffee break

15:40 **Marcel Weber**

"Individuals, Cells, and the Special Composition Question"

16:15 **Nicholas Binney**

Commentary

16:30 Discussion

16:40 **Isabella Sarto-Jackson**

"Ontologies of Protein-Ligand Binding Complexes"

17:15 **Ann-Sophie Barwich**

Commentary

17:30 Discussion

Wednesday, 3 September 2014

09:55 **Eric Rogers**

"Selection or Sorting: The Conceptual Obscurity of Species Selection"

10:20 Coffee break

10:40 **Celso Antônio Alves Neto**

Commentary

10:55 Discussion

11:10 **Vidyanand Nanjundiah**

"Arbitrariness in Information Transfer and the Autonomy of Biology"

11:45 **Pierre-Luc Germain**

Commentary

12:00 Discussion

12:10 Lunch

14:00 **James DiFrisco**

"Time Scale and Levels of Organization"

14:25 **Marco Tamborini**

"Ontological Issues in Paleobiological Data: What is the Fossil Record?"

14:50 **Daniel Brooks**

Commentary

15:05 Discussion

15:20 Coffee break

15:40 **Marco J. Nathan**

"On the Role of Counterfactual Reasoning in the Biological Sciences"

16:15 **Maximilian Huber**

Commentary

16:30 Discussion

16:40 **Daniel J. Nicholson**

"Are Biological Mechanisms Real?"

17:15 **Joeri Witteveen**

Commentary

17:30 Discussion

Thursday, 4 September 2014

09:30 **Zdenka Brzović**

"Multiple Realizability of Functional Kinds"

09:55 **Jörg Räwel**

"De-ontologization of Individuality in Evolutionary Biology""

10:20 Coffee break

10:40 **Paola Hernández-Chávez**

Commentary

10:55 Discussion

11:10 **Eric Garnier**

"Using Ontologies for Ecological Research"

11:45 **Antoine Dussault**

Commentary

12:00 Discussion

12:10 Lunch

14:00 **Eva Fernández-Labandera Tejado**

"Regulation and its Main Features"

14:25 **Emanuele Ratti**

"The Hybridization Between Data-driven and Hypothesis-driven Research: A Proposal Based on the Debate About the Relation Between Discovery and Justification"

14:50 **Marko Jurjako**

Commentary

15:05 Discussion

15:20 Coffee break

15:40 **Matteo Mossio**

"Organization and Biological Individuation"

16:15 **Argyris Arnellos**

Commentary

16:30 Discussion

16:40 **Francesca Merlin**

"The Limited Extended Nature of Biological Inheritance"

17:15 **Mathieu Charbonneau**

Commentary

17:30 Discussion

Friday, 5 September 2014

09:30 **John Dupré**

"Living Systems: Processes or Things?"

10:05 **Antonine Nicoglou**

Commentary

10:20 Coffee break

10:40 Discussion

10:50 General Discussion

11:50 Seminar closing

12:10 Lunch

Abstracts

Species Cohesion and Individuality

Celso Antônio Alves Neto *(Hannover)*

I address the problem of attributing cohesion to species and evaluate its consequences for the 'species-as-individuals' thesis. In particular, I analyze an argument developed by BARKER & WILSON (2010) according to which species do not have the same type of cohesion as organisms have, and therefore are not individuals.

BARKER & WILSON (2010) distinguish between two different phenomena described as cohesion. On one hand, 'responsive cohesion' refers to a unitary and homogeneous product of different elements responding to external common factors at the same time. On the other, 'integrative cohesion' refers to a unitary product of causal interactions among different elements. They claim that species do not have integrative cohesion. At the same time, these authors defend that individuals must have integrative cohesion, presupposing (1) that organisms are models of individuality and (2) that organisms have integrative cohesion.

I make two different replies to such an argument. First, I discuss the concepts of 'organism' and 'integrative cohesion' drawing on recent debates about biological individuality (CLARKE 2010). I show that there is no unique paradigm of individuality, because there can be no unique characterization of 'organism' (HABER 2013). As a consequence, 'organism' and 'integrative cohesion' should be understood in a relaxed sense. I do not deny (1) or (2) but propose that such assumptions are more context-sensitive than BARKER & WILSON think, and in principle do not warm the 'species-as-individuals' thesis.

Second, I claim that species are individuals even if they do not have integrative cohesion. I define the theoretical role of 'cohesion' as in the 'species as individuals'

thesis: a horizontal identity criterion for individuals (HULL 1976). Then I describe that such an identity is based on relations, not on qualitative properties (similarity). So long as the distinction between individuals and natural kinds reflects the distinction between these two different identities, species are still analogous to organisms, because organisms have relational identities. I claim that the natural kind theory (HPC kinds) favored by BARKER & WILSON does not succeed in attributing relational identity to species (ERESHEFSKY 2010). Hence, even if they do not have integrative cohesion, species are analogous to organisms in an important sense and, therefore, are individuals.

While not offering a positive definition of 'cohesion,' I make a case for a certain theoretical role it plays in the species-as-individuals thesis. 'Cohesion' points out a theoretical demand to be fulfilled by individuals in a relational way (horizontal identity). From this point of view, the analogies and dissociations among the concepts of 'organisms,' 'species,' and 'individuals' shed new light on the ontology of biology.

Barker M, Wilson R (2010) Cohesion, gene flow and the nature of species. *J Philos* **107**:61-79

Clarke E (2010) The problem of biological individuality. *Biol Theory* **5**:312-325

Ereshefsky M (2010). What's wrong with the new biological essentialism? *Philos Sci* **77**:674-685

Haber M (2013) Colonies are individuals: Revisiting the superorganism revival. In: Bouchard F, Huneman P (eds) *From Groups to Individuals: Evolution and Emerging Individuality.* MITP

Hull DL (1976) Are species really individuals? *Syst Zool* **25**:174-191

An Organizational Account of Organisms

Argyris Arnellos *(Klosterneuburg)*

From an organizational perspective, organisms should not only be capable of reproducing each of their own differentiated parts but also the dynamic and functional interrelationships between those parts, i.e., their own global/collective organization. Moreover, apart from their constructive dimension, organisms are also agents engaging in interactions with their environments, in a way that these interactions are in a functional and reciprocal relation (at least) with the maintenance of their global organization. Then, one should not focus on how aggregations of parts become temporary cohesive systems, but on how they may turn into the respective highly organized and functionally integrated and differentiated wholes that adaptively interact with their environments.

This is quite challenging, especially with respect to biological organisms, where the concept of functional integration is often accused of looseness that allows for an excessive plurality of collaboratively produced heterogeneous organismal wholes. Indeed, from the early stages of collaboration in the biological world, entities assemble into groups, bringing forth several types of relatively stable cellular associations (e.g., biofilms, filaments, colonies, various types of aggregations, multicellular systems, modular systems, etc.). All these aggregations comprise a number of different cell types, and they are characterized by specialized intercellular interactions, thereby exhibiting a degree of functional integration. In turn, this integration results in apparent forms of collective agency through which the group expands its overall adaptive capacity.

We begin by explaining why the minimization or even the complete elimination of the possibility of conflicts between the cells (alignment of fitness) together with the achievement of a clear and functional division of labor (export of fitness) are not enough for organismal wholes, since — the underlying integration in such cases notwithstanding — the agential dimension is not satisfied. We then suggest a general scheme of

organizational conditions and requirements for the realization of organisms. More specifically, we will argue that an organismal whole endogenously constructs its own developmental regulation, and the various operational patterns of such regulation are modulating and control the generation and integration of the constitutive aspects in such a way that they are in a functional and reciprocal correspondence with its interactive aspects. We briefly discuss the structural and operational characteristics of this endogenously produced regulation, showing that it is due to the combination of inductive signaling and of physicochemical morphogenetic transformations and movements at the tissue level of organization, as these are taking place in a specially internalized environment.

We conclude by discussing some implications with respect to the role of regulation in organisms, and by arguing that organismal wholes are not just the result of the generation of functional diversity, but that its control through the regulatory relationships among the (increasingly complex) components and modules of the system is equally or even more important.

Theory and Observation in Olfaction: How the Historicity of Observational Evidence leads to a better Understanding of Theorising in the Life Sciences

Ann-Sophie Barwich *(Klosterneuburg)*

I develop a historicised notion of observational evidence relevant for understanding theorising in the life sciences. The issue of theorising in biology, while rich in its history, has received little attention in recent philosophical debate. Surrendering the notion of theory to physics, with the theory of evolution as the salient exception, philosophers of biology favoured analysis of experiments, models and social factors underlying disciplinary developments in the life sciences. In parallel with this practice-oriented turn, attention was directed at the historical variation of scientific objects through the historicity of knowledge-making practices in experimental contexts. Integrating philosophical and historical analysis, I rehabilitate the notion of theory for the life sciences by drawing attention to the historicity of observational evidence.

Using the case of olfaction, I present an epistemic history of the emerging experimental system investigating the molecular basis of smell. Tracing the disciplinary developments through which the mechanism of odour recognition became investigated within a small community of researchers, I examine the conditions that inform past and present scientific judgement in olfactory research. Unknown in its details up to today, inquiry into the biological foundations of smell perception has been strongly theory-driven. Lacking an experimental basis throughout almost the entire 20th century, olfactory researchers had to develop research strategies under which the sense of smell became empirically accessible and to find an empirical starting point through which theorising was appropriate in the first place. Starting from comparative anatomical and psychophysical studies at the end of the 19th century, followed by the rise of synthetic chemistry at the beginning of the 20th century, and with the dawn of biochemical and molecular biological studies up to the triumph of genetics in the second half of the 20th century, olfaction has passed through several disciplinary identities. Elucidating the different

strategies of modelling facts and conducting experiments in the course of olfaction theory, the question I will address is how the underlying concept of observational evidence has changed and how, in turn, these changes were dependent on the ways in which theorising in other domains of the life sciences was practiced.

Historicising the notion of observation with the example of olfaction, I will argue for a different outlook on theory in the life sciences. By 'historicising' I mean that in order to understand what kinds of observation counts as evidence for (or against) a theory concerns not only its analysis within the specific temporal context within which an observation is made, but also its impact on later scientific judgements of the historical trajectory through which a scientific practice is reached. Different from being a collection of models (semantic view) or propositional structures (syntactic view), I argue that theory in the life sciences pertains to historically developed collections of practices as emerging in parallel with an ontological understanding of life processes in terms of their disciplinary defined nature (e.g., the olfactory mechanism as an evolutionary product, as integrated in a biological system, or as a causal interaction with external stimuli).

Granularity and Adequatism: Two Key Concepts in a Realist Ontology

Martin Berzell *(Linköping)*

Reductionism of science in philosophy of science is a common idea. But in the field of biomedical ontologies a non-reductionist view has been proposed, for example, by BARRY SMITH. This view is an Aristotelian-like description of the categories that make up different levels of reality. It is a realism made up of states of affairs on different levels of reality, and these levels can be of science or social life, for example. Whereas the reductionist strives to explain every thing that exists via another more basic level, the type of ontology that SMITH proposes doesn't. In this ontological project, every level of aggregation is assumed to exist — and none of the levels 'take priority' or are 'more basic' than any of the other levels.

According to SMITH, an ontology has to be able to fulfill its descriptive purpose. It needs to be able to answer question like: "What classes of entities are needed for a complete description and explanation of all the on-goings in the universe?" It is a way of asking what it takes for a theory to be true. As a defender of a theory that says that "all swans are white," one would commit oneself to the existence of 'swans' and something like 'whiteness.' This means that when we make scientific explanations of all the on-goings in the universe, we commit ourselves to an ontology including the entities and properties used in the statements describing them.

In this view, there is also a collection of key concepts, including, among others, 'adequatism' and 'level of granularity.' The idea that every level of granularity contains adequate information to describe itself without the need for reduction is what is called 'adequatism.' But what exactly does this mean? One thing it does entail is that we have to accept that different sciences operate with different ontologies, and that no one specific science is the most basic one, that takes priority in explanation.

The question is how these key concepts can be analyzed in more detail; and maybe more importantly, what does it mean in the life sciences to accept a non-reductionist

view of science? This paper will try to first define these terms more clearly and, second, see what role they would play in the life sciences.

Applying Ontology: The Possibility of Promiscuous Nosology

Nicholas Binney *(Exeter)*

The classification of disease, or nosology, is central to medical practice. The act of diagnosis itself can be understood as one that identifies a particular sort of patient. If ontology is understood as the subject that considers what sorts of things there are, then when making diagnoses doctors at the bedside are doing ontology.

However, doctors at the bedside may not consider paying close attention to their ontology and metaphysics a good use of their time. Doctors may be in agreement with the logical empiricists and consider metaphysics a meaningless exercise, of little use at the bedside. Being concerned with very practical matters, like the management of patients and the relief of their suffering, it is right for medics to focus their attention on matters that directly affect their work. In order to convince the medic of the value of metaphysical musing, philosophers must show how holding different metaphysical positions affects medical practice. I argue here that medics' metaphysics can indeed affect their work, and consequently is important at the bedside. I will argue that philosophical investigations into ontology can be usefully applied at the bedside.

My argument proceeds in four stages. I argue that medics already adopt strong ontological positions, as is revealed by their efforts to classify patients according to the disease from which the patient is suffering. However, this by itself does not show that medics should think about their ontology, as it does not show that ontology affects practice at the bedside. In order to show this, I draw attention to the ontology of a very early advocate of classification, THOMAS SYDENHAM (1624-1689). I will argue that SYDENHAM took the view that a single system of classification for disease would be suited to any context in which the medic may be working. This view is shared by many medics today. SYDENHAM argued that there was a close analogy between the classification of plants (taxonomy) and the classification of disease (nosology). Taking a lead from philosophers who have criticized the universal application of a single taxonomy in botany, I criticize the universal application of a single nosology in medicine.

Using examples from the medical literature, I will argue that in some instances the adoption of a pluralist ontology for disease may be profitable, and for the possibility that diseases may be usefully viewed as promiscuously real.

The possibility of applying ontology in this way provides an example of how philosophy of science may be put into practice. This possibility raises questions about whether or not philosophers want to focus their attention on this kind of work.

Bio-ontologies: Orienteering Tools for Biomedical Research

Federico Boem *(Milano)*

If someone would search for the term ‘ontology’ on Google she would be surprised to realize that the first entries mainly refer to a domain of computer science called *applied ontology*. In this battle for notoriety, ‘ontology’ in a more traditional and philosophical sense is defended just by Wikipedia and a few other websites. Since its origins (see PLATO’s praise for “contemplative life” or ARISTOTLE’s endorsement of epistemic virtues over other ones), philosophy has been detached from any technological or pragmatic application. Indeed ‘knowledge’ has been traditionally conceived as a purely speculative enterprise from which any kind or application should simply follow.

While philosophical ontology was just devoted to speculation, engineers and computer scientists revitalized the ontological way of thinking in the light of its possible application. Thus a computational ontology is a way to model and represent a domain of interest or a particular area of knowledge so that a computer can process it. Ontologies constitute a tool that allows comparison among data that were originally produced and stored in different manners. Moreover, ontologies are conceived as the mode to translate a specific knowledge at a certain level of description to other levels. Therefore ontologies are also said to be the ‘semantic level’ of scientific modeling. Within biomedical research bio-ontologies constitute a promising tool in many areas. Due to the pervasive and increasing role of bio-ontologies in biomedical research, a genuine epistemic problem would be to understand how the information they provide should be interpreted, and how it should be used by scientists. A mainstream position in this field is in favor of a sort of realism since these ontologies would be ‘windows on the world.’ Indeed, if ontologies are definitely representing knowledge, they do offer a vision on reality, a reality that is obviously filtered by the epistemic framework in which science operates. We will then argue that the categories of a bio-ontology do not simply refer to ‘objects in the world,’ but that they rather represent a high degree of theoretical idealization and epistemic abstraction as they are the result of a complex interaction between experimental findings, technical constraints, and semantic analysis.

Annotations and terms, as they represent the integration of experimental data, should not be conceived as ‘real entities’ but rather as *orienteering tools* on which to elaborate new experimental strategies. As in the orienteering game, bio-ontologies are those tools helping researchers to find directions on unfamiliar territory.

In Defense of Levels: Productive Ambiguity and the Hierarchical View of the World

Dan Brooks *(Bielefeld)*

Representing the world as hierarchically organized into a number of discrete levels of organization is so deeply embedded in biological science that it is rarely given explicit attention by working scientists. Similarly, philosophers of science routinely make reference to this stratified picture of the world for many topics, such as scientific explanation, the nature of causation, and theory structure in science. Despite this ubiquity in science and philosophy, there remain 'levels skeptics', who claim that the concept of organizational levels is a misleading, or even vacuous, notion for understanding how scientists produce knowledge about the natural world. Two different kinds of arguments are typically offered to this effect. One line of argument focuses, quite correctly, on the lack of clarity with which levels talk is applied in the literature: ‘Levels’ can simply mean too many things. Another line of argument asserts exactly the opposite, namely that the concept imparts a view of nature and science that is too rigid to be of use. Regardless of this skepticism, however, ‘levels’ endures as a pervasive theoretical concept in the biological sciences, and is heavily referenced in scientific texts of all degrees of specialization whether in general textbook or original research articles.

The purpose of this paper is to offer a response to this ‘levels skepticism’ by articulating more precisely why the concept of levels continues to be important for investigating the complex phenomena inherent to the biological sciences. One common misunderstanding all too often ascribed to levels of organization is an outdated ‘layer-cake’ character developed in the mid-20th century, and strongly associated with theoretical reductionism. These associations are unwarranted, however, as the articulation of levels in science proceeds in a heavily localized manner with a well-defined stratification of the phenomenon it is meant to describe, and within a specific disciplinary setting. Protein structure serves as an exemplary case in this regard. The term's admitted ambiguity also presents problems. While it is doubtful that a singular

concept of levels can adequately perform the roles that are ascribed to it, a plurality of more particular, mutually complementary levels concepts is possible. In other words, what the critics charge as vacuity in the concept of levels of organization, proponents may defend as a virtue of flexibility in the concept's range of application.

This moderate defense of levels makes room for a more sustained analysis of the importance of the concept of levels in science. Unlike other organizing concepts in biology like the ‘tree of life,’ the concept of levels of organization is more directly applied by scientists themselves for self-identification of their work among the many sub-disciplines of biological research, but also to orient their research towards objective features of the natural world. More particularly, the concept is central to conceptualizing explanatory contributions of particular disciplines for complex phenomena that are investigated by multiple disciplines that, alone, are unable to explain such phenomena.

Multiple Realizability of Functional Kinds

Zdenka Brzović *(Rijeka)*

This paper examines if the HPC theory of natural kinds can be defended against the recent objection that it fails to capture many scientific kinds (ERESHEFSKY and REYDON, forthcoming). It is argued that the HPC theory cannot accommodate non-causal kinds, functional kinds, and heterostatic kinds because of its insistence on the underlying causal basis of kinds responsible for the clustering of similar properties of kind members. I will focus on the claim that the HPC theory cannot capture functional kinds. In their criticism of the HPC theory, ERESHEFSKY and REYDON presuppose that functional kinds are multiply realizable, which in turn means that the function characterizing a kind can be performed by entities that differ in structure and properties. This is a problem for the HPC theory because of its requirement that members of the kind should share a cluster of common properties. As an example of a functional kind, ERESHEFSKY and REYDON use of the concept of gene in molecular biology.

I will defend the view that scientifically interesting functional kinds are not multiply realizable, and that ERESHEFSKY and REYDON's criticism of HPC is unjustified since even functional kinds must share an underlying causal basis. In order to make my case I will borrow the arguments already presented in the debate on functional kinds in philosophy of mind. The first type of argument, endorsed by KIM (1992) BICKLE (1998), and BECHTEL and MUNDALE (1999), invokes the success of the guiding methodological principle in neuroscience, which assumes that underlying neural mechanisms are continuous within and across species. Since this principle, which is at odds with the thesis about multiple realizability, is so successful in scientific practice, we should reject the multiple realizability thesis. In a similar vein I will try to show that the scientific practice in molecular biology (the example offered by ERESHEFSKY and REYDON) reveals that the underlying structure, and not only function, plays an important part in kinds individuation.

The second type of argument endorsed by KIM (1992) claims that multiply realizable

functional kinds are not projectible, which makes them poor candidates for scientific kinds; if there is no underlying causal basis we cannot make projections and inductive generalizations about kind members. I agree with KIM that scientific kinds ought to support inductive practices while ERESHEFSKY and REYDON seem to drop this requirement. I will argue that ERESHEFSKY and REYDON, in an effort to encompass all successful classificatory practices, have mistaken some heuristic practices for natural kinds.

Bechtel W, Mundale J (1999) Multiple realizability revisited: Linking cognitive and neural states. *Philos Sci* **66**:175-207

Bickle J (1998) *Psychoneural Reduction: The New Wave.* MITP

Ereshefsky M, Reydon T (forthcoming) Scientific kinds. *Philos Stud*

Kim J (1992) Multiple realization and the metaphysics of reduction. *Philos Phenomenol Res* **52**:1-26

Re-embodying the Extension of Darwinism

Mathieu Charbonneau *(Klosterneuburg)*

Projected extensions of Darwinism into a larger encompassing theory (e.g., from Darwin's organisms to the different levels of biological organization, Universal Darwinism, Generalized Darwinism, etc.) offer insightful case studies on the role of ontology in the evolutionary half of the biological sciences, of the relationship between theoretical frameworks and the range of ontologies these frameworks can accommodate, but also on how epistemological and methodological frameworks can deal with these multiple, sometimes conflicting ontologies. Indeed, through abstracting what is supposed to be the 'core of Darwinism,' if any such thing exists, proponents of the extension of Darwinism must deal with the — often conflicting — ontological frameworks of the biological sciences (the source domain) and the domain to which Darwinism is to be extended (the target domain, e.g., culture).

This problem of conflicting ontologies has been dealt through an abstraction-driven, disembodied view of Darwinism through the 'de-ontologizing' of the source and the target domain. The abstracted schema is spelled out in terms of logical concepts, such as sets and ensembles, logical operators, principles, and lists of sufficient and necessary conditions for evolution by natural selection to obtain. The rationale behind this strategy is that by evacuating ontology from the abstract entities, we gain a domain-neutral, encompassing Darwinian theory. Ontology is then pushed back as a local, intra-domain problem: Darwinism spelled large is ontologically neutral (hence 'Universal' or 'Generalized' appellations of Darwinism).

I argue that this received view, by evacuating ontology from the extension project, is epistemologically and methodologically flawed. The view is committed to a three-step logical recipe for extending Darwinism, which consists in (1) abstracting the core conceptual scheme of natural selection as a logical, ontologically neutral scheme, (2) choosing a target domain, and (3) mapping the abstracted scheme onto the target domain. Many problems emerge from this construal; among others, we can identify

construing evolving populations systems as sets or ensembles, understanding inheritance and selection as statistical notions (transgenerational covariance in variation distribution), and systematically black-boxing variation-generating mechanisms as noise leading to imperfect transmission.

These flaws are due to a misconception of the epistemology of explanatory analogies and inter-domain theoretical transfer. I argue that a closer look at the use of explanatory analogies suggests a different picture where abstraction and mapping are constrained by explanatory pragmatics and methodological reification, respectively. Instead of adopting a naive mapping view that abstracts away from each domain through the evacuation of the objects and relationships that populate them, using explanatory analogies in fact focalizes the extension project on the individuation and embodiment of putative evolutionary processes and mechanisms. The extension strategy I defend is thus an embodiment-oriented approach for methodology-driven science that not only reintegrates ontology, but also shows that any such transfer of theory is based on a specific ontological interpretation of each domain, which in turn shapes the extension process.

Time Scale and Levels of Organization

James DiFrisco *(Leuven & Exeter)*

The idea that nature is structured hierarchically or according to different levels of organization is an important ontological principle in the sciences, and particularly in the life sciences. WIMSATT (2007) expresses a commonly shared sentiment when he writes: “Levels of organization are a deep, non-arbitrary, and extremely important feature of the ontological architecture of the natural world.” Hierarchy concepts have increasingly taken on a central role for a variety of problems in philosophy of science, featuring prominently, for example, in debates about reductionism and emergence, downward causation, multilevel selection and units of selection, and biological individuality.

For the most part, accounts of hierarchical levels of organization aim to provide a general schematic representation of the causal structure of the world, such that intra-level entities are those that interact causally and directly whereas inter-level entities interact indirectly, via upward or downward causation or constraint (ELDREDGE & SALTHE 1984; SALTHE 1985). In view of this aim, however, more recently some authors have questioned the coherence and even the importance of general hierarchy theories (RUEGER & MCGIVERN 2010; POTOCHNIK & MCGILL 2012; ERONEN 2013). For any proposed hierarchy, where levels are distinguished on the basis of a consistent criterion (e.g., composition, spatial scale, etc.), it is possible to find exceptions — causal interactions that violate the putative segregation of levels. No one hierarchy can then be chosen over others as describing the ‘true’ causal structure of the world, and hence, it is argued, the project of developing a general, overarching theory of levels of organization should be abandoned.

This paper aims to assess the concept of hierarchical levels in biology in light of the criticisms addressed to it, and to evaluate whether it should indeed be abandoned or whether some suitable alternative can be found to fulfill its role.

Although traditional hierarchy concepts have their intuitive basis in compositional (part-whole) relations, I argue that hierarchical relations and compositional relations should be dissociated, because the latter do not by themselves permit defining levels across horizontally distinct entities — which is precisely the interest of a general hierarchy theory (ERONEN 2013; cf. CRAVER & BECHTEL 2007). I argue that this traditional, compositional levels-of-organization scheme ought to be replaced by a hierarchy of time scales. This hierarchical schema has its roots in ecology (ALLEN & STARR 1982; O'NEILL ET AL. 1986; POTOCHNIK & MCGILL 2012), and represents a middle position between the traditional levels of organization concept and the complete denial of levels, having several advantages over the former while preserving its motivation against the latter. Because scale is continuous, 'levels' are not discrete and typologically fixed but are purely relational, and revisionary with respect to compositional-organizational types (cell, organism, population, etc.). Moreover, time-scalar differences provide a more reliable guide to the segregation of causal interactions than space-scalar or compositional differences, and usefully prioritize the ecological factor of matter-energy exchange.

Having developed and defended a time scale criterion for hierarchy theory, I conclude by considering its limitations as a basis for a general hierarchy theory, as well as possible implications it would have, recursively, on the debates in which hierarchy concepts are employed.

Allen T, Starr T (1982) *Hierarchy: Perspectives for Ecological Complexity.* U. of Chicago P.
Craver C, Bechtel W (2007) Top-down causation without top-down causes. *Biol Philos* **20**:715-34
Eldredge N, Salthe S (1984) Hierarchy and evolution. *Oxford Surv Evol Biol* **1**:184-208
Eronen M (2013) No levels, no problems: Downward causation in neuroscience. *Philos Sci* **80**:1042-1056
O'Neill R, DeAngelis D, Waide J, et al. (1986) *A Hierarchical Concept of Ecosystems.* Princeton U. P.
Potochnik A, McGill B (2012) The limitations of hierarchical organization. *Philos Sci* **79**:120–140
Rueger A, McGivern P (2010) Hierarchies and levels of reality. *Synthese* **176**:379–397
Salthe S (1985) *Evolving Hierarchical Systems: Their Structure and Representation.* Columbia U. P.
Wimsatt WC (2007) *Re-engineering Philosophy for Limited Beings.* Harvard U. P.

Living Systems: Processes or Things?

John Dupré *(Exeter)*

This talk will address an ancient and fundamental ontological issue in biology, whether the living world should be thought of as a hierarchy of objects, or rather as composed of processes, and thus as essentially dynamic. I shall spend some time attempting to clarify the question. What is the difference between a thing and a process? Does a process require a thing, or things to which it happens? I also propose to reflect on the status of this question, and the kinds of ways we might attempt to address it. Is it an empirical question, to be answered by the progress of science, or at least by philosophical reflection on the progress of science? Or is it something that might be answered by a priori reflection? Might the question be partly normative? Finally, does it matter? Does it matter to science how we resolve this kind of ontological issue?

What Was at Stake Between Tansley and Clements?

Antoine C. Dussault *(Montréal)*

It is commonplace to interpret the debates between founders of the science of ecology in terms of standard philosophical polarities like emergentism vs. reductionism, or order vs. chaos. In such readings, the CLEMENTS/GLEASON debate is viewed as one between pictures of the ecological world emphasizing order, predictability and uniformity, vs. pictures emphasizing chaos, randomness and heterogeneity; whereas the CLEMENTS/TANSLEY debate is described as one between organicists (strong emergentists) and outright reductionists (see, e.g., WORSTER 1977; TOBEY 1981; BARBOUR 1996). ELIOT (2011, 2007) and NICOLSON & MCINTOSH (2002) have done some great work at rectifying commonplace readings of the CLEMENTS/GLEASON debate. The purpose of my presentation is to contribute to tempering too strongly polarized readings of the CLEMENTS/TANSLEY debate. Although such rectification is more directly concerned with the history of ecology, my presentation also has import for the philosophy of the life sciences in its aim to illustrate the importance of being careful when reading scientific debates in the light of philosophical (here metaphysical) categories. As, in the hands of ecologists, metaphysical debates frequently intertwine with empirical and theoretical ones, overlooking the latter can foster incomplete and sometimes overstated accounts of the controversies in which ecologists are involved.

In order to illustrate this, I will first show that CLEMENTS was not as strongly an emergentist as it is sometimes assumed. I will maintain that, although CLEMENTS (1936), influenced by his admirer JOHN PHILLIPS, became fond of the views of SMUTS (1927) and emergent evolutionists (e.g., MORGAN 1923), his explanations of ecological phenomena, as ELIOT (2011, 2007) and HAGEN (1992, 1988) have clearly shown, were plainly reductionist, involving only causes situated at the level of interacting species and organisms. I will suggest that CLEMENTS's holism determines his ecological hypotheses not at the level of causal explanations, but rather at that of his teleological and essentialist picture of ecological succession and climax (which cohabited peacefully with his causal reductionism). For CLEMENTS, succession toward the climatic climax was not

a predictive law, but a statement about what occurs in ecologically normal circumstances, 'normal' here meaning something akin to medical and physiological understandings of the term (WACHBROIT 1994).

Next, I will turn to TANSLEY (1935) and show that, although he vigorously attacked CLEMENTS and PHILLIPS for their abuse of organismic analogies, he did not aspire to rid ecology of holistic thinking. Rather, by introducing the concept of ecosystem inspired from the work of HYMAN LEVY (1932), he sought to provide such thinking with what he deemed a more scientifically credible foundation, namely, that of systems physics. TANSLEY's critique must be read, on the one hand, in the context of an empirical debate in ecology about the correctness of CLEMENTS's view of climate as the sole determiner of the orientation of ecological succession (VAN DER VALK 2014); and on the other hand, as a methodological debate over whether, given that ecosystems are wholes, they can nevertheless be appropriately studied through a reductionist analytical method (JAX 1998). What I will emphasize is that despite his criticism of ecological organicism, TANSLEY did not reject CLEMENTS's teleological view of succession and ecological normality.

Barbour MG (1996) Ecological fragmentation in the Fifties. In: Cronon W (ed) *Uncommon Ground: Rethinking the Human Place in Nature*. Norton

Clements FE (1936) Nature and structure of the climax. *J Ecol* **24**:252-284

Eliot CH (2007) Method and metaphysics in Clements's and Gleason's ecological explanations. *Stud Hist Philos Sci C* **38**:85–109

Eliot CH (2011) The legend of order and chaos. In: deLaplante K, Brown B, Peacock KA (eds) *Philosophy of Ecology*. Elsevier

Hagen JB (1988) Organism and environment: Frederic Clements's vision of a unified physiological ecology. In: Rainger R, Benson KR, Maienschein M (eds) *The American Development of Biology*. U. of Pennsylvania P.

Hagen JB (1992) *An Entangled Bank: The Origins of Ecosystem Ecology*. Rutgers U. P.

Jax K (1998) Holocoen and ecosystem: On the origin and historical consequences of two concepts. *J Hist Biol* **31**:113-142

Levy H (1932) *The Universe Of Science*. Watts

Morgan CL (1923) *Emergent Evolution*. Williams and Norgate

Nicolson M, McIntosh RP (2002) H. A. Gleason and the individualistic hypothesis revisited. *Bull Ecol Soc Am* **83**:133–142

Smuts JC (1927) *Holism and Evolution*. Macmillan

Tansley AG (1935) The use and abuse of vegetational concepts and terms. *Ecology* **16**:284-307

Tobey RC (1981) *Saving the Prairie: The Life Cycle of the Founding School of American Plant Ecology, 1895-1955*. U. of California P.

van der Valk AG (2014) From formation to ecosystem: Tansley's response to Clements' climax. *J Hist Biol* **47**:293-321

Wachbroit R (1994) Normality as a biological concept. *Philos Sci* 61:579–591

Worster D (1977) *Nature's Economy: The Roots of Ecology*. Sierra Club Books

Regulation and its Main Features

Eva Fernández-Labandera Tejado *(Donostia / San Sebastián)*

Regulation is a fundamental issue when analyzing how complex systems achieve robust self-maintenance while embedded into variable environmental conditions. It is necessary to ensure quick and targeted actions. A system without regulation is self-organized through spontaneous formation of patterns, but they drastically limit plasticity in response to different situations a system is subject to throughout its existence. To develop the responsiveness needed for problem solving, it requires a system of feedback mechanisms and the ability to send instructive signals that go from the local response to a wider one, through all intermediate ranges of possible states of the system.

This necessarily involves an increase in structural complexity, and the consistency needed for maintaining such a system is given exclusively by regulation. The most distinctive feature of a regulated system is the presence of a functionally specialized system, able to differentiate one or a set of various states, from the multiplicity of possible states a regulated system can go through, based on an assessment of the system conditions and production of control signals which induce relevant changes in functional status. These features reduce the cost of increasing the error ratio that comes with any increase in structural and functional complexity, and regulatory processes that can correct errors, repair damage, and adjust the activity of procedures to constantly changing circumstances. In others words, the regulated system is known for its ‘robustness’, a compensation mechanism for internal and/or external perturbations. Nevertheless, this is CHRISTENSEN's definition of regulation, and it is very general. The interaction of feedback regulation, homeostasis and adaptation remains as an intuitive draft, but without enough clarification to distinguish it from other compensatory mechanisms, or to discern the degree of complexity of the various regulatory phenomena.

A new hypothesis from the lasts years suggest to abandon the usual phenomenological approach in favor of a more comprehensive study of organizational properties and their contribution to the system, in order to characterize the various compensatory mechanisms that come into play in the ongoing and continuous exchange with an unstable environment into which a biological system grows. For this purpose, two functional architectures are distinguished: constituent functions and regulatory meta-functions. The former refer to work of self-production and self-maintenance carried out by metabolism. The latter represent diverse response mechanisms of constitutive functions to internal and external perturbations so the system remains viable.

The question is that control mechanisms of compensation may operate at both levels. However, even the simplest system may exhibit some robustness (like the emergence of patterns from simple structures mentioned above), yet it could not be said to be proper regulation, but simply dynamic stability. Resistance to certain variations can be achieved through compensations between processes or coupled subsystems. However, regulation requires a distinct and functional architecture unique of biological systems. Regulation needs a level hierarchy, so it can manage both structural and functional complexity of living systems, modulating the action of its mechanisms depending on which perturbation or set of perturbations it is facing.

I will expose some of the diverse accounts of regulation, and highlight various issues philosophical speculation must face when relating concepts like organizational closure, autonomy, and regulation itself, inter alia.

Using Ontologies for Ecological Research

Eric Garnier *(Montpellier)*

Ecology is currently undergoing a major transformation to become a ‘data- intensive’ science, which requires combining very heterogeneous datasets. Semantic heterogeneity is a primary issue, and corresponds to the diverse natures of the data concerned (e.g., gene distribution, taxonomy, community structure, ecosystem fluxes, climate), the multiplicity of terms, and more generally, of concepts used in ecology, making the interoperability of existing data difficult. The development of generic and domain ontologies is seen as a key step toward a better formalization of concepts, allowing one to confront the data with interpretations, thereby enabling emergence of new understandings. I will discuss recent advances in this emerging field of research in ecology.

‘Rediscovery’ and the Self-vindication of Computational Biology

Pierre-Luc Germain *(Milano)*

From an epistemological point of view, there are great advantages in adopting an ontology in the scientist's sense–i.e., not necessarily as a realist metaphysical commitment, but as a provisional consensus on what there is (approaching one of Quine's senses of ontology). For instance, current ‘omics’ approaches in biology are possible only because of a broad agreement on relevant biological entities and activities. More or less formalized bio-ontologies are digitizing entities, terms, and their relations, thereby making ‘dirty biology’ amenable to computation and enabling high-throughput approaches. As a consequence, so-called unbiased approaches are in fact designed to detect very particular kinds of things, which has led to renewed concerns about theory-ladenness and self-vindication.

Indeed, contemporary experimental biology does not start with observation, but rather with production: its phenomena are not given by nature but produced by its very methods. This creates circularity, as both the methods of production and the methods of observation/analysis are designed on the basis of the same grammar and repository of entities and activities. Such circularity is not necessarily bad, and in fact it has been argued that it is a condition of the possibility of laboratory sciences, enabling an iterative improvement of the coupling between techniques and our categories. However, it does imply that there is contingency in how our bio-ontologies develop, and suggests the risk that our view on what there is could be stuck in local, sub-optimal maxima.

In principle, the only way to circumvent this problem is to cultivate constant attempts to reconceptualize ‘what there is’ more or less autonomously from conventional tools (in itself a potentially interesting program for so-called complementary philosophy of science). Indeed, efforts for the computational ‘rediscovery’ of established facts and distinctions are often represented as further proofs of their reality (or adequacy). I propose to examine the case of the ‘rediscovery’ of cell types as an example of such

approaches, and to discuss its limitations as an independently converging digitalization of biology.

The Proximate/Ultimate Distinction Faces Cognition

Paola Hernández-Chavez *(México D.F.)*

The proximate/ultimate causation is an influential, though debatable, distinction in evolutionary theory and philosophy of biology. In his famous "Cause and effect in biology" (1961), ERNST MAYR advocated the use of two complementary notions of causality: proximate causes related to immediate factors such as how an environment shapes an organismal trait, and ultimate causes related to evolution by means of natural selection, as in the historical explanations of why an organism has a specific trait. According to MAYR, biology can focus either on the functioning of a system (proximate causes) or on the evolutionary history of a system (ultimate causes).

I will apply the proximate/ultimate distinction to cognitive issues in order to illustrate the tension between environmental (proximal) and genetic (ultimate) approaches. I will claim that in order to understand how human cognition works, proximal explanations seem to precede (but, obviously, not to exclude) evolutionary explanations. Mainstream approaches to cognitive architecture assume, as their main explanatory resource, that the cognitive abilities we presently have emerged in the context of our ancestors' competition for resources. I will show why evolutionary speculations are insufficient to understand how our cognitive structure is made of and how it works.

In biology, ultimate causation relates to studying the environmental factors that contribute to survival and reproduction. In such fashion, Darwinism is linked to natural selection, where the final 'aims' are gene transmission and species survival. An extreme example of this explanatory pattern is memetics. On the other hand, proximal causation implies studying environmental/immediate factors, which can be independent or even go contrary to evolution. In such a scenario, proximal and ultimate causation could not be conciliated. In brief, proximal causation seems to be mainly concerned with accounting for the organisms' and populations' adaptive processes. It usually states 'how?'- questions. In contrast, ultimate causation implies formulating hypothesis about

the possible evolutionary origins of the biological traits or behaviors. It usually states ‘what?’- or ‘why?’-questions.

In order to support the claim that to elucidate how our cognitive processes work it is suitable to study their characteristics and proximal causes in the first place, I will deal with the visual system. The human visual system is highly modularized, genetically rooted, and is involved in many cognitive processes. Empirical evidence points out that despite its genetic basis, the visual system is highly permeable.

Briefly, in contrast to current evolutionary theories aiming to explain our cognitive architecture based on speculations of our ancestors’ adaptive conditions, I contend that our cognitive architecture can be better understood if we focus on proximal causation. Studying proximal causation in regards to cognition is imminent once we realize that cognitive theories have implications for cognitive impairments studies. For such theories, the only possibility to understand and treat a cognitive disorder comes from understanding the proximal causes of the impairment, such as the environmental conditions of the subject’s development, the resulting residual dysfunctions, and the brain rewiring it involves.

The Ontological Perplexity of Synthetic Organisms

Sune Holm *(København)*

Scientific research and rapid advances in technology are accelerating our ability to manipulate biological systems. The core aim of the emerging field of synthetic biology is to enable the design of living systems with new functions that do not exist in nature, and the redesign of already existing functions. A recent book on synthetic biology and its promises and perils (CARLSSON 2010) proclaims that biology is technology: Organisms and their constituent parts are engineerable components of larger systems, and the possible products of synthetic biology are commonly described as living machines. While these locutions are extremely effective when it comes to proclaiming and communicating the engineering aspirations of synthetic biology, they are also philosophically perplexing. However, little investigation has focused on the ontological status of the products that synthetic biologists announce that they will construct. I explore the ontological nature of synthetic biology products.

My focus will be on the analysis suggested by PABLO SCHYFTER (2012). SCHYFTER discusses how should we understand the material products of synthetic biology. He focuses on two aspects of the ontology of synthetic organisms. The first concerns the appropriateness of characterizing synthetic biology products as technology, i.e., as synthetic biological artifacts. His claim is that there is "both an analytic suspicion and a commonsense impression that engineered organisms must somehow differ from corkscrews, airplanes, and towers," and that this impression "rests on a series of ontological issues." In particular he considers whether synthetic organisms satisfy the following four criteria of artifactuality: materiality, intentional design, functionality, and normativity (KROES & MEIJERS 2006), and he argues that synthetic biology products will only fit them "imperfectly." What distinguishes synthetic biological artifacts from corkscrews and airplanes is that they reproduce and self-maintain, and they can evolve, thereby 'subverting' their designers' intentions. In the first part of this paper and drawing on recent work on artifact ontology I discuss the interrelation between the criteria of

intentional design, functionality, and normativity of synthetic biological artifacts in order to understand the sense in which such objects are technological.

In the second section I consider synthetic organisms in the light of theories of natural kinds. SCHYFTER finds that synthetic organisms may present complications for the homeostatic property cluster account of natural kinds and suggests that the promiscuous realism of DUPRÉ (1993) will provide a better framework for establishing the kinds of things produced by synthetic biology. I critically assess SCHYFTER's claim that the ontology of synthetic biology products is "a messy affair."

Carlson R (2010) *Biology is Technology*. Harvard U. P.

Dupré J (1993) *The Disorder of Things*. Harvard U. P.

Kroes P, Meijers A (2006) The dual nature of technical artefacts. *Stud Hist Philos Sci A* **37**:1-4

Schyfter P (2012) Technological biology? Things and kinds in synthetic biology. *Biol Philos* **7**:29-48

What, Exactly, is Biological Possibility?

Maximilan Huber *(Genève)*

Morphospace is a twofold representation of organic form. First, the range of biologically possible organic form is delimited. Second, the actual distribution of organic form is depicted; the reasons or causes resulting in the actual distribution have been at the heart of a contagious debate between adaptionism and developmental biology (e.g., AMUNDSON 1994). Surprisingly, the more fundamental metaphysical notion of biological possibility has only received little attention. Even though it is commonly accepted that biological possibility is distinct from logical, physical, and historical possibility, explicit definitions are rare.

An important exception is DENNETT (1995) who defines biological possibility based on the thought-experiment of the Library of Mendel. In this library, every possible genome (up to a certain length) is stored and for each genome, there is a reader-constructor capable of producing the corresponding phenotype. Now, for some genome G1, x is is biologically possible if and only if x is an instance of a genome G2 or a feature of G2's phenotypic products, and G2 is accessible from G1. This definition has two nice features. First, the tree of life is included in the Library of Mendel as distinguished accessibility pathway between certain genomes. Second, biological possibility has a very local or historical feel since it is defined relative to a certain genome; so what is biologically possible depends on the exact position in the Library of Mendel respectively the tree of life. The crux of this definition is of course the notion of accessibility; unfortunately, DENNETT leaves it largely unexplained. I will improve on the given definition of biological possibility by making the notion of accessibility more precise. For this purpose, I will formalize the Library of Mendel using three different modal logics and discuss the advantages and disadvantages of each approach. What follows is a brief and informal overview over this strategy.

First, as a variation of the classical semantics for counterfactual conditionals (LEWIS 1973), it is interpreted, for each genome, as a nested system of spheres arranged by

biological similarity and populated by genomes. This requires a rewrite of LEWIS' criteria of similarity; these criteria are phrased in terms of the general laws of physics but need to be replaced or at least supplemented by the special laws of biology (see DUNN 2011 for such a rewrite with respect to thermodynamics). Second, the Library of Mendel is interpreted on the basis of a probabilistic modal logic (FRISCH & HADDAWY 2013) where accessibility is a conditional probability between genomes. This approach arguably captures DENNETT's (1995) intuition that some biological possibilities are 'more possible' than others. Third, a propositional dynamic logic (FISCHER & LADNER 1979) allows, on the one hand, to give content to accessibility by interpreting it as evolutionary program, and, on the other hand, to accommodate the reader-constructor corresponding to each genome by interpreting it as developmental program.

Amundson R (1994) Two concepts of constraint: Adaptationism and the challenge from developmental biology. *Philos Sci* **61**:556–578

Dennett DC (1995) *Darwin's Dangerous Idea: Evolution and the Meanings of Life.* Simon & Schuster

Dunn J (2011) Fried eggs, thermodynamics, and the special sciences. *Brit J Philos Sci* **62**:71–98

Fischer MJ, Ladner RE (1979) Propositional dynamic logic of regular programs. *J Comput System Sci* **18**:194–211

Frisch AM, Haddawy P (2013) Probability as modal operator. Computing Research Repository, 1304.2352:109–118

Lewis DK (1973) *Counterfactuals.* Blackwell

McGhee GR (1999) *Theoretical Morphology: The Concept and Its Applications.* Columbia U. P.

What is Natural Selection? A Tip from Cancer Research

Marko Jurjako *(Rijeka)*

I will focus on the question: how should we best characterize Darwinian natural selection? In particular, we will examine the prospects of a mechanistic answer to that question, such as the one defended in BARROS' (2008) paper. With the account advanced in that paper, the so-called new mechanistic philosophy of science has made its most explicit contribution to the issue of evolutionary mechanisms and has joined the debate between the two leading philosophical interpretations of the nature (ontology) of Darwinian selection, i.e., the force and consequence interpretations (for an overview, see BRUNNANDER 2007). In answering the above question, we will proceed as follows: in the first part of the paper, BARROS' account of natural selection as a mechanism in a rather strict sense will be more closely analyzed. Accordingly, since Barros' corresponding account develops a more comprehensive version of the so-called MDC account of mechanisms (see MACHAMER et al. 2000), and rejects the other influential mechanistic account (see, e.g., GLENNAN 2002), relevant underpinnings of putative evolutionary mechanisms will also be addressed to a certain degree. In the second part of this paper, natural selection — considered as one of the main 'ingredients for human cancer disasters' (see ALBERTS et al. 2008) — will be described. Human cancer as a 'micro-evolutionary process' (see MERLO et al. 2006) in this regard offers suitable data resources for at least two related reasons: (1) the onset of human cancers provides a more direct access to evolution by natural selection, which draws on a determined time range of human life; (2) the proximity of natural selection in tumorigenesis and, more broadly, in cancerogenesis to the biological mechanisms in a more restricted sense. Both reasons will help in making progress toward a satisfying answer on what, after all, is the nature of natural selection. In that regard, we will argue in favor of the view according to which Darwinian natural selection is most adequately understood as a certain kind of process-mechanism.

Alberts B, Johnson A, Lewis J, et al. (2008) *Molecular Biology of the Cell.* 5th ed. Garland Science

Barros BD (2008) Natural selection as a mechanism. *Philos Sci* **75**:306-322

Brunnander B (2007) What is natural selection? *Biol Philos* **22**:23-246

Glennan S (2002) Rethinking mechanistic explanation. *Philos Sci* **69**:S342-S353

Machamer P, Darden L, Craver CF (2000) Thinking about mechanisms. *Philos Sci* **67**:1-25

Merlo LM, Pepper JW, Reid BJ, et al. (2006) Cancer as an evolutionary and ecological process. *Nature Rev Cancer* **6**:924-935

How Behavioral Scientists Deal with Explanatory Complexity

Maria Kronfeldner *(Bielefeld)*

The talk will address how behavioral sciences deal with the ontologically given complexity of living systems. After analyzing the relations between three kinds of complexity — semantic, developmental, and explanatory — the talk aims at two things: (1) Making sense of causal selection: Scientists regularly ignore most of the ontologically given causal factors involved in the production of certain behaviors. They do so in order to reduce the complexity they encounter. This so-called causal selection (i.e., a biased selection of causes that are ontologically on a par) will be defended as a useful heuristic strategy. For this, I shall use a revised version of COLLINGWOOD's (1938) pragmatic-pluralist 'control principle' of causal selection. (2) Defending an integrative pluralism: LONGINO (2013) claims that the "causal spaces" used in different approaches to the behavior of living systems (in particular human behavior, the most complex one) are incommensurable. The approach defended here argues against LONGINO's incommensurability claims. The perspectival ways of choosing between relevant and irrelevant causes are commensurable. For specific problems, the partial knowledge produced from one perspective can be integrated with similar partial knowledge from other perspectives. The pluralism that results from scientists' selective reactions to complexity is not a 'tower of Babel'-pluralism, but an integrative one.

Collingwood RG (1938) On the so-called idea of causation. *Proc Aristot Soc* **38**:85-112

Longino HE (2013). Studying human behavior : How scientists investigate aggression and sexuality. U. of Chicago P.

Ontological Issues in Developmental Biology: Taking Variation Seriously

James Lowe *(Exeter)*

New methods and techniques (and changing organismal practices) in developmental biology are allowing experimenters to include more organisms in their experimental set-ups. As the sheer number of samples in MORGAN's 'fly-room' aided the detection of even rare mutations in Drosophila (KOHLER 1994), the increasing number of samples amenable to observation and analysis is currently leading to a greater appreciation of the variation exhibited between living forms of the same species. Additionally, in the last twenty years new emphasis has been placed on the discovery (and integration into wider explanatory frameworks) of developmental and evolutionary mechanisms which generate, maintain, eliminate, and harness variation (such as those approaches covered by the labels 'evolutionary developmental biology' and 'ecological developmental biology'; see, e.g., HALL & HALLGRÍMSSON 2005; GERHART & KIRSCHNER 2007; KLINGENBERG 2010; GILBERT 2012; HALLGRÍMSSON et al. 2012). The investigation and explanation of variation is therefore increasingly central to developmental and evolutionary studies. While extensive and successful efforts have been made to analyze and conceptualize the philosophical and scientific consequences of new departures in developmental biology (e.g., ROBERT 2004; AMUNDSON 2005; BURIAN 2005), so far the significance of variation in development has received little attention in the philosophical literature.

My aim is to correct for this by accounting for how we might approach well-established ontological categories in developmental biology taking variation seriously. This requires three things. First, to establish the extent and significance of variation in development, and to clarify what exactly we mean by variation, and the different ways in which entities and processes can vary. Second, to look at key terms that incorporate certain assumptions about variation and which form part of the ontological framework of modern developmental biology. I will focus on one such key term that is central to much

experimental work, normal development, though I will also consider differentiation and specification. Normal development will be defined, and its key role in experimental systems outlined, which will include a brief history of its use. Third, I will directly relate normal development to how variation is conceptualized and managed in developmental biology.

I argue that given the extent of variation exhibited by developing organisms, the sort of questions that scientists are increasingly asking concerning variation, and the greater need to take account of variation in development, the ontological status normal development traditionally and currently holds in developmental biology must be called into question. Finally, I suggest how this approach might lead to a similar analysis of concepts such as differentiation and specification, and their ontological correlates, the differentiated or specified cell or tissue.

Amundson R (2005) *The Changing Role of the Embryo in Evolutionary Thought.* Cambridge U. P.

Burian R (2005) *The Epistemology of Development, Evolution, and Genetics.* Cambridge U. P.

Gerhart J, Kirschner M (2007) The theory of facilitated variation. Proc Natl Acad Sci USA 104 Suppl. **1**:8582-8589

Gilbert SF (2012) Ecological developmental biology: Environmental signals for normal animal development. *Evol Devel* **14**:20-28

Hall BK, Hallgrímsson B (eds) (2005) *Variation: A Central Concept in Biology.* Elsevier Academic

Hallgrímsson B, Jamniczky HA, Young NM, et al. (2012) The generation of variation and the developmental basis for evolutionary novelty. J Exp Zool B: *Mol Dev Evol* **318**:501-517

Klingenberg C (2010) Evolution and development of shape: Integrating quantitative approaches. *Nat Rev Genet* 11:623-635

Kohler R (1994) *Lords of the Fly.* U. of Chicago P.

Robert JS (2004) *Embryology, Epigenesis, and Evolution: Taking Development Seriously.* Cambridge U. P.

The Limited Extended Nature of Biological Inheritance

Francesca Merlin *(Paris)*

This talk will address the question of the nature of biological inheritance in the light of the fact that now biologists consider that organisms inherit much more than just DNA. What is biological inheritance? And how far should its definition be extended in order to take into account new forms of 'non-genetic' transmission (epigenetic, parental, behavioral, ecological, and cultural)? Starting from recent proposals to reconceive inheritance, I will show that one of the main assumptions in the scientific and philosophical literature of the last twenty years is not supported by evidence. The analysis of four distinctions, mainly empirical–and of the lessons drawn from them–will allow me to propose a redefinition of inheritance that brings to the fore its privileged linked to the process of reproduction at the ontological level, and the specific theoretical role of this concept in evolutionary biology. I will conclude by showing the epistemic gain provided by my answer to the ontological question of what inheritance is.

Organization and Biological Individuation

Matteo Mossio *(Paris)*

I will put forward an account of biological individuation grounded on a precise characterization of biological organization. I will suggest that biological organization should be conceptualized as a causal regime realizing a closure between those components that act as constraints on the underlying thermodynamic flow of energy and matter. Because of the mutual dependence and integration between the components that it entails, organizational closure pertinently grounds biological individuation. I will focus on two main issues related to this account of individuation.

On the one hand, I will claim that organizational closure provides an understanding of biological individuation in terms of a complex and specific interplay between constraints and processes, between conservation and change. Biological individuals are such precisely because, some of its components do not change at the relevant time scales and, because of their conservation, they are able to constrain processes and reaction, and realize organizational closure. On the other hand, I will discuss the question whether organizational closure is a necessary, or a necessary and sufficient condition for biological individuation. In the latter case, any system realizing closure is ipso facto a biological individual: for instance, insofar as they seem to be pertinently organized, ecosystems would count as individuals. In the former case, which I favor, organized systems are individuals only if they meet additional requirements, under which they can be taken as autonomous systems; accordingly, the concept of biological individuals would likely apply to unicellular and multicellular organisms, but presumably not to ecosystems.

Arbitrariness in Information Transfer and the Autonomy of Biology

Vidyanand Nanjundiah *(Bangalore & Klosterneuburg)*

Living matter is characterized by an intricate web of interactions at all relevant scales. The consequence is a breakdown of autonomy: the quantitative or qualitative state of one partner is influenced by the other (for simplicity we stick to pair-wise interactions and ignore 'bystander' and other many body effects). The influence can be mediated by physical means — e.g., pressure — or by chemical means — e.g., a hormone. Pressure and hormones are signals: they convey information and elicit a response. Is the response related to the signal? In some cases, yes; the response is implicit in the signal. Consider an enzyme that catalyzes the breakdown of a substrate. The enzyme has a 3-dimensional structure that recognizes a certain portion of the substrate and therefore binds to it; as a result, it speeds up the rate at which the substrate is converted to product. This makes it possible to design an enzyme for a specific purpose by the logical application of physical and chemical principles. In other cases the link between signal and response appears to be wholly arbitrary. In biology, the best-known example is the genetic code. The only (current) 'explanation' for why a particular nucleotide triplet in DNA corresponds to a specific amino acid in a protein is that it is an accident of evolution. One is unable to deduce the nature of the amino acid from that of the DNA triplet: in principle any code could work. Arbitrariness opens up a huge range of possibilities for the functioning of living matter, constrained by physics and chemistry but not (necessarily) deducible from their principles. The talk will attempt to develop the idea that arbitrariness in information transfer is evidence of the independence of biology from physics and chemistry.

On the Role of Counterfactual Reasoning in the Biological Sciences

Marco J. Nathan *(Denver & Milano)*

NELSON GOODMAN's influential *Fact, Fiction, and Forecast* begins with the famous remark that "if we lack the means for interpreting counterfactual conditionals, we can hardly claim to have any adequate philosophy of science." Half a century later, GOODMAN's problem still remains unresolved; yet philosophy of science steadily proceeds along its path, seemingly unscathed by the lack of an uncontroversial and widely accepted account of counterfactuals. Indeed, even a cursory glance at the extant literature reveals that counterfactuals have received — and continue to receive — very little attention in scientifically informed circles.

This tension invites some obvious questions. On the one hand, how can the paramount importance of counterfactuals for the philosophy of science be reconciled with the evident observation that they are so overtly and persistently ignored? On the other hand, how could the significance of a viable account of counterfactuals for philosophy of science be dismissed, given that these statements lie at the core of various influential accounts of laws of nature, law-like generalizations, explanation, dispositional properties, causal attributions, and other concepts central to philosophical discussions of the metaphysical foundations of science. The goal of this talk is to articulate this dilemma and to sketch a solution. By focusing on biological examples, I argue that counterfactuals do play an important role within scientific theorizing, as they constitute explanatory hypotheses regarding and alleged similarity between a theory (or model) and the world. Nonetheless, the thesis defended here requires a radical revisiting of the traditional conception of the ontology and foundations of biology.

Are Biological Mechanisms Real?

Daniel J. Nicholson *(Exeter)*

One of the most conspicuous developments in the philosophy of science over the past fifteen years has been an increasingly central concern with elucidating the role that mechanisms play in scientific practice. Much of the philosophical attention has focused on developing an account of mechanisms that does justice to the way the term is used in scientific explanation, especially in the biological sciences. Although there is little agreement over how best to characterize this concept — MACHAMER ET AL. (2000), GLENNAN (2002), and BECHTEL & ABRAHAMSEN (2005) are the three most influential accounts — there is at least close to universal agreement regarding their metaphysical status.

Whatever else they are, one thing we can be certain of is that mechanisms are "real systems in nature" (BECHTEL 2006); that is, that they are "real and local," as the title of a recent paper makes explicit (MCKAY & WILLIAMSON 2011). The reason why there is a general consensus on this issue has to do with the way we tend to think about paradigmatic mechanisms like a clock or a fridge. These are clearly "real and local," and are of course "real systems in nature."

But is this still the case when 'mechanism talk' is applied to biological phenomena? When one considers the history of the usage of the concept of mechanism in biology one realizes that the term was employed for several centuries as a synonym of 'machine' or 'machinery,' and that it was only in the second third of the 20th century that it came to be widely used to designate processes that are not machine-like, such as natural selection, inheritance, or the immune response (on this history, see NICHOLSON 2012). The term 'mechanism' as it is used in biology today has lost its mechanical and machine connotations. Biologists speak of mechanisms without thinking about machines anymore.

The term 'mechanism' has become a dead metaphor and its meaning has become

vague. Although it pervades biological discourse, unlike other terms like ‘microtubule,’ ‘mitosis,’ or ‘metabolism,’ ‘mechanism’ does not have a precise definition. It does not appear in the glossaries of biology textbooks, nor is it listed in its indexes. Instead, ‘mechanism’ is a term that simply ‘comes up’ in scientific practice, and its meaning is inferred from the explanatory context in which it is invoked. Most philosophers have assumed that one thing that has remained attached to the usage of the term ‘mechanism’ in biology is the conviction that biological mechanisms are ‘real things in nature’ (like machines such as clocks and fridges).

I challenge this conviction. I do so by taking seriously two implications that follow from an ontic view of biological mechanisms. If biological mechanisms are ‘real and local,’ we should be able to answer two key questions: (1) how many mechanisms make up an organism? (2) When is a description of a biological mechanism complete? By showing the impossibility of providing principled answers to these questions I will show that the best way to understand biological mechanisms is not as real things but as idealized spatiotemporal cross-sections of organisms that heuristically pick out certain causal features over others in order to account for how given functions within the organism are carried out.

The Timing of Development

Antonine Nicoglou *(Paris)*

Since 1980, a new conceptual framework has appeared in biology, EvoDevo, whose aim is to gather developmental and evolutionary explanations (GILBERT, OPITZ, & RAFF 1996). Nevertheless, the issue of whether and how such a gathering should be achieved raises difficulties. In a certain way, one could consider that "problems concerned with the orderly development of the individual are unrelated to those of the evolution of organisms through time" (WALLACE 1986). And since development can be depicted as the trajectory of an individual from the zygote stage to the adult stage, in a process in time, at least its timescale appears clearly decoupled from the evolutionary timescales (HALL & OLSON 2006).

Furthermore, developmental process may include various processes at distinct space and time scales (molecular, cellular, etc.), which can be further analyzed on their own. I suggest that by focusing on the character, instead of the developmental stage (DE BEER 1940), developmental biology has lost the temporal dimension of its process, which was further considered with the stage–a distinct section arbitrarily cut from the temporal axis of an organism's life. I argue that a way to reassess the importance of time in developmental process (in order maybe to achieve afterwards a gathering of development and evolution) is to address the specifics of the developmental timing, its specificities and its relation to other time scales. This would offer a clarification of the separation between evolutionary and developmental time scales, and show how a developmental theory might integrate the various processes at distinct space and time scales that I identify.

Indeed, a more restrictive definition of 'development,' following the embryological tradition that focuses on the constraints of form (NEWMAN & BHAT 2008) rather than on genes (e.g., developmental genes, etc.) (CARROLL 2008), would allow one to pay more attention to specific biological interactions, as differentially correlated to various aspects of forms and moments of their emergence. In a way, each interactive process along

development (such as adhesion, cohesion or chemical waves, etc.) (FORGACS & NEWMAN 2005, POURQUIÉ 2003) possesses and delineates a specific timing. This leads to a further task, namely to understand how different types of processes can be built (and beyond this what is the basis of a difference between processes) in order to define and distinguish at the end, different types of models or different types of theories, their possible synthesis and/or incompatibilities. If one can pinpoint differences during developmental periods, one can also distinguish different kinds of interactions at different levels (e.g., chemical interactions at the unicellular level, cell interactions at the multicellular level, etc.).

Carroll SB (2008) Evo-Devo and an expanding evolutionary synthesis: A genetic theory of morphological evolution. *Cell* **134**: 25–36

de Beer GR (1940) *Embryos and Ancestors*. Oxford U. P.

Forgács G, Newman SA (2005) *Biological Physics of the Developing Embryo*. Cambridge U. P.

Gilbert SF, Opitz JM, Raff RA (1996) Resynthesizing evolutionary and developmental biology. *Dev Biol* 173:357–372

Hall BK, Olson WM (eds) (2006) *Keywords and Concepts in Evolutionary Developmental Biology*. Harvard U. P.

Newman SA, Bhat R (2008) Dynamical patterning modules: Physico-genetic determinants of morphological development and evolution. *Phys Biol* **5**:015008 (14pp)

Pourquié O (2003) The segmentation clock: Converting embryonic time into spatial pattern. *Science* **301**:328–330

Wallace B (1986) Can embryologists contribute to an understanding of evolutionary mechanisms? In: Bechtel W (ed) *Integrating Scientific Disciplines*. Springer

The Return of Potencies in Evolutionary Biology: Towards an Ontology of Possibility

Laura Nuño de la Rosa *(Klosterneuburg)*

In 1978 ERNST MAYR claimed that the disciplines converging into the Modern Synthesis had rejected the presence of any (phenomenal or causal) kind of finalism in evolution: palaeontology had proved the non-existence of evolutionary trends, and molecular biology had shown the intrinsic randomness of genetic change. A decade later, the disciplines later converging in the new developmental synthesis started to challenge the randomness and contingency of evolutionary change. On the one hand, the investigation of the tempo and mode of evolution has brought with it an increasing interest in the directionality of evolutionary change and the logics of morphospace. On the explanatory side, the evolutionary jargon has been populated with 'teleological' terms (possibilities, potentialities, dispositions, variability...) emphasizing the inherency of evolution, namely "the tendency to organize and change along preferred routes" (NEWMAN & MÜLLER 2006).

The introduction of a 'teleological' component into evolutionary theory has led several practitioners of EvoDevo to confront the ontology of chance and necessity underlying the received view of evolution. My talk will address what I take to be the main ontological issue associated with the incorporation of generative principles in evolutionary theory, namely the ontological status of developmental systems as the targets of evolution. The variational properties of developmental systems (such as modularity) cannot be interpreted as individual properties that contribute to the fitness of the organisms composing a population (WAGNER & ALTENBERG 1996). Contrary to what has been recently claimed (MERLIN 2010), I will claim that if the targets of evolution are not the individuals composing populations but the variational properties of developmental systems, the notion of evolutionary chance is radically contested, and an alternative ontology of possibility craves our philosophical attention.

Integrating Expanding Data in Pluralistic Models of Heredity: Toward an Organizational Framework

Gaëlle Pontarotti *(Paris)*

Contemporary literature shows an increasing interest for extended inheritance. Whereas the multiplication of data regarding non genetic mechanisms–epigenetic, behavioral, ecological, symbiotic–responsible for transgenerational similarities encourages critics to claim for the adoption of pluralistic (MAMELI 2005), multidimensional (JABLONKA & LAMB 2005), or inclusive models (DANCHIN et al. 2011), a few authors try to assess the effects of non genetic processes on evolutionary trajectories (HELANTERA & ULLER 2010; BONDURIANSKY, CREAN, & DAY 2012). However, the multiplication of inheritance channels may mainly have a significant and so far neglected impact on the very concept of heredity, urging specialists to redefine key notions such as inherited factors. Indeed, such a conceptual clarification might be indispensable in a pluralistic framework that might otherwise lead to the problematic conflation of inherited factors with any stable developmental resources (GRIFFITHS & GRAY 1994; MAMELI 2005), and the consecutive expansion of a key biological category, which may from now on include parts of parental extended phenotypes such as environmental or behavioral features (BONDURIANSKY 2012). In this view, the multiplication of mechanisms underpinning the like-begets-like phenomenon, if promising at first sight, might turn inheritance into a vague process responsible, all in all, for ill-defined patterns of extended similarities. It might finally lead to what could be identified as a 'holistic trap.'

I argue that the expansion of data regarding non-genetic mechanisms of inheritance first and foremost demands a conceptual reform capturing the patterns of extended similarities to be explained in pluralistic models, a step that may further allow outlining the shared properties of inherited factors related to those similarities, and maintained through various inheritance processes. After describing the holistic trap induced by pluralistic models, I sketch the first elements of a conceptual reconstruction based on the theory of organized systems developed, among other authors, by MOSSIO & MORENO

(2010, forthcoming). I suggest that the patterns of trans-generational similarities to be studied concern, rather than extended phenotypes, extended biological systems whose spatial limits and cohesion might be captured by the concept of organizational closure, namely the narrow integration of differentiated parts, acting as constraints in a given system and exhibiting interdependence for their own maintenance and that of the system the belong to. In this respect, heredity might be defined as the organization-begets-organization phenomenon. This approach allows an accurate characterization of the relevant inherited factors to be considered. Being responsible for characterized organizational similarities, those factors appear as persisting constraints, that harness flows of matter and energy across generations of such extended systems subject to closure. In other words, the organizational account of heredity allows the integration of an expanding knowledge into a coherent theoretical framework and leads to the emergence of a genuine biological category to be distinguished from that of stable developmental resources. Drawing new contours for extended heredity, such a conceptual clarification might furthermore be fruitful when integrating extended inheritance into various fields of investigation such as evolutionary biology. Indeed, in outlining the limits of reoccurring extended phenotypes, and in defining more precisely replicated items, it might shed a new light on evolutionary ontology (DAWKINS 1976; HULL 1980) and open the way to a renewed perspective on ‘replicators’ and ‘interactors.’

Evolutionary Novelty, a Concept Still in Search of a Definition

Thibault Racovski *(Exeter)*

The definition of the concept of evolutionary novelty poses several ontological and epistemological problems. A commonly accepted intuitive definition of novelty exists: an evolutionary novelty is a phenotypic trait bringing a qualitative difference, rather than a quantitative one, compared to traits already present in the lineage. This definition can serve as a starting point but is insufficient because of the several possible ways to interpret the notion of qualitative difference. Some authors have insisted on the need to produce a definition of novelty as theory-independent as possible (e.g. MÜLLER & WAGNER 1991), in particular neutral towards the mechanisms responsible of the origin of novelties. However most definitions have to rely on theoretical terms to cash out the quantitative/qualitative distinction, such as function (e.g., MAYR 1960; PIGLIUCCI 2008) or homology (e.g., MÜLLER & WAGNER 1991; MÜLLER 2010).

The distinction between the description of novelties and their explanation is often waved as a methodological principle, but its very possibility and its epistemic value is rarely overtly discussed. A good example is the influential definition of novelty as a "structure that is neither homologous to any structure in the ancestral species nor homonomous to any other structure of the same organism" (MÜLLER & WAGNER 1991). This definition is at odds with the dominant definition of homology in systematics according to which each trait can in principle be homologized (e.g. WILEY & LIEBERMAN 2011). To restrict the extension of the concept of homology, MÜLLER AND WAGNER rely on a "biological concept of homology" (WAGNER 1989) that is grounded in a theory of how trait develop and that, in consequence, is not neutral towards the mechanisms of the origin of novelty.

Even if a restrictive view of homology is adopted, the establishment of traits with no homolog faces epistemological problems with ontological consequences. The grain problem (CRACRAFT 1990) applies to the taxonomic level at which novelties are individuated. Many examples of novelty are defined at high taxonomic levels when only

the species level would be adequate. The asymmetry problem is related to the evidence on which claims of absence of homology are based. Evidence of the existence of intermediate forms falsifies a hypothesis of evolutionary novelty while the absence of evidence of intermediates does the not falsify a hypothesis of absence of novelty.

Another strategy is to define novelty or, more precisely, different types of novelty by the specific mechanisms responsible for their origin (e.g., MÜLLER 2010). Epigenetic mechanisms, phenotypic plasticity or the overcoming of strong developmental constraints are candidates. But because they can have clearly quantitative effects as well as apparently big qualitative effects, these mechanisms also prove insufficient. It is concluded that this absence of a satisfying definition does not threaten novelty as a general explanandum of life, but threatens evolutionary novelties as a real kind of evolutionary events.

De-ontologization of Individuality in Evolutionary Biology

Jörg Räwel *(Zürich)*

The history of biology can be interpreted as a progressive de-ontologization of its (established) knowledge. The paradigmatic ‘what?’-questions of ontology (what something is in a predetermined manner, what the being or essence of an entity is) have been, at least since DARWIN, replaced by ‘how?’-questions. The foreground is now dominated by the question as to how differences come into the world constructively, as distinct from that as to what something is in a pre-determined manner. Since DARWIN, biology has been based on the paradigm of functionalism.

In specific terms, this question found its expression in so-called population thinking, which in turn enabled the rejection of ontology or essentialism. “DARWIN showed that one simply could not understand evolution as long as one accepted essentialism. Species and populations are not types, they are not essentialistically defined classes, but rather are biopopulations composed of genetically unique individuals. This revolutionary insight required an equally revolutionary explanatory theory of evolution: Darwin's theory of variation and selection” (MAYR 2001).

I argue that, given the individual-based perspective, whether conceptually represented by, for example, genes, organisms, or groups subject to natural selection, a strong residue of essentialism is nonetheless traceable in biology. One of the consequences of the kind of essentialism evinced above may then well be the ‘units of selection’ problem.

I have recourse to the concept of ‘autopoietic systems’ (MATURANA & VARELA) in order to attempt to de-ontologize the concept of individuality in biology by radicalizing population thinking. For this purpose, the concept of autopoietic systems, originally related to the constitutive dynamics of cells, will be related to the evolutionary dynamics of populations or species. Accordingly, populations and species are understood simultaneously as product and the producer (of themselves), “organized (defined as a unity) as a network of processes of production (transformation and destruction) of

components which: (1) through their interactions and transformations continuously regenerate and realize the network of processes (relations) that produced them; and (2) constitute it [the system, J.R.] as a concrete unity in space in which they (the components) exist by specifying the topological domain of its realization as such a network“ (MATURANA & VARELA 1980).

Populations and species understood as autopoietic systems thus constitute the performative unit of evolution. Variations of the particular genome of each organism, through mutation, genetic recombination (as with sexual reproduction), as well as epigenesis, concern reproduction as elementary operation within autopoietic perpetuation. Survival permitting reproduction, or respectively where the premature demise of organisms renders reproduction impossible, is a matter of the structures of a species or of a population, where these are seen an autopoietic unit.

Consequently, I do not propose to consider individuals as units that are no longer deconstructable, and are selected as ontic entities in the course of evolution through natural selection. Instead, I understand them as operative moments (survival/demise) within the evolutionary dynamics of populations or species as autopoietic systems. The survival of organisms as entities capable of reproduction then manifests as positive selection, and the premature demise of organisms, rendering reproduction impossible, as negative selection. Thus, there are no objects for selection. Rather more, the question as to the units of selection appears as an atavism generated by a perspective, which, at least rudimentarily, cleaves firmly to essentialism.

The Hybridization Between Data-driven and Hypothesis-driven Research: A Proposal Based on the Debate About the Relation Between Discovery and Justification

Emanuele Ratti *(Milano)*

In the debate on the nature of data-driven research, a proposal has recently emerged. The proposal states that there is not a dichotomy between data-driven (DD) and hypothesis-driven (HD) research. In fact, DD and HD are 'hybridized,' 'integrated'; they are complementary rather than competitive. Let us call this proposal the hybridization thesis. I illustrate, through the case study of genome-wide association (GWA) studies, the inferential path from data to hypotheses. However this example (like many others) shows merely how DD juxtaposes with HD but it does not say what is exactly the relation between DD and HD. Here I propose to see the hybridization thesis in the light of the old debate on the relationship between the 'logic' of discovery (in the sense of a methodology to generate hypotheses, like DD) and the 'logic' of justification (in the sense of a methodology to test the hypotheses proposed by the methodology of discovery, like HD). In the debate, there were two positions on how the relation should be conceived. First, discovery is merely logically contingent to justification, but it promotes efficiency. Whatever the methodologies employed in the discovery phase, these are used merely in order to help to accelerate the phase in which hypotheses will be tested. For example, in GWA studies there is a methodology of discovery aimed at reducing the number of hypotheses (the number of single nucleotide polymorphisms, SNPs) to be tested in the post-GWA study phase. This methodology is highly efficient: it reduces the number of SNPs from millions to few dozens. Although the methodology of discovery of GWA studies promotes a sort of 'economy of research,' the same few dozens SNPs might be found, logically, with any other method. Hence, there is nothing special in the logic of discovery actually employed by GWA studies. The second position is that methodologies of discovery have a special epistemic weight. One thing is to say that what happens in a particular discovery context merely promotes efficiency

in the justification context. Another thing is to say that what happens in the discovery context carries probative weight per se in the context of justification (this is called the 'per se thesis'). If the per se thesis is right, then some moves made in the context of discovery are more than simply logically contingent to justification. DD research, in a context of data deluge, clearly promotes the efficiency of HD. However, in this talk I will endorse the thesis that DD carries a special epistemic weight with respect to HD, because it does not merely say which hypotheses should be prioritize in the HD phase (i.e., fostering efficiency), but also it gives clues on how hypotheses should be treated experimentally. I will illustrate this thesis by showing how the discovery phase of GWA studies influences the post-GWA phase.

Selection or Sorting: The Conceptual Obscurity of Species Selection

Eric Rogers *(Cincinnati)*

One ongoing debate over the ontological status of natural selection and random drift is divided into two camps. Some have argued that selection and drift are best understood as mere statistical descriptions of variation and change of within-population fitness. Others have argued for a more traditional dynamical understanding of selection and drift as causal forces responsible for this change. By and large this debate has centered on selection at the organismal level, yet there are similar tensions in the scientific literature within the context of hierarchical selection theories. In particular, one long-standing conflation between species selection and species sorting has resulted in confusion over whether selection at the species level should be understood descriptively or dynamically.

I will argue that a descriptive understanding that equates species selection with sorting fundamentally obscures further species-level concepts, especially species drift and effect macroevolution. In the descriptive mode, selection, drift, and effect macroevolution are viewed as kinds of effects or patterns. As patterns, they lack sharp conceptual distinctions; it is rarely if ever possible to determine a priori what kinds of patterns constitute selection versus drift, for example. Moreover, as some have pointed out, the probabilistic character of statistical description means it is likely impossible to make this distinction even in principle. If so, on the descriptive interpretation, species selection and species drift, like selection and drift more broadly, are conceptually indistinct.

Instead, I argue, only a dynamical understanding of selection as a causal process can provide the necessary clarity. This approach neatly delimits selection from sorting, and serves also as a basis for defining species drift and effect macroevolution. A dynamical understanding is therefore required to make holistic sense of species selection theory. While empirical problems remain, this approach has a threefold advantage. First, it is in line with the traditional understanding of selection as a kind of physical mechanism that

effects directed change within a population. Second, it grants selection the desired explanatory power (for in the descriptive mode, selection is itself in need of explanation). Lastly, reasoning from a dynamical understanding allows us to make predictions about the kinds of statistical effects we would expect to see, thus motivating the descriptive function of biostatistical analysis.

Applied to hierarchical selection theories, the dynamical understanding has one major flaw. If processes at a higher level can be constituted by processes at a lower level, there may be no distinction between species-level selection and selection processes at the organismal level. If so, species selection may be at best a redundant concept. At worst, any given pattern of species-level sorting may be alternatively attributable to a causal locus at either the organismal or the species level. In either case, the major advantage of the dynamical understanding–its conceptual clarity–is neutralized. I will show how the answer to this question turns at least partly on the ontological relation of individuals to species, and will conclude by exploring some possible solutions. If the dynamical understanding doesn't provide the desired clarity, it may be the case that a descriptive understanding is preferred on practical grounds.

‘Synthetic Protocell Philosophy’: Fabricating New ontological Constructs, *in vitro* and *in silico*, to Establish More Solid Epistemological Bases for Biology

Kepa Ruiz-Mirazo *(Donostia / San Sebastián)*

Philosophy is not dying out, as some scientists are inclined to state. In the next years it will become increasingly evident that science needs philosophy to properly fulfill its promise and the expectations it has created of producing truly transdisciplinary knowledge: a type of knowledge that is bound to provide an unprecedented potential for social transformation. However, this challenging task requires scientifically well-trained philosophers and philosophically well-trained scientists working together in the process of generation of that knowledge. It is not just a question of analyzing the implications of scientific progress, once this is made, but of designing and developing research avenues that apply diverse approaches to a specific problem of high scientific and philosophical relevance.

Within that general context, my talk will focus on the interesting pathways that ‘synthetic biology’ and ‘systems chemistry’ are opening in recent years in order to tackle the problem of origin of life. These involve the production of new types of systems, in-between the inert and the living, and in-between the artificial and the natural, through the combination of various methodologies of work, both *in vitro* and *in silico*. More precisely, I will argue that those two emergent research fields, by means of fabricating novel empirical constructs — proto-cellular constructs in particular, though not exclusively — are bound to provide fundamental insights about the organizational principles underlying biological systems. I will further argue that their potential to achieve such an ambitious goal would be notably increased if philosophical work is integrated in their actual development. Conceptual reflection — analytic and synthetic — is not only required to distill the epistemological consequences of a set of scientific results; or to establish connections across disciplines, relating apparently different lines of investigation; conceptual reflection, in addition to that, should be regarded as a useful

activity *within* science; as a complementary tool to drive research, to detect blind spots, put forward new ideas and try to contrast them, through the implementation of concrete experiments or computer simulations. Along these lines, I will try to demonstrate that the merging of philosophy with science (with chemistry and biology, in our case) is fruitful, giving added value to scientific results and biasing the generation of ontological constructs towards the satisfaction of more global and transdisciplinary epistemic needs.

Ruiz-Mirazo K, Briones C & de la Escosura A (2014) Prebiotic systems chemistry: New perspectives for the origins of life. *Chem Rev* **114**:285-366

Ruiz-Mirazo, K. & Moreno, A. (2013): Synthetic biology: Challenging life in order to grasp, use or extend it. *Biol Theory* **8**:376-382

Ruiz-Mirazo, K. & Moreno, A. (2012): Autonomy in evolution: From minimal to complex life. *Synthese* **185**:21-52

Ontologies of Protein-Ligand Binding Complexes

Isabella Sarto-Jackson *(Klosterneuburg)*

A key concern in molecular biology is the study of macromolecules and macro-molecular mechanisms in living beings. To understand such mechanisms, research focuses on the characterization of the components involved, e.g., the investigation of protein-protein or protein-ligand interactions, in order to understand protein function and to utilize this knowledge in medicine and pharmaceutics.

In the classical view, complex formations between proteins and ligands were described by the *lock and key* model. This model assumes a well-defined geometrical structure of binding partners that allows for interaction of complementary interfaces, but neglects any putative conformational changes. Due to increasing experimental evidence this view was rejected, and KOSHLAND (1958) suggested the *induced fit* mechanism to take the imperfect complementarity of the binding partners' interfaces into account. This model emphasized a change in the structure of one or more partners upon binding. A few years later a third model, termed *conformational selection*, was put forward by MONOD, WYMAN, & CHANGEUX (1965). It assumed that one or both of the interaction partners exist in multiple low-energy conformations in the unbound state. The balance of the population in these conformations is defined by the Gibbs free energy differences between these states, and can be shifted upon binding of the interaction partners.

Currently, the primacy of one of the two latter mechanisms over the other remains unclear. This is largely due to an apparent lack of methods that would allow the experimental discrimination between them (GIRALDO 2004). Nonetheless, it is import to be aware which mechanism is theoretically assigned to a given class of macromolecules since many other assumptions derive from it. The *conformational selection* model has undoubtedly gained an enormous importance for pharmaceutical drug design over the last decades. This model suggests that a (more or less) large, but distinct conformational heterogeneity of proteins already exists spontaneously in the absence of regulatory ligands (i.e., the existence of different 'kinds' of proteins). A ligand

then selects a protein with a complementary interface, stabilizes a certain conformational state of the interaction partner, and conveys appropriate signal transduction in the cell. Such structural ontologies are the rationale for the development of lead compounds that have potential to interact and stabilize a protein state of desired biological activity. This underlying concept also sets the preconditions for structure-based bioinformatics approaches such as homology/comparative modeling, *in silico* ligand docking, or the generation of pharmacophore models.

In contrast, the *induced fit* model assumes that a class of proteins exhibits an initial, single, stable conformation under given experimental conditions. Only upon binding, a ligand induces the interaction partner to adopt its adequate conformation. In this view, conformational differences are causally related to ligand binding and emphasis is put on the process rather than structure. Such an underlying concept challenges data-intensive methods focusing exclusively on protein structure and classical bioinformatics approaches, because of their presumably limited predictive power on the biological activity.

I will discuss these models and their subsequent implications for wet-lab methodologies, rational drug design, and bio-ontologies.

Koshland DE (1958) Application of a theory of enzyme specificity to protein synthesis. *Proc Natl Acad Sci USA* **44**:98-104

Monod J, Wyman J, Changeux J-P (1965) On the nature of allosteric transitions: A plausible model. *J Mol Biol* **12**:88-118

Promotion vs. Causation: A Metaphysical Distinction?

Guillaume Schlaepfer *(Genève)*

In a recent paper focused on aprioricity of causal models in evolutionary biology, E. SOBER (2011) raises the question of the difference between two types of causal statements: causation and promotion. While he doesn't make any positive claim about a metaphysical difference between the two kinds of statements, he describes various epistemic differences.

A first difference is the fact that 'A promoted B' only entails the occurrence of A while 'A caused B' entails both the occurrence of A and B. Furthermore, promotion doesn't entail causation, since promotion can occur without causation. Conversely, causation doesn't entail promotion either, for promoting an event raises its probability while it isn't necessarily so with causation. Observations can be used in a Bayesian way to move from 'would promote' statements to 'actually promoted' and to 'actually caused' statements.

While SOBER doesn't adopt any metaphysical stance, the issue recalls the debate in the framework of probabilistic causation, where SOBER (1984), along with others, advocated the need for two concepts of causation. This debate relies on cases, referred to by SOBER, in which an event seems to lower the probability of another event, but actually causes it in the end. It is claimed that probabilistic causation does a good job at the level of types, but fails in defining causation at the level of tokens.

This proposal has been tackled by HITCHCOCK (1995), who convincingly argues that causation is contrastive in nature, and that the cases at stake are ambiguous in that regard. For example, a bad swing in golf might increase the probability of hole-in-one in comparison to no swing at all, while lowering it in comparison to a perfect swing.

It seems to me that while HITCHCOCK brings important clarifications, he doesn't solve the problem. If you consider only the cause to find out the effect in a probabilistic framework, things might always occur in an unexpected way. The mistake in SOBER'S

examples is to take a God's eye perspective to say what actually happened. This cannot be done in a framework of probabilistic causality. It takes further observations and Bayesian assumptions to find out afterwards what actually happened. Hence, both causal claims are probabilistic in nature. The difference is only the epistemic perspective. My claim is that in a probabilistic framework of causation, the difference of epistemic perspective is sufficient to explain the difference between promotion and actual causation. Mostly, the first is stated prior to the causal event while the second is posterior, but all this remains pure probabilistic causation.

Hitchcock C (1995) The mishap at Reichenbach Fall: Singular vs. general causation. *Philos Stud* **78**:257–291

Sober E (1984) Two concepts of cause. *PSA 1984* **2**:405-424

Sober E (2011) A priori causal models of natural selection. *Australasian J Philos* **89**:571–589

Neuro-predisposedness? On the Concept of 'Neurobiological Predispositions' in the Light of the Embodied Dynamicism Perspective

Ewelina Sokołowska *(Uppsala)*

The embodied-embedded approach to cognition seems to have made a strong case against the seemingly undead issue of neuroreductionism, i.e., the belief that mental states are nothing more than states of the nervous system, that mental states *are* brain states. According to the proponents of the embodied-embedded approach, it is a mistake to locate the mind in the brain, as processes crucial to cognition cut across the brain-body-world division and are impossible to disentangle from each other.

Yet, even if accepting that the mind cannot be reduced to the brain, there are still many who argue that certain brain structures can be said to predispose people to certain behaviors. In this spirit, many of our differences in behavior are to be accounted for by our biological differences in the brain. And so, differences in the structure and functioning of the brain are accordingly being reported to exist between men and women (and their respectively different learning abilities as well as their capacity to empathize with others), between violent and non-violent people, between conservatives and liberals, to name just a few examples.

The question I will address is thus the following: How are the statements that we are 'biologically predisposed' to certain traits and behaviors, because of the specific structure and functioning of our brains, to be interpreted? For, even though the term 'predisposition' has started to be used in an inflationary way in research connecting biology (especially our genes and brains) to our psychology and behavior (often to escape the bad fame of biological determinism, as the term 'predispositions' sounds naturally more probabilistic), the concept itself seems to have seldom been pondered upon. I want to try to rectify this deficiency and explore the issue of neurobiological-behavioral 'predispositions' explicitly in the context of embodied dynamicism.

Ontological Issues in Paleobiological Data: What is the Fossil Record?

Marco Tamborini *(Heidelberg)*

My talk intends to historicize the practices of paleobiology in order to point out the turning points in the constitution of paleobiological data. Paleobiology is a new approach to the fossil record born during the 1970s. It aims to (1) making paleontology more theoretical and less descriptive; (2) introducing models and quantitative analysis into paleontological methodology; (3) importing ideas and techniques from other disciplines (especially biology) into paleontology; (4) emphasizing the evolutionary implications of the fossil record (SEPKOSKI 2012). This discipline is characterized by the use of a great deal of data, databases, and computer simulations. However, paleontologists have been struggling with a problem since the birth of their discipline: how the imperfections of the fossil record do affect our ability to study the past life (FOOTE & MILLER 2007). Hence, the quality, not the quantity, of the data seems to characterize paleontological investigations. This ontological issue is still pivotal nowadays.

By the means of a historical epistemology, I will address a simple question: what is the fossil record? This question is important not only for the paleontological investigations, but also for all the data-driven disciplines. In fact, the fossil record has the peculiarity to be a historical datum and the comprehension of this particularity is fundamental in order to understand the common structures and the differences among all the data-driven disciplines. To answer this question, I will briefly analyze and compare German paleontology between the mid-19th and the early 20th centuries with the conceptualization of the fossil record between the 1940s and 1970s. As a result, I will be able to provide some insights into the nature and the limits of paleobiological data.

Emergent Properties in an EvoDevo Biological Context

Vanessa Triviño *(Murcia)*

There is an important debate in philosophy of biology with respect to the possibility or not of reducing the different branches of biology (evolutionary, systematic, developmental, ecology...) to molecular biology. This reductionist approach in biology has its origins in the first half of the 20th century, when molecular biology started to develop and it was considered that the so-called 'classical genetics' (associated to Mendel and others) could be reduced to it. This approach reaches its maximum height with the discovery of the molecular structure of the DNA by WATSON & CRICK (1953a,b). This discovery allowed some authors such as SCHAFFNER (1969) to consider that, in fact, not just the phenotypic properties studied by 'classical genetics' can be reduced to molecular biology but all the behaviors and different processes that take part in an organism can, since, as WATSON & CRICK have highlighted, the organism is made of chemical components. Due to these considerations, other philosophers such as WIMSATT (1976, 1980), SARKAR (1998), and KELLER (2010) have defended the possibility of reductionism. KELLER, for example, considers that recent development in the field of cybernetics and Bernard Machines could allow us to achieve the reduction of the high-level to the lower one. The consideration of being able to reduce all the aspects and behaviors of the organism to the lower level is behind of the idea that all the branches of biology can be reduced to molecular biology. But there are other authors that have rejected this possibility: FODOR (1974), KITCHER (1984), or DUPRÉ (2012) among others. DUPRÉ, for example, has pointed to the difficulties that polygeny and pleiotropy raise for the reductionist approach.

In this work I intend to explore the issue of the possibility of reductionism beyond the field of molecular biology itself. In order to do so, I will consider some proper-ties studied by evolutionary developmental biologists, in particular, I will focus on the property of fitness — not by attending to the role it plays in evolution but as an organism's property (or capacity) itself. I have a twofold aim. On the one hand, I will try to see whether this property can be reduced to chemical and/or physical properties of

either the environment or the organism or both, or it resists such a reduction. On the other hand, I will explore whether some of the anti-reductionist arguments that have been developed in the context of molecular biology could be extended to developmental biology.

Dupré J (2012) Processes of Life: *Essays in the Philosophy of Biology*. Oxford U. P.

Fodor JA (1974) Special sciences. *Synthese* **28**:77-115

Keller EF (2010) It is possible to reduce biological explanations to explanations in chemistry and/or physics. In: *Contemporary Debates in Philosophy of Biology*. Wiley-Blackwell

Kitcher P (1984) 1953 and all that: A tale of two sciences. *Philos Rev* **93**:335-373

Schaffner KF (1967) Approaches to reduction. *Philos Sci* **34**:137-147

Schaffner KF (1969) The Watson-Crick model and reductionism. *Brit J Philos Sci* **20**:325-348

Watson JD, Crick FHC (1953a) Molecular structure of nucleic acids: A structure for deoxyribose nucleic acid. *Nature* **171**:737-738

Watson JD, Crick FHC (1953b) Genetical implications of the structure of deoxyribose nucleic acid. *Nature* **171**:964-967

Individuals, Cells, and the Special Composition Question

Marcel Weber *(Genève)*

Philosophers seeking to understand biological individuality have for the most part sought a general, modally robust criterion that an entity must satisfy in order to qualify as a biological individual or organism. For example, several authors have recently analyzed individuals in terms of natural selection theory, arguing that some abstract theoretical principle such as the Price equation provides some kind of a structuralist criterion for biological individuality (e.g., CLARKE 2012, FRENCH 2012).

I will show that such a criterion only works if some other criterion of biological individual or living thing is already presupposed. Thus, these accounts at best give us an answer to what VAN INWAGEN (1983) calls the 'special composition question' or SCQ (what conditions must obtain for some x to compose something?). VAN INWAGEN's own answer to this question is notoriously vague (the x compose something if and only if the activities of the x constitute a life). In any case, the SCQ presupposes obviously that we can already individuate the components. This in itself is not an objection against an account of biological individuality, but it does put pressure on an account of biological individuality to say more about the composing units. An obvious choice for the latter is the living cell.

Thus, the problem of biological individuality is perhaps best construed as the question: under which conditions does a collection of cells compose a multi-cellular individual? (The question of how to individuate cells will not be considered here). I will not defend any monistic answer to this question. Instead, I will argue that the exact conditions for composition depend on the context of inquiry. In particular, the composition conditions may or may not include a criterion for monoclonality. There is, however, an important composition criterion that plays a role in may different disciplinary contexts: the condition of functional integration. I shall conclude with some remarks about the metaphysical implications of this view. One of the most interesting implications, perhaps, concerns the modal robustness of the concept of organism: Our concept of the

organism is *modally local*, that is, it is only applicable in a set of possible worlds that are not too far from actuality.

Clarke E (2012) Plant individuality: A solution to the demographer's dilemma. *Biol Philos* **27**:321-361

French S (2012) The resilience of laws and the ephemerality of objects: Can a form of structuralism be extended to biology? In: Dieks D, et al. (eds) *Probabilities, Laws, and Structures.* Springer

Van Inwagen P (1983). *An Essay on Free Will*. Oxford U. P.

On the Ontology of Biological Space

Russell Winslow *(Santa Fe)*

At the beginning of his 1951 essay *Experimentation in Animal Biology*, GEORGES CANGUILHEM offers an example of an experimental fact in order to distinguish biological 'facts' from biological 'meaning.'

> In a lesson on muscular contraction, contraction is defined as a modification of the form of the muscle without variation in volume; when necessary this is established by experimentation, following a technique whose illustration is reproduced in every schoolbook: an isolated muscle, placed in a jar filled with water, contracts under electrical excitation, but the water level stays the same. One is happy to have established a fact. Yet it is an epistemological fact that an experimental fact thus taught has no biological meaning. (p. 4)

For CANGUILHEM, the unique and original biological object of investigation does not come into view in these sentences that describe the isolation of organic material touched and compelled into contraction by a bolt of electricity. Here, a severed muscle floating in water could be compared to almost any object of investigation, whether living or non-living. That is to say, for him, there is no biological meaning evident in the experiment. On the following page, CANGUILHEM indicates what is missing from this experimental fact that would help to situate it into a structure of meaning.

> It is here a matter of nothing less than what might be called... "the life of relation": the problems of posture and locomotion posed by the animal organism's daily life, whether peaceful or dangerous, whether confident or menaced, whether in its usual environment or in a perturbed one. (p. 5)

For CANGUILHEM, "the life of relation" characterizes the ontological situation of every living thing. In biological investigation, one must perform experimentation, to be sure, but it is perhaps a mistake to call these facts — which are severed from "the life of relation" of the organism to which they belong — knowledge.

Biological meaning is derived from the lived situation and this illuminates the experimental facts within a certain totalizing frame, not the other way around.

There are, of course, many objects of biological knowledge that would be affected by the elucidation of the narratives of "the life of relation." Perhaps the most obvious object from the given experiment would be the biological self- motion of animals (a theme CANGUILHEM develops in the essay). However, I am particularly interested in the consequences for an understanding of biological space. After all, if a fundamental characteristic of the being of biological entities lies in their "life of relations," then the ontological situation of the space of the laboratory in the above examples is so abstract as to be devoid of biological meaning. In the artificial and indifferent space described above, there exists no possibility for peace or danger, for confidence or menace; indeed there is no environment there. Does the being of biological space differ from this laboratory milieu? Or does it possess the same ontological meaning?

One might feel compelled to cite the date of this publication and to ask the question: have we not progressed beyond these concerns in the biological sciences? Are these conceptual problems outdated in the philosophy of biology? I do not think so. In fact, there may be need to revive these questions in light of the milieux of microorganisms. I propose the following topic for the seminar: does the tradition of microbiological cultures and the systems of knowledge that it organizes rest on a metaphysical presupposition with respect to the meaning of the being of biological space? A meaning of being not unlike that account of the milieu described above. It seems to me that there are enormous consequences for rethinking the meaning of the being of biological spaces when we consider the following.

A) *Contemporary trees of life:* The mode of being necessarily extrapolated from our perceptual experience of the living beings around us (fungi, animals, plants) are but a tiny fraction of the forms of being, the modes of being, that exist and that are not perceptually experienced by us (PACE 2005). Would an examination of these other "lives of relation" reconfigure our understanding of the being of biological spaces?

B) *Cultured spaces:* A majority of microbiological species cannot be cultivated (EPSTEIN 2009). Is it because we've not located the appropriate technological tools for them to grow as individuals? Or might their modes of being not be compatible with the cultured milieu, itself enframed by a conceptual scheme? Does our ontology of space impose a

conception of the organization of space by biological organisms that remains foreign to the majority of forms of life on Earth?

C) *Metagenomics and single-cell genomics:* Insofar as metagenomics focuses on the extraction of genes from a milieu (RINKE et al. 2013), are there unquestioned metaphysical presuppositions subtending the concept of milieu supporting the knowledge composed by such genetic facts.

Epstein SS (ed) (2009) *Uncultivated Microorganisms*. Springer

Pace N (2005) The large-scale structure of the tree of life. In: Sapp J (ed) *Microbial Phylogeny and Evolution*. Oxford U. P.

Rinke C, Schwientek P, Sczyrba A, et al. (2013) Insight into the phylogeny and coding potential of microbial dark matter. *Nature* **499**:431-437

Rethinking 'Population Thinking'

Joeri Witteveen *(Utrecht)*

If ERNST MAYR (1904-2005) is to be believed, 'population thinking' marks an important breakthrough in metaphysics. MAYR characterized population thinking as a way of approaching biological phenomena that recognizes them for their biological ontology, as opposed to their physical, chemical, or, more generally, 'typological' constitution.

There are good reasons not to believe MAYR. A close examination of the genesis of MAYR's population/typology dichotomy shows that it is conflation — a mixture of cross-cutting methodological, conceptual, and theoretical distinctions that MAYR 'compacted' into a meaningless construct (WITTEVEEN, in progress).

And yet, MAYR's confusing use of 'population thinking' does not automatically force us to purge the term from our vocabulary. Population thinking continues to be invoked in a number of scientific contexts, as a way of drawing out meaningful contrasts with other ways of approaching particular domains of study. I therefore suggest that, rather than being a term to be dispensed with, population thinking is a term whose confounded meanings need to be pulled apart.

Following GODFREY-SMITH's (2001) 'classification and clarification' of different notions of adaptationism, I will propose a distinction between different kinds of population thinking. I will show that a considerable amount of debate concerning the meaning, significance, and adequacy of population thinking results from hidden category mistakes. A classification of kinds of population thinking can therefore be used to distinguish real disputes from semantic confusion.

After offering a basic classification, I will briefly discuss three domains that can benefit from it. First, I will review a historical debate about the origins of population thinking. I will show that SOBER (1980), ARIEW (2008), and LEWENS (2009) unwittingly rely on different notions of population thinking when disputing one another's claims about the origins of this mode of thinking. Next, I will turn to a debate in cultural evolutionary

theory, in which scientists from different traditions claim to be population thinkers on what turn out to be rather different grounds, rooted in different kinds of population thinking (RICHERSON & BOYD 2005; CLAIDIÈRE ET AL. in press). Finally, I will show that my classification can clarify where the real tension between neo-Darwinists and 'evo-devotees' lies (AMUNDSON 2005).

Amundson R (2005) *The Changing Role of the Embryo in Evolutionary Thought: Roots of Evo–Devo*. Cambridge U. P.

Ariew A (2008) Population thinking. In: Hull DL, Ruse M (eds) *Oxford Companion to Philosophy of Biology*. Oxford U. P.

Claidière N, Scott-Phillips T, Sperber D (in press) How Darwinian is cultural evolution? *Phil Trans R Soc Lond B*

Godfrey-Smith P (2001) Three kinds of adaptationism. In: Orzack SH, Sober E (eds) *Adaptationism and Optimality.* Cambridge U. P.

Lewens T (2009) Evo-devo and "typological thinking": an exculpation. *J Exp Zool B: Mol Dev Evol* **312**:789-796.

Richerson PJ, Boyd R (2005) *Not by Genes Alone: How Culture Transformed Human Evolution*. U. of Chicago P.

Sober E (1980) Evolution, population thinking, and essentialism. *Philos Sci* **27**:350–383

Witteveen J (in progress). 'Temporary oversimplication': Mayr, Simpson, Dobzhansky and the origins of the population/typology dichotomy

Notes

Acknowledgments

The Third European Advanced Seminar in the Philosophy of the Life Sciences was supported by:

Warm thanks to Eva Lackner and Isabella Sarto-Jackson for their marvelous administrative assistance.

Cover motif by: Peter Kogler
Photographed by: Stefan Sarto
Graphic design by: Isabella Sarto-Jackson