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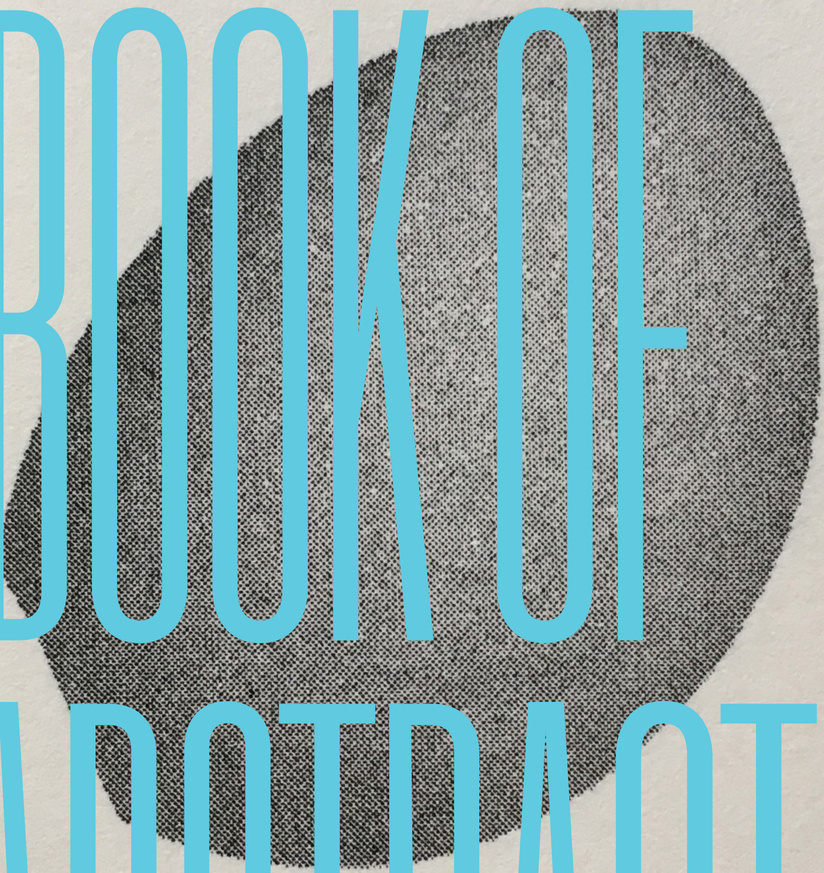

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Keynote lectures

8 JULY
MONDAY

Lessons learned from waterfleas, whales and bees: A journey into environmental controversies in the search for sustainable food

Fern Wickson, NAMMCO and GenØK, Norway

Ecology seeks to understand how organisms interact with their environment. It is a biological science that looks at how things are interconnected, how they interrelate. I am an ecologist interested in how we, the human species, interact with our environment. My work is transdisciplinary; researching the human/nature relationship through overlapping lens of biological science, ecological ethics and environmental politics. In this talk I will present some of the lessons I have learned about how ethics and politics are entangled in the science of environmental harm. These are lessons I have learned from working with waterfleas, whales and bees.

How we feed ourselves, as a species, is one of the foundational ways we construct and conduct our interaction with nature/the environment/our ecological community. It is a key mode of entry into our relationship with the rest of life on Earth. Today there is increasing recognition that modern industrial food systems have created extensive environmental damage and there is an urgent quest to find sustainable solutions. In this quest though, certain technologies and practices generate intense socio-political controversy over their role in a sustainable future.

This presentation will explore two such sustainable food controversies: genetically modified organisms (GMOs) in agriculture and the hunting of whales and seals in the North Atlantic. Through my ongoing engagement with these issues, I will demonstrate how the question of what constitutes environmental harm is a splendid swirling nexus of science, ethics and politics. And that in this complexity, there is much we can learn from being attentive to waterfleas, whales and bees. Indeed, to all the other species we share this extraordinary planet with.

Fern Wickson is an Australian citizen who has been living in Norway for over a decade. She is a Research Professor of Environmental Governance and holds an interdisciplinary PhD across biology and political science. Her work has focused on the science/policy interface and specifically, the integration of science, indigenous knowledge, stakeholder views and environmental philosophy in the pursuit of sustainable food systems.

DR. FERN WICKSON is the Scientific Secretary of the North Atlantic Marine Mammal Commission (NAMMCO) and a Senior Advisor at GenØk Centre for Biosafety in Tromsø, Norway. Committed to ecological ethics and a politics of socio-ecological care, the primary objective of her work has been to advance sustainability in food systems and responsibility in research and innovation arenas.

Fern has served as an expert delegate to the Intergovernmental Panel on Biodiversity and Ecosystem Services (IPBES) working group on the diverse conceptualization of values in nature. She has also been a member of the Norwegian Biotechnology Advisory Board and past President of the international Society for the Study of New and Emerging Technologies (S.Net).

In her spare time, Fern enjoys hiking, snowboarding, kayaking and trying to grow her own food. She is also a yoga and meditation teacher and runs her own studio in Tromsø called The Peaceful Wild.

9 JULY
TUESDAY

Epistemic landscapes for the century of life

Gísli Pálsson, University of Iceland, Iceland

The last century has been variously named the century of genetics, biology, and the gene. The 21st Century, in contrast, seems primarily associated with life and the environment. Such a shift, I argue, has at least two kinds of momentum. On the one hand, it continues from recent concepts of "local biologies", "body worlds", and "biosocial relations", conflating genomes, organisms, and context, erasing the boundaries between inside and outside the organism. On the other hand, it recognizes an emergent momentum in the history of life, characterized by the alarming threat of mass extinction as a result of human activities, witnessed by a recent UN report. Probing the advent and implications of the 'environment' is at the core of the growing field of "epigenetics", identified by Conrad Waddington in the 1940s. Applying Waddington's visualization of epigenetic landscape to epistemic shifts in the century of life – partly turning Waddington on Waddington – I suggest one may interrogate the development of the notions of "epigenome" for the purpose of understanding and respecting "life itself" in the current century of life.

GÍSLI PÁLSSON is Professor of Anthropology at the University of Iceland. He has written extensively on a variety of issues, including human-environmental relations, slavery, biomedicine, and genomics. He has done fieldwork in Iceland, the Republic of Cape Verde, the Canadian Arctic, and the Virgin Islands. He is the author, editor, or co-editor of many books, including *Anthropology and the New Genetics* (2007), *Biosocial Becomings: Integrating Social and Biological Anthropology*, co-edited with Tim Ingold (2013), *Nature, Culture, and Society: Anthropological Perspectives on Life* (2016), *Can Science Solve the Nature/Nurture Debate?*, with Margaret Lock (2016), and *The Man Who Stole Himself* (2016).

Pálsson has a keen interest in photography and human/other-than-human relations. Recently he has embarked on a new project that combines scholarship and the arts, science and history: the fate of the Great Auk (*Penguinus impennis*), which became extinct by the mid-19th century.

Diverse format sessions

Unculturable organisms in the big data era

ORGANIZER

Holly Andersen, Simon Fraser University, Canada

Many techniques for analyzing DNA require large numbers of cells for DNA extraction. However, many species, including protists like radiolaria, cannot be cultured in the lab; individual organisms cannot provide sufficient DNA to be analyzed with standard techniques. Krabberød and his co-authors faced the issue of how to sequence individual radiolarians that can only be collected in the field and kept alive for a certain period, and innovated a method of amplification of genetic material from a single cell using the transcriptome. This amplification of the genetic material for testing has revolutionary implications for understanding the place in the tree of life for organisms that cannot be cultured in a lab.

While single cell genetic amplification provides methodological access to a single organism, another method, often called Metagenomics, takes a very different approach. It basically involves sequencing all the genetic material in a sample containing hundreds or thousands of microbial species (e.g. water, soil or gut samples) without having examined it visually. Based on the genetic material, it is possible to infer which species are present, or which genetic pathways are present. For many environments, many of the microorganisms have a genetic composition that is unknown to us. These are often the unculturable organisms.

Technological innovations and improvements in the last ten years have made the sequencing of transcriptomes and genomes something that can be achieved in days instead of what was previously years. Right now these techniques are generating quantities of data that many biologists don’t know how to analyse. The same technological advances are used both to sequence DNA from single cells and from metagenomics. This is why bioinformatics has become an important and integral part of biology.

Krabberød, an engineer, researcher, and bioinformatician, will present his work on single cell amplification using the transcriptome, in particular on radiolarians. Creel will discuss how this connects with similar Big Data issues in other sciences, and situate the amplification of genetic material using the transcriptome into terms of comparable issues in computer science. Andersen will focus on the issue of unculturability, including its implications for our basic understanding of the characteristics of life on Earth, but also for exobiology.

The goal is a panel-style discussion to centre the methodological issues of genetic analysis of unculturable organisms, the implications of unculturability for our understanding of diversity of life on earth, and how such "small-batch science" fits into big data trends in biology.

PARTICIPANTS

Anders Kristian Krabberød, University of Oslo, Norway
Kathleen Creel, University of Pittsburgh, USA
Holly Andersen, Simon Fraser University, Canada

Reassessing the role of narratives in psychiatry

ORGANIZER

Nina Atanasova, The University of Toledo, USA

Narratives have traditionally played a significant role in psychiatry as diagnostic tools. Their uses, however, have been a subject of an ongoing discussion. Controversial questions include: In what sense, if any, are narratives crucial for distinguishing between normal, abnormal, adaptive, and maladaptive behaviors? Does reporting history of childhood abuse make a difference in identifying as adaptive behaviors which may otherwise be considered deviant?

Narratives in the form of self-reports by patients can help medical professionals to embed a symptom complex in a wider conceptual framework that goes beyond the prevalent evidence-based practice. Hence, such narratives can provide an interesting tool for grappling with the etiology and temporal progression of a disorder. For example, reports of auditory hallucinations are often an indication of pathology.

Whereas reporting the personal history of childhood abuse may help in identifying deviant behavioral patterns with a psychopathological abnormality.

It has been stressed that narratives could lead to normalizing of a behavior, which may be considered pathological on the face of it (Meehl 1973). Should such normalization be regarded as professional bias or is it instead a sign of deepened understanding of the individual that exhibits the seemingly deviant behavior (Gurova 2013)? In addition, narratives contribute to the dynamics of mental illness through self-reflection of patients. Correspondingly, they can exacerbate psychological trauma (Sarto-Jackson 2018) or enable the formation of coping strategies (Kirmayer and Crafa 2014).

On a larger scale, recognizing the social and cultural determinants of the very conceptualization of various psychiatric disorders also calls for reevaluation of the significance of narratives in psychiatry. Certain practices and behaviors may be considered deviant in some cultures all the while being part of the mainstream behaviors of other cultures. For example, daily alcohol consumption is frequent in many European cultures whereas it would be considered symptomatic in the US. Narratives function as tools for interpretation of the cultural significance of such behaviors. Conversely, when absorbed by popular discourse, psychiatric constructs may influence the reconceptualization of mainstream culture (Kirmayer and Crafa 2014).

The goal of the proposed symposium is to reassess the role of narratives in clinical practice by drawing attention to and exploring in detail certain underappreciated functions of narratives in the conceptualization, diagnostics, and treatment of mental disorders. The proposed analyses are expected to strengthen the case for adopting narratives as valuable tools of biopsychosocial approaches in psychiatry.

PARTICIPANTS

Nina Atanasova, The University of Toledo, USA
Lilia Gurova, New Bulgarian University, Bulgaria
Paola Hernández-Chávez, University of Pittsburgh, USA
Isabella Sarto-Jackson, Konrad Lorenz Institute for Evolution and Cognition Research, Austria

Animal consciousness

ORGANIZER
Jonathan Birch, London School of Economics and Political Science, UK

In recent years, an interdisciplinary community of animal consciousness researchers, drawn from neuroscience, evolutionary biology, comparative psychology, animal welfare science and philosophy, has begun to emerge (as indicated, for example, by the founding of the journal *Animal Sentience* in 2016). The aim of this field is to study the inner lives of animals – their subjective experiences and feelings – in a scientifically rigorous way, on the model of the scientific study of human consciousness. The field faces significant methodological hurdles, since non-human subjects cannot verbally report their experiences. However, animal sentience research is founded on the belief that by synthesizing the insights and methods of multiple disciplines, and by constructing clear behavioural, cognitive and neurological criteria for attributing sentience, these hurdles may be overcome.

At present, the field is characterized by heated controversy: foundational disagreement over the nature of sentience and the criteria for its attribution leads to intense debate over issues such as the presence or absence of sentience in fish (see, e.g. Key 2016, and the 45 commentaries on the article) and in invertebrates such as cephalopods and arthropods (Mather 2007; Klein and Barron 2016). Philosophers have an essential role to play in placing this emerging interdisciplinary field on secure philosophical foundations, enabling researchers to move beyond the impasses that result from unresolved foundational disagreement. What is needed is a conceptual framework for thinking about consciousness as an evolved phenomenon that varies along several dimensions and a deeper understanding of how these dimensions relate to measurable aspects of animal behaviour and the functional organization of the nervous system.

This double session will bring together leading experts in philosophy of biology, evolutionary biology, the neuroscience of consciousness and animal ethics to advance these debates. Its main aims are

1. to integrate philosophical debate on the nature of animal consciousness with the latest empirical research,
2. to evaluate the current state of evidence for animal sentience,
3. to consider possible accounts of the evolution of consciousness, and to assess the consequences of animal consciousness research for ethics.

The session will consist of short talks followed by a panel discussion.

PARTICIPANTS, PART 1
Eva Jablonka, Tel Aviv University, Israel
Zohar Bronfman, Tel Aviv University, Israel
Lars Chittka, Queen Mary, University of London, UK

PARTICIPANTS, PART 2
Adam Shriver, University of Oxford, UK
Catherine Wilson, CUNY Graduate Center, USA
David Rudrauf, University of Geneva, Switzerland

Roundtable: Philosophy of biology before and after "Biologie"

ORGANIZER
Cécilia Bognon-Küss, Université Paris 7 Diderot, France and IHPST (CNRS), France

Despite the appearance of more specialized scholarship over the past few decades, it is still standard to trace the usage of the term "biology" back to Treviranus and Lamarck around 1800. It is widely agreed among historians that biology as a science of the functioning and development of living bodies emerged in the beginning of the 19th century, integrating methodological or empirical advances in various disciplines, namely physiology, embryology, comparative anatomy and medicine. The fact that the word "biology" was simultaneously and independently coined by several authors from different national and disciplinary backgrounds (Hanov (1766), Bichat (1800), Lamarck (1809), Treviranus (1802–1822)) is commonly seen as testifying to this epistemic emergence (Duchesneau (1982), Barsanti (1994, 2000), McLaughlin (2002), Wolfe (2011, 2019)). Even though scientists were of course discussing living phenomena earlier, what is striking here is the constitution of a unified framework for investigating "vital" phenomena.

"Philosophy of biology" in turn is a fairly recent area of academic expertise. It developed from the post-positivist tradition of the philosophy of science in the 60s, has its specific journals (*Biology and Philosophy*, *Studies C*, *Biological Theory*, etc.), scientific societies (ISH-PSSB) and a core group of issues that mostly revolve around evolutionary biology and molecular biology and that are supposed to be relevant at the same time for metaphysics and theoretical biology: e.g. molecular reductionism, adaptationism, units of selection, genetic information. Biologists such as Ernst Mayr and Stephen Jay Gould were very influential in this growing subfield of philosophy. So conceived, philosophy of biology is quite exclusive of historical concerns, even though its "founding parents" (Michael Ruse, Marjorie Grene, David Hull) have devoted a significant amount of their work to the history of biology (see Gayon 2009 and passim, on this question of the gradual self-definition of philosophy of biology as a discipline).

We have recently edited a volume (Bognon-Küss and Wolfe eds. 2019) on the interplay between philosophy and natural science in the mid to late Enlightenment as a dynamic in the constitution of biology as a science in the early 1800s. What we term "Philosophy of biology before biology" is the combined historical and philosophical focus on this constitution, which also has implications for the constitution of the philosophy of biology in the 1960s (since this relies on a historical narrative about the science of biology). We believe this roundtable will produce a fresh but also systematic perspective on both the history of biology as a science and on the early versions of what came to be called the philosophy of biology. Additionally, due to its conceptual and metaphysical focus, it should build a bridge between more historical understandings of these materials, and contemporary philosophy of biology.

B. Demarest, C. Bognon-Küss, L. Nyhart, G. Toepfer, and C. Wolfe discuss the idea of "philosophy of biology before biology", while P. Honenberg and M. Chirimuuta focus on competing paradigms in the constitution of philosophy of biology and its Continental rivals.

PARTICIPANTS
Charles T. Wolfe, Ghent University, Belgium
Boris Demarest, Universität Heidelberg, Germany
Philippe Honenberger, University of Nevada, USA
Lynn Nyhart, University of Wisconsin, USA
Georg Toepfer, Leibniz-Zentrum für Literatur- und Kulturforschung, Germany

Individuation, process, and scientific practices

ORGANIZER
Ruey-Lin Chen, National Chung Cheng University, Taiwan

Individuation, Process, and Scientific Practices, edited by Otávio Bueno, Ruey-Lin Chen, and Melinda Bonnie Fagan, was published by Oxford University Press in October 2018. This book offers a new approach to the individuality problem, arguing that research on the problem can be advanced by examining processes of individuation in scientific practices. The volume consists of a long introductory chapter and twelve contributed chapters. These chapters examine the individuation of scientific entities, explore different aspects of individuation, highlight individuation in experimental practices, and extend the issue of individuation to wider contexts.

This book is motivated by a classic philosophical question: "What things count as individuals?" But rather than addressing it from a purely theoretical or analytical perspective, the volume proceeds to reformulate the question in terms of scientific practices. So reformulated, the new question is: "How do scientists individuate the things they investigate and thus count them as individuals?" Insights about criteria of individuation emerge from piecemeal investigations of different practices of individuation. Hence, these investigations focus on individuation in scientific practice, rather than on a fundamental theory or more abstract metaphysical speculations. In reformulating the classical question, the chapters in this book develop themes concerning experimental practice, biological processes, and pluralism. The results exhibit the strengths of a practice-based philosophy of science.

This session is designed to introduce and explore the central approach advanced by Individuation, Process, and Scientific Practices. The organizers, who are the editors of the book, have selected one of the editors and two authors to be panelists. The panel will introduce the new approach and illustrate how this approach can open new discussions about individuation in biology. Hence, the aim of this session is to introduce a new discussion about individuation (rather than rehearse the contents of the book).

PARTICIPANTS

Marie I. Kaiser, University of Bielefeld, Germany
C. Kenneth Waters, University of Calgary, Canada
Ruey-Lin Chen, National Chung Cheng University, Taiwan
Otavio Bueno, University of Miami, USA
Rose Trappes, University of Bielefeld, Germany

Representing protein dynamics

ORGANIZER

John Dupre, University of Exeter, UK

This session derives from an AHRC (Arts and Humanities Research Council, UK) funded project, Representing Biology as Process (http://www.probioart.uk), which, in turn, grew out of John Dupré's ERC-funded project, A Process Ontology for Contemporary Biology. The latter project developed the argument that Biological Systems of all kinds should be understood as processes rather than substances or things. This raised questions about the best ways of visually representing biological systems without occluding their dynamic nature.

Core members of the interdisciplinary team are Dupré, artist Gemma Anderson, and cell biologist James Wakefield, and the team will address problems of representation across a range of biological scales. Anderson has been collaborating with a diverse range of scientists for several years, and following pioneering work by artists such as Paul Klee, she has had a longstanding interest in representing transformation through two-dimensional images. The first, largely completed, target of the present project was mitosis, especially the spatial and energetic landscapes of spindle formation. Anderson and Wakefield collaborated in generating a series of entirely novel images of mitosis, and the team continues to work on exploring the meaning and utility of these images.

The current phase of the project addresses protein dynamics, beginning with a treatment of the energy landscape associated with protein folding. Here, Anderson is collaborating with protein biophysicist Jonathan Phillips. The conventional image for representing protein dynamics in biology is the "folding funnel", an irregular, roughly conical shape that corresponds to an energy landscape down which the nascent protein is imagined to transition as its structure achieves lower energy formations. While this image represents some features well, others are obscured. In particular, important aspects of the intrinsic behaviour of molecular species are absent, or poorly represented, such as stochastic change and parallel pathways. Thus, a gap exists in our ability to represent and interact with fundamental dynamic processes in a visual manner that is intuitive and instructive.

The proposed presentation at ISHPSSB, Oslo will describe the methods of interdisciplinary collaboration and the objectives of the project, and then present the images developed for protein folding and some discussion of their significance. As with the mitosis project, a number of novel modes of representation are being explored. We will present a series of new images that function as visual metaphors for the protein energy landscape. These draw on the structure of a maze, and we also experiment with the maze as a metaphor for processes beyond proteins, such as mitosis and speciation. Anderson, Phillips and Dupré will jointly present this work, providing philosophical, art-theoretic, and scientific, perspectives on the project and its results.

PARTICIPANTS
John Dupre, University of Exeter, UK
Gemma Anderson, University of Exeter, UK
Jonathan J. Phillips, University of Exeter, UK

Doing philosophy through performance

ORGANIZER
Sophia Efstathiou, Norwegian University of Science and Technology, Norway

History and philosophy of science has traditionally used the empirical methods of historians, and developed in close connection to particular scientific disciplines and their methods. With the growth of interdisciplinary work, different modes of philosophical research have become established as of added value in philosophy, including philosophy using empirical methods developed within the natural and social sciences, and experimental philosophy. This session explores influences from the arts: joining artistic research and philosophy and focusing on the performance arts, in the mode of performance philosophy, or performance HPS.

What is the method of philosophy?

Can applied theater and art be how we do philosophy?

This session investigates these questions by proposing to engage session participants in performance-based activities designed as philosophical think-modes. Before we describe these exercises we dub 'gameformances' let us say a bit about our motivation.

Philosophy, by which we mean analytic, Western philosophy, has been paradigmatically geared to investigate and cultivate logos: capacities for "clear" reasoning –logic – speech, argumentation. This does not mean that philosophers do not make use of other rhetorical and literary instruments in their work. One need only think of the analogies and thought-experiments that philosophers across the ages have developed to bring their points across. Audiences of philosophy have been urged to imagine that our senses deceive us (R. Descartes), or to imagine diverting a trolley hitting people tied on the rails (P. Foot), or having a famous violinist attached to our kidney system for nine months without our consent (J. J. Thompson). Imagination, moral imagination and feeling are crucial parts of philosophical reflection.

What we explore in this session is the possibility to create situations that engage participants in philosophical reflection in an embodied and open-ended way through a mode of play, recognizing this as an important mode of philosophical research, teaching and productivity.

The session will have a three-fold structure, engaging three issues important for philosophy of science and biology through three exercises or "gameformances".

1. First we shall perform an exercise geared to investigate classification, dubbed Apples and Oranges –audience members are invited to pick a token of a particular kind of thing and to develop an intimate relationship with it.
2. Second we will play a game investigating the ethics of technology and technological scripts, dubbed Virtuous Designs –participants are invited to collaboratively re-design ordinary things (biological entities, social processes/ institutions, everyday objects) following new, invented, "virtuise" verbs e.g. "fairorise" a cup: make a cup facilitate fairness, or "generositate" a virus: make it enable generosity.
3. Third we will do a performance exercise called the Response-able Walk to investigate the notion of social emergence and social response-ability.

PARTICIPANTS

Sophia Efstathiou, NTNU, Norway
Joyce Havstad, Oakland University, USA
Leah McLimans, University of South Carolina, USA

Exogenous homologies and experimental graduate pedagogy; Or, How to write a paper in a day

ORGANIZER

Matt Haber, University of Utah, USA

This session will be in two parts. First, will be the presentation of a paper, "Exogenous Homologies", written by the University of Utah Philosophy of Biology Lab group. Part two will be a round table open discussion on the process of writing that paper as a lab group, and on the general topic of graduate pedagogy in philosophy of biology and other ISHPSSB fields.

Part One *(30 minutes)*. In biology, we can take as a working definition of "exogenous factors or parts" those that originate outside of an organism. Recently, there has been a growing appreciation for the role exogenous parts play in biology, for example, in terms of individuality and identity (e.g., Pradeu 2012), or functionality or development (e.g., McFall-Ngai and Ruby 1998). Here we consider whether homologies might meaningfully be exogenous. Though initially counter-intuitive, we argue that exogenous homologies are distinct from endogenous ones, and ought to be understood as existing along a gradient. Where endogenous homologies are encapsulated in evolving lineages, exogenous homologies are located in distinct but entangled lineages. For example, highly reliable pseudo-vertical transmissions will generate reliable exogenous homologies. This will result in a gradient of cases that function as exogenous homologies to a greater or lesser degree. This will range from clear, exemplar cases (face mites), to borderline cases (chanterelle mushrooms), to cases where pseudo-vertical transmission is so infrequent that there are not, in any meaningful sense, exogenous homologies (squid-vibrio symbioses). We end by considering hard cases (e.g., termite mounds).

Part Two *(60 minutes)* This paper was jointly written as a Philosophy of Biology Lab project. Part two of this session will begin with a brief presentation of the writing process, and explanation of it as a training exercise for graduate students in philosophy of biology. The Philosophy of Biology Lab Group aims to bring some of the training mechanisms from the sciences to philosophy, and aspires to be more than just a reading group. In this case, that meant adopting a joint project with the goal of producing a co-authored research paper. To facilitate this, we set ourselves the goal of "writing a paper in a day", which required a thoughtful, strategic approach. We will share the success and failures of this project, with the hope of generating a broader discussion about innovative and engaging methods for graduate training in philosophy of biology and other ISHPSSB fields.

PARTICIPANTS
Matt Haber, University of Utah, USA
Stephen M. Downes, University of Utah, USA
Derek Halm, University of Utah, USA
University of Utah Philosophy of Biology Lab Group, University of Utah, USA

Should we stay or should we go now? An open workshop with examples from the histories, philosophies, and sociologies of systems biology

ORGANIZERS
Karen Kastenhofer, Austrian Academy of Sciences, Austria
Niki Vermeulen, University of Edinburgh, UK

The contexts of doing science and technology studies in a broad sense have changed considerably in the past decades. Not only have our studies proliferated quantitatively, diversified and produced their own turns and waves, their practice has also been molded by new funding environments with ever changing hypes and shifting public discourses. It seems safe to say that scholars are now more used to changing their research topics on a frequent basis. The question of which topic to pic up and how to best frame it has become more and more salient. With an augmenting projectification that cuts our scientific lives into slices of two to five years and a focus on reporting success stories, we seldom have the time to discuss our own research trajectories and how we leave past research topics behind, including failures, disappointments, and unforeseeable surprises. This workshop is dedicated to this theme and welcomes scholars from all topical fields to focus on the question how, why and when we quit with a research topic.

With a shared decade long interest in and engagement with systems biology, its epistemology, sociology, societal implications and governance we will start with this case, summarizing how the interest of science and technology studies in this field emerged in different contexts, what the main disciplinary strands of these studies have been in the past and where we stand now. At least in our opinion(s). We will invite other scholars to contribute their views before this workshop and hope for all of you to join the discussion with your own perspectives, experiences and opinions. Scholars from other topical fields like synthetic biology, nanotechnology or neuroscience are highly welcome! Also, we hope for participants with diverse disciplinary backgrounds. The targeted outcome of this session is twofold:

1. to get a better idea about where we stand now with the multidisciplinary study of systems biology and
2. to put the general issue of how, when and why to quit or stick with a research topic on the table.

PARTICIPANTS

Karen Kastenhofer, Austrian Academy of Sciences, Austria
Niki Vermeulen, University of Edinburgh, UK

What's new in *The New Mechanical Philosophy?* Book symposium with Stuart Glennan

ORGANIZER

Lena Kästner, Saarland University, Germany

In *The New Mechanical Philosophy* (OUP 2017), Stuart Glennan offers a comprehensive treatment of his mechanistic worldview and situates it within the expanding body of literature on contemporary mechanist philosophy. Overall, *The New Mechanical Philosophy* develops an account of mechanisms that synthesizes important aspects of the new mechanist philosophy. Rather than engaging in trench warfare, Glennan takes a birds eye view on certain recent debates and advances an integrated account, which attempts to dissolve certain controversies within the new mechanist philosophy.

For instance, Glennan emphasizes both scientists' craving for general explanations of phenomena and that they unusually study and discover the inner workings of particular mechanisms responsible for a phenomenon. Naturally, there is a tension between seeking generality and looking at particulars. To address this, Glennan provides

i. an ontological account of mechanisms in the world as well as
ii. an epistemological account of how scientists develop and employ models of mechanisms.

Despite the importance of this distinction, his accounts invite further questions: First, (i) crucially depends on how exactly to determine the boundaries of mechanisms. Radomski will focus on this "carving problem" in the context of research on cancer mechanisms. Second, (ii) crucially depends on a clarification of the roles of idealization in modeling. To this end, van Eck will discuss several distinct explanatory roles served by idealizations in mechanistic modeling and explanation derived from systems biological research.

By developing both an ontological and an epistemological account, Glennan crucially emphasizes the importance of both ontic and epistemic considerations in modeling (ch. 2), explanation (ch. 8) and mechanism classification (ch. 5). Indeed, as Kästner will argue, Glennan's discussion of mechanism classification may be read to suggest that ontic and epistemic considerations serve as two dimensions jointly setting up a space for mechanism classification.

Third, Glennan further elaborates his famous mechanistic theory of causation (ch. 6 & 7) according to which c is a cause of e if and only if there is a mechanism connecting c and e. Glennan defends this view in great detail and argues that with his account we can finally make sense of the notoriously problematic issue of interlevel causation in mechanisms. While much of his overall framework is appealing, Krickel will detail some remaining worries and offer a solution based on her own account of causation in mechanisms.

In this session, Glennan will personally reply to the four contributions listed above. In the final discussion (chaired by Carl Craver), we shall ask how much news there is in *The New Mechanical Philosophy*. What is the impact of Glennan's view for our understanding of explanations in biology? What progress has been made in reconciling opposition among new mechanist philosophers? Are there any important issues being swept under the carpet? And what work still remains to be done?

PARTICIPANTS

Lena Kästner, Saarland University, Germany
Beate Krickel, Ruhr-University Bochum, Germany
Bartosz Radomski, Ruhr-University Bochum, Germany
Dingmar van Eck, University of Amsterdam, Netherlands and Ghent University, Belgium

Philosophy in an Age of GWAS, Polygenic Prediction, and SNP Heritability

ORGANIZER

Lucas J. Matthews, University of Virginia, USA

Investigations of the genetic underpinnings of human behavior are advancing rapidly. Before, twin and family studies assessed the influence of genetic differences on complex behavioral traits, such as intelligence, depression, and schizophrenia. Decades of quantitative genetics evinced one provocative-yet-indisputable empirical fact: the more genetically similarity between individuals, the more phenotypic similarity. It eventually became the First Law of

Behavior Genetics: all behavioral traits are heritable. But what does it mean for a trait to be heritable? The advent of fast and cheap DNA sequencing technology provides new approaches to answering this old question. Genome Wide Association Studies (GWAS) flag small genetic differences – known as Single Nucleotide Polymorphisms or "SNPs" – as statistically associated with behavioral differences. Polygenic Risk Scores (PRSs) allow researchers to estimate the quantity of genetic differences relevant to specific traits. Genome Complex Trait Analysis (GCTA) allows researchers to calculate a new "molecular heritability" estimate, which is grounded strictly in DNA differences. The field of behavior genetics, which started somewhere with quantitative heritability, has now returned back to a new and poorly understood, "molecular heritability". The primary goal of this symposium will be to address hard questions about the latest developments in genomic technology and evidence. Are SNPs causal? Can GWAS results lead to meaningful mechanistic explanations? Can the NIH "All of Us" research initiative live up to its bold promise of preventing health disparities? How do we address the recent emergence of genomic race science?

PARTICIPANTS
Lucas J. Matthews, University of Virginia, USA
Jonathan M. Kaplan, Oregon State University, USA
Carl F. Craver, Washington University, USA
James G. Tabery, University of Utah, USA

Philosophy, history, and social studies of the life sciences: A tribute to Jean Gayon

ORGANIZER
Francesca Merlin, CNRS & University of Paris 1 Panthéon-Sorbonne, France

Jean Gayon (1949–2018) was Professor of History and Philosophy of Science and Director of the Institute for the History and Philosophy of Sciences and Techniques at Paris 1 Panthéon-Sorbonne. After studying philosophy, he followed Canguilhem's advice and trained in biology for a decade before embarking onto a PhD program that led to his book on the history of Darwinian theory of natural selection. During this period, Jean travelled frequently to the United States where he contributed to the emergence of philosophy of biology and built lasting connections with its founding members such as David Hull, Ernst Mayr, Michael Ruse, Marjorie Grene, and Richard Burian. In the 1990s and 2000s, while moving from the Université de Bourgogne to the Sorbonne, Jean analysed the philosophical history of central biological concepts (heredity, natural selection, gene, life, function); the epistemology of model organisms in biomedical research; the ethical and social dimensions of medical and biological research (human enhancement, race, eugenics); the history of disciplinary formations (genetics, population genetics, microbiology, evolutionary biology); as well as the relation between history and philosophy of science in major French and North American figures (Canguilhem, Dagognet, Grene, Hacking). Jean's detailed studies of scientific knowledge combine analytic precision and historical depth and are based on a variety of methods that go beyond traditional disciplinary borders in order to explore conceptual puzzles prompted by present-day issues. Jean's legacy as a philosopher and a historian rests not only on an impressive publication list and on him being internationally active, but also on his role as a mentor in training graduate students.

A recently edited collection *Philosophie, biologie, histoire: mélanges offerts à Jean Gayon* (Merlin & Huneman, 2018) and *La Connaissance de la vie aujourd'hui* (Gayon & Petit, 2018) – soon to appear in English translation as *Knowledge of Life Today)* – have illustrated Jean's central place in the community of historians and philosophers of life sciences. Bringing together scholars from France, the United Kingdom, Mexico, the United States, and Canada, this session builds on this recent scholarship and aims primarily at honouring the career and the thought of Jean Gayon and to showcase the continued relevance of his interdisciplinary work. It proposes to do so in examining some of his most significant contributions to the philosophy, history, and social studies of biology. Speakers will address Jean's analysis of core biological concepts such as heredity (Müller-Wille) and chance in biology (Merlin) as well as his perspective on the history of the Modern synthesis (Smocovitis) and evolutionary theory (Huneman). Turning to methodology, other participants will explore the tension between philosophy of biology and historical epistemology in Jean's work (Méthot) and examine his views on the relation between history and philosophy of science (Depew) using the history of French genetics as a case study (Burian). The co-author of *Knowledge of Life Today* will also provide insights into his work with Jean Gayon (Petit).

PARTICIPANTS, PART I
Richard Burian, Virginia Tech, USA
Pierre-Olivier Méthot, Faculté de philosophie, Université Laval, Québec, Canada
David Depew, University of Iowa, USA
Victor Petit, Université de Technologie de Compiègne, France

PARTICIPANTS, PART II
Staffan Müller-Wille, University of Exeter, UK
Francesca Merlin, CNRS & Université Paris 1 Panthéon-Sorbonne, France
Vassiliki Betty Smocovitis, University of Florida, USA
Philippe Huneman, CNRS & Université Paris 1 Panthéon-Sorbonne, France

The psyche and the life sciences

ORGANIZER
Håvard Friis Nilsen, Østfold University College, Norway

What is the state of the relation between the psyche and the life sciences today? The history and philosophy of psychiatry, psychology, psychoanalysis and allied sciences form an integral part of the history of biology in the late 19th and 20th centuries. In the 1940s and 50s, Freudian psychoanalysis seemed to take the world by storm. Beginning in the late 20th century, revolutionary breakthroughs in the development of psychotropic drugs provided new remedies for age-old ailments: Prozac produced an overnight revolution in treatment of depression, and Viagra contributed to an immediate relief from sexual impotency (one of the most common reasons for males seeking psychiatric counselling).

Today, the increase in pharmaceutical psychotropic drugs for alleviating psychic disturbances or tensions is matched by the disturbing rise in addictive and toxic substances and drugs for a general, illegal market. The laboratory-produced remedies for psychological or existential needs seem endless: whether dealing with anxiety, sexual disturbances or just plain boredom, the world of science as well as that of drug cartels seem to be able to offer a previously unsurpassed variety of quick fixes, as envisaged by Aldous Huxley in his 1934 classic *Brave New World.* The rise in psychotropic drugs goes hand in hand with an international general criticism of traditional forms of therapy and talking-based cures. This session invites participants and papers addressing the boundaries between biology and the psychiatric/psychological fields, and historical perspectives are most welcome.

PARTICIPANTS
Anna Lindemann, Sigmund Freud University, Austria
Håvard Friis Nilsen, Østfold University College, Norway

Digital history and philosophy of science: The reconstruction of scientific phylomemies as a tool for the study of the life sciences

ORGANIZER
Thibault Racovski, CNRS/IHPST, France

The transfer of theories and methods from evolutionary biology to the social sciences has a rich history. Notable examples are memetics, the application of Richard Dawkins' theory of genetic replicators to the evolution of culture, and the application of methods from phylogenetics to the study of the evolution of languages. More specifically, history and philosophy of science have been enriched by the use of a selectionist approach, initially developed by Stephen Toulmin and David Hull, to understand the evolution of science in terms of competition between theories.

Both the selectionist and the phylogenetic approaches bring a quantitative dimension in the study of their object. Traditionally however, philosophers of science have only relied on the study of limited samples of the scientific production to devise theories about the processes of scientific change. Yet, at present, the quantitative dimension appears especially relevant for the study of the evolution of science. Firstly because of the ever-growing volume of the scientific production that makes it impossible to track it by close reading. Secondly, because to adequately produce and test theories about processes of scientific change, it is necessary to retrieve quantitative patterns of change in order to detect the presence or absence of "signatures" of these processes.

In the last couple of decades, a technical and methodological shift, brought on by new computational tools, the existence of accessible databases of scientific journals (PubMed, Arxiv, Web of Science, etc.) and the development of text-mining methods and complex networks analysis, has made possible a quantitative reconstruction of scientific evolution in the same way as postgenomic techniques made possible the science of genomic networks and architectures. However, the majority of quantitative analyses of science productions (scientometrics, science of science, etc.), bar a few, do not try to analyse the temporal evolution of science. They rather focus on a measure of scientific activity at a given time, construct citation networks, possibly monitor the activities of fields and research centers to identify research fronts, but can hardly track the conceptual innovations within fields, the extinction or emergence of concepts, or the conceptual bifurcations and merging, as it is required by any attempt to capture patterns of scientific evolution.

This symposium will focus on a method that embraces this ambition: phylomemy reconstruction (Chavalarias & Cointet, 2013). This method allows the reconstruction of science dynamics by text-mining corpora at a large scale. It characterizes quantitatively the different phases of the evolution of scientific fields and automatically build "phylomemetic" topic lattices (an analogy with phylogenetic trees of biological species) representing this evolution. This method promises to indirectly help devise better theories and models of science evolution. It also improves the testing of theories by avoiding sample biases. Additionally, it is a tool for historians and philosophers of the life sciences that can provide new insights on historical case studies.

PARTICIPANTS
David Chavalarias, CNRS/EHESS /ICS-PIF, France
Bernd Amann, Sorbonne University, France
Ian Jeantet, University of Rennes 1, France
Thibault Racovski, CNRS/IHPST, France

Individuals out of interactions: Reproduction, symbiosis and syntrophic consortia

ORGANIZER
Derek Skillings, University of Pennsylvania, USA

The debate on biological individuality has usually been focused on the definition and characterization of evolutionary individuals. Addressing this topic has helped clarify the discussion about units of selection and the requirements for evolution by natural selection. Less attention has been paid to other kinds of individuality (i.e. non-evolutionary based accounts), among which the main alternative to evolution to ground biological individuality has been constituted by organismal physiology. Non-evolutionary accounts of biological individuality are still underdeveloped in comparison to evolutionary ones. This is especially evident in relation to interactive cases (i.e. host-microbe symbioses, microbe-microbe symbioses (biofilms), colonies, reproducing biological systems) that transcend the "traditional organism".

On the one hand the very notion of organism has been challenged by cases of cohesive entities emerging from interactions. Recent research on host-microbiota and, more generally, symbiotic relationships characterized by close functional ties, for example, might seem either to question the possibility to establish clear functional boundaries for living organisms, or to call for further work of characterization of the different ways functional interactions can be establish within a system or between systems. On the other hand, where generalization has been attempted, criteria involved in physiology, metabolism, organisms, anatomy, and ecology all tend to get bundled up together with very few distinctions to be made about why they go together.

The need for precise accounts based on conceptual or theoretical criteria is therefore especially apparent given new understandings of a wide range of interactive biological entities, from host-microbiota to pregnancy. In this symposium this issue will be discussed from different perspectives: physiological, organizational ecological, immunological, etc.. The possibilities of forms of biological individuals arising out of interactions and new ways to identify and account for non-evolutionary individuals beyond organisms will be explored in four talks, from syntrophic and physiological symbiotic individuals to the case of reproduction and pregnancy.

PARTICIPANTS
Jonathan Grose, University of Southhampton, UK
Derek Skillings, University of Pennsylvania, USA
Leonardo Bich, University of the Basque Country, Spain

Precision biology: Concepts and measurements

ORGANIZER
Ana M. Soto, Tufts University School of Medicine, USA and Centre Cavaillès, ENS, France

Two types of discourse predominate in the bio-medical sciences. First, that there are no "laws" in biology and thus there is no generalization without a corresponding exception; oftentimes, this stance is followed by the conclusion that theorization is not possible in biology. And second, that genetic reductionism and its "brainchild", precision medicine, lead to a tight linkage between an individual's genotype and a clinical disease, implying that the search for causal factors should focus on molecules, especially DNA. Statistical methods, especially deep learning on large data sets would make theorization superfluous. The first stance predicates that scientific knowledge can flourish in the absence of a theoretical framework, and second embraces a position based on a group of metaphors (information, program, signal) which were never endowed with a precise theoretical meaning and do not match the precise mathematical theories of information.

This session explores the possibility of developing a theoretical framework by adopting precise biological concepts. As an example, these concepts should shed light on measurements which are the tools of experimental biology.

1. Introduction (C. Sonnenschein): Using physics as a case study for the construction of theories we identified fundamental differences between physical and biological objects. These differences provided a starting point for constructing principles for a theory of organisms. These principles are 1) biological inertia, 2) variation, and 3) organization

2. Principle of biological inertia (A. Soto): The principle of inertia is central to classical mechanics: it identified a physical observable (momentum) and a conservation law (momentum conservation) and allowed physicists to analyze what modifies inertial movement. Based on the cell theory, we propose a biological principle of inertia, the "default state of proliferation with variation and motility". That proliferation is the default state is axiomatic for biologists studying unicellular organisms. From this theoretical commitment, what requires explanation is proliferative quiescence, lack of variation, lack of movement.

3. Principle of variation (A. Pocheville): Darwin introduced the notion that random variation may lead to unpredictable changes of living forms through time. We propose that biological variation should be given the status of a principle in biology.

Biological objects (e.g. organisms) should be considered as specific objects; they are distinct individuals. We formalize this principle in terms of symmetry changes, where symmetries underlie the theoretical determination of the object. In contrast, physical objects are generic (e.g. different objects can be assumed to be identical) and evolve in well-defined state spaces. Implications of this principle are: biological objects are historical and contextual, and variation is the source of novelty and plasticity.

4. Principle of organization. Integration of these principles and corollary (M. Montévil): Organization constitutes an overarching hypothesis that frames the intelligibility of biological objects. We offer a specific characterization of organization in terms of closure of constraints. The adoption of organization as a principle fosters an original approach to biological stability. We elaborate on its articulation with the two other theoretical principles addressed in this session and use them to discuss what it means to access empirical objects in biology. Finally, we address measurement and precision in biology.

5. General discussion.

PARTICIPANTS

Carlos Sonnenschein, Tufts University School of Medicine, USA and Centre Cavaillès, ENS, France

Ana M. Soto, Tufts University School of Medicine, USA and Centre Cavaillès, ENS, France

Arnaud Pocheville, Université Toulouse III. France

Maël Montévil, Centre Pompidou, France

An interdisciplinary roundtable on: *Collecting experiments: Making big data biology*

ORGANIZER

Bruno J. Strasser, University of Geneva, Switzerland

Collecting experiments: Making big data biology (U. Chicago Press, 2019), by Bruno J. Strasser, offers a new narrative for the history of biology over the last three centuries, as well as arguments about the present and future of biological and biomedical research. The book traces the development and uses of collections in the experimental life sciences from early twentieth century collections of live organisms to present databases of genomic data. Instead of a narrative centred on the rise of experimentalism (the "laboratory revolution") and the decline of natural history, *Collecting Experiments* argues that the contemporary life sciences (and the current "big data" revolution) are best understood as the coming together of two older ways of knowing – collecting and experimenting, commonly associated with the museum and the laboratory. The book suggests that, after more than a century of experimental research focussed on model organisms, we are witnessing a return to comparative studies in the laboratory involving a wide range of organisms. These research practices – centred on collecting, comparing, and computing data – have far-ranging epistemic as well as social consequences. They have contributed to transforming the norms of data access and sharing ("open science") and to renewed ideals about public participation in scientific research ("citizen science").

PARTICIPANTS
Edna Suárez-Díaz, UNAM, Mexico
Joel Hagen, Radford University, USA
James Griesemer, UC Davis, USA

Novel perspectives on the major transitions

ORGANIZER
Walter Veit, University of Bristol, UK

Life is hierarchically structured, with replicating entities nested within higher order self-replicating structures. Take, for example, multicellular life: the multicellular entity replicates, as do the cells that comprise the organism. Inside cells are mitochondria that also have the capacity for autonomous replication; the same is true of chromosomes within the nucleus, and of genes that comprise chromosomes. Such a hierarchical structure reflects a series of major evolutionary transitions in which lower order self-replicating entities have been subsumed within higher order structures. Typically this involves the lower level entity "giving up its right to autonomous replication" and with this "sacrifice" comes enslavement to the "needs" of the higher order "corporate body". Posed in these terms it is difficult to see how evolutionary transitions unfold; how selection might shift levels and why life is hierarchically structured. Necessary for progress is clarity concerning what needs to be explained.

How evolution transitions from one level to the next has been a major research program on its own since John Maynard Smith and Eörs Szathmáry (1995) published their seminal work The Major Transitions in Evolution. This panel is concerned with the provision of novel perspectives on the major transitions. We will present four different papers covering recent work and progress in microbiology, theoretical biology and philosophy of biology. Our interdisciplinary panel will offer novel insights and challenge the orthodoxy in the literature providing suggestions for new mathematical models and experiments. We emphasize a special focus on the emergence of proto life cycles and the role of ecology within the Major Transitions. Collectively, the papers aim to illuminate and clear up confusions within the literature, and if successful move the field further.

PARTICIPANTS

Paul B. Rainey, Max Planck Institute for Evolutionary Biology, Germany & Ecole Supérieure de Physique et de Chimie Industrielles de la Ville de Paris, France
Walter Veit, University of Bristol, UK
Eörs Szathmáry, Eötvös Loránd University, Hungary
Pierrick Bourrat, Macquarie University, Australia

Traditional sessions

The concept of the environment in biology: Historical, philosophical, and sociological perspectives, part I

ORGANIZERS
Jan Baedke, Ruhr University Bochum, Germany
Tatjana Buklijas, University of Auckland, New Zealand

In recent years the relationship between the organism and the environment has been much debated within conceptual, historical, and sociological studies of the biosciences. Yet while the concept of the organism is discussed widely, the concept of the environment itself is rarely addressed in detail. This double session takes, first, a closer look at some central past meanings of the term, such as milieux environnants (Lamarck), conditions of existence (Darwin), “Umwelt” (Uexküll), constructed environment (Lewontin), and others. Second, it discusses the historical conditions and consequences of past and present concepts of the environment: as collective or individual, homo- or heterogeneous, invariant or spatio-temporally flexible, selective or constructed, passive or actively generative, experienced or “acted on”, external or internal. This discussion will include analyzing the challenges these views have faced in biological practice, ranging from experimental setups to explanatory standards. Third, the session addresses the biomedical and larger societal developments and problems that different conceptualizations of the environment prompt today. Among others, these include, new trends towards shaping environments to fit individual and collective needs; fears of environmental determinism; and a new awareness of generation-spanning environments (e.g., in epigenetics). These three – historical, philosophical, and sociological – dimensions will be discussed in six case studies spanning the long twentieth century, and looking at theoretical biology, niche construction, eco-evo-devo, medical genetics, environmental epigenetics, and tropical medicine/infectious diseases.

Reciprocal, experienced and fit: Environmental debates in early 20th century theoretical biology

Jan Baedke, Ruhr-University Bochum, Germany

In the early 20th century, many biologists showed an increasing interest in the unit of the organism and the organism-environment relationship. As a consequence, the concept of "Umwelt" or "environment" was widely addressed in biotheoretical and -philosophical debates. In contrast to Darwin's earlier view that the organism finds itself in a struggle for existence with the conditions of life and that organismic variation depends (in large parts) on environmental variation, theorists in the first decades of the 20th century developed more complex views of the environment. Central figures in this trend were the biochemist Lawrence Joseph Henderson and theoretical biologist Jacob von Uexküll. While both adopted the idea that there exists a reciprocal dependency between organism and environment, this reciprocity thesis was spelled out in different ways. Henderson argued that, besides seeing organisms as adapted, we should also understand the specific physico-chemical properties of the environment as adapted, as they support the development of life. In contrast to this "wide" (cosmic) theory of reciprocity, Uexküll developed a "narrower" (sense-physiological) theory. He argued that the environment is constructed through the sensual exploration of the organism. Thus, every organism creates its own environment as it subjectively perceives it and acts in it. In this paper, first, I discuss Henderson's and Uexküll's different views on organism-environment reciprocity and agency, as well as their impact on environmental debates in British organicism and German holistic biology. Second, I discuss how these views of the environment became increasingly contested by a focus on collective rather than individual environments, and static/selective rather than dynamic/constructed environments. Finally, third, I compare these earlier debates about the environment with similar discussions in today's developmental and evolutionary biology about the reciprocal relationship between organisms and their environment.

The environment: An ambiguous concept in Waddington's biology?

Laurent Loison, Institut d'Histoire et de Philosophie des Sciences et des Techniques & French National Center for Scientific Research, France

Waddington is usually acknowledged as one of the first promoters of a unified Eco-Evo-Devo theory where the environment is supposed to play an important role both in development and evolution. When standard population genetics and the Modern Synthesis tend to reduce the environment to only an external and constant selective entity, Waddington favored a much more elaborate concept. For instance, as early as decades before the contemporary debate on niche construction, he emphasized that the environment is not something mechanistically imposed on animals, but that organisms choose and actively modify their environmental niche. Yet, while it is decidedly true that Waddington's biology puts in the forefront a more subtle concept of environment than what was classically at work at the time of the rise of the Modern Synthesis, the way he articulated this concept in juxtaposition with the concept of development remains paradoxical. On the one hand, Waddington never stopped claiming that the phenotype is the outcome of both the genome and the environment. But on the other hand the topology of his famous epigenetic landscape was rooted only in the genome, the variation of the environment being treated as an external perturbation that might be able to switch the rolling of the ball from one pathway to another. In other words, the genes and the environment were sometimes considered as symmetric agents in the epigenetic systems, and sometimes not.

The aim of this presentation is to explore the significance of this tension in Waddington's theoretical framework. I will show that even if some statements remain retrospectively ambiguous, Waddington's biology is best characterized as an asymmetric understanding of the causal role of genes and environment both in development and evolution. His theory of genetic assimilation was based on the idea of differential hereditary responsiveness to environmental variations, which gives the genome a leading role in the interacting process that drives organic morphogenesis. I will conclude by supporting the view that this asymmetry should not be seen as a weakness, but rather as a strength.

Environments of 21st century medicine

Tatjana Buklijas, University of Auckland, New Zealand

My talk examines the understanding of environment in environmental epigenetics and related fields (developmental origins of health and disease, reproductive biology) in the last two decades. Airs and waters once determined the health of the individual but in the nineteenth century the environment was relegated to the secondary place. At the time when Lamarck's notion of an active environment was replaced by Darwin's more passive one, Claude Bernard developed the idea of "milieu intérieur", the cornerstone of human physiology and medicine for decades to come. It understood the organism as a self-contained unit whose regulatory functions maintained homeostasis against environmental perturbations. Through the late nineteenth and twentieth centuries, much of medicine was place-neutral, except for those fields defined by their place – such as tropical medicine and industrial hygiene. Concerns about environmental degradation in the 1970s gave rise to the models of disease in which environment figured prominently. Yet the "natural" environment of the 1970s differs profoundly from the more individual, "personal" environment of the 21st century medicine. In this talk I will examine the kinds of resources that environmental epigenetics – a growing field focusing on the ways in which external influences received, especially, during early life change gene expression and, in turn, modify disease risk – uses to construct the notion of environment. What kinds of environments are taken into account, and what is left out? How explicit are the environmental epigeneticists when it comes to defining relevant environment? And what kind of implications – including political ones – do such (implicit or explicit) definitions have?

The concept of the environment in biology: Historical, philosophical, and sociological perspectives, part II

Malaria as an “environmental” disease: Swahili and bio-medical conceptions from Zanzibar, 1950–2018

Melissa Graboyes, University of Oregon, USA

Among bio-medical researchers and global health practitioners, malaria is recognized to be a deeply environmental disease. This paper, which is part of a larger book project, examines Swahili and bio-medical conceptions of what makes malaria an environmental disease by focusing on the East African island of Zanzibar. Zanzibar is an ideal location for asking these questions due to its sustained engagement with international malaria elimination attempts over the past century. Since the early 1900s, the island has served as a natural laboratory for malaria control measures led by the British colonial government, the World Health Organization (WHO), the Centers for Disease Control (CDC), the US Agency for International Development (USAID) and most recently the Gates Foundation. This paper discusses and deconstructs the definitions of “environment” used by these various groups.

An important goal of this paper is to integrate African vernacular knowledge into the history of biology, juxtaposing bio-medical conceptions of what makes malaria an “environmental” disease with Swahili conceptions from the 1950s through the present. Interviews and ethnographic observations in Zanzibar show that people regularly reference the mazingira (environment) when talking about malaria. Examples are presented about how Zanzibari’s link malaria to the landscape, flora, and fauna in various ways, and how Swahili conceptions of the disease differ significantly from contemporary bio-medical framings of what makes it “environmental.” These discrepancies are under-recognized by contemporary global health practitioners and have important implications for creating successful and appropriate malaria elimination and control campaigns today. Preliminary findings based on fieldwork in Zanzibar and archival research in Europe and Africa indicate that Zanzibari vernacular knowledge challenges many biomedical epistemic frameworks.

To broaden or to narrow: Teratologists and competing definitions of the Environment and Birth Defects (1956–1970)

Heather Dron, Stanford University, USA

Between 1956 and 1960, an embryologist, a geneticist, and a pediatrician organized the Teratology Society, a professional society in the US concerned with studying environmentally-mediated birth defects. Their vision of environmentally mediated anomalous prenatal development used a broad definition of the environment (effectively anything not inherited) and a narrow definition of birth anomalies (primarily anatomical differences visible at birth). Despite this expansive definition of environmental factors influencing development, many of their research studies wielded diet, chemical products, and radiation to study anomalous development in animals. With the rise of the late 1960s popular environmental movement's emphasis on chemical pollution derived from industrial activities, these physicians and scientists increasingly found themselves at odds with new approaches to reproductive toxicology that favored more diffuse and low dose exposures and broader definitions of resulting prenatal anomalies. For instance, in 1967, the World Health Organization defined teratogenesis to include not just unusual anatomy associated with dysmorphic organogenesis but also disturbances in growth, gender, neoplasia, intellectual deficit, and behavioral changes. This paper argues that teratology's' explanatory insecurities about inference from animal and human epidemiological models, reinforced by disagreements between different approaches to interpret chemical exposure during pregnancy, favored consolidation of expertise about inherited or spontaneously occurring genetic mutations,

presumably less unruly and subject to popular sensationalism or hijacking by citizen science.

The environment in the emergence of amniocentesis in West Germany

Birgit Nemec, Heidelberg University, Germany

In 1971, molecular biologist Carsten Bresch, head of the German Research Foundation's (DFG) senate commission for environmental research proposed a new approach to control environmental mutagenicity ("Umwelt-Mutagenität"), i.e. genetic anomalies induced by exogenous factors. Amniocentesis, a newly available technique of prenatal diagnosis, Bresch argued, if used in large scale population monitoring schemes could be a more effective "defensive measure" than methods contained in previous regulatory approaches: state regulatory approaches based on animal mutagenicity tests. His arguments convinced decision makers in politics, research and the industry; soon afterwards "Prenatal Diagnosis of Genetic Defects" was launched within the DFG priority program "for the case when careful mutagenicity testing is not enough" (DFG 1973).

In this talk I first analyse Bresch's concept of environment as an "outer world" ("Außenwelt", Bresch 1977: 230) charged by man-made hazards to organismal development: radiation, pollution, virus infections, industrial and consumer goods, i.e. pharmaceuticals. Within the German context, he stood for an evolutionary perspective on the organism-environment relationship, with Christian-spiritual elements (referring to Pierre Teilhard de Chardin), as well as for its popularization. I will then analyse how by 1970, in a period of growing environmental concern, Bresch and his interdisciplinary team used established explanatory standards (environmental burden, steady accumulation of genetic load, i.e. congenital anomalies) to argue for the introduction of amniocentesis as an individualised clinical-practical procedure. To conclude, I discuss the work of the Ulm pioneers of amniocentesis Karl and Henriette Knörr ("The Knörrs") to explain, how, later on, experience from gynecological and cytogenetic practice led to the technology's reframing as a tool to diagnose and prevent mostly internal and generation-spanning (inherited or spontaneously occurring) anomalies, shifting from the management of collective environments to the management of individualised, patient-focused environments.

New narratives in the history, philosophy, and social study of biological engineering

ORGANIZERS

Dominic Berry, London School of Economics and Political Sc., UK
Janella Baxter, University of Pittsburgh, USA

This panel highlights new approaches in the history, philosophy and social study of biological engineering. Emphasising the need for interdisciplinary investigation and interpretation of such areas, we draw together historians, philosophers, and social scientists studying biological engineering across CRISPR, “Genome Project write”, and in the making of biotech itself. We corral these different approaches through reflection on, or by attending to, narrative as an epistemic tool or way of knowing available to scientists and engineers in our cases, and the uses to which narrative is there put. Our results can therefore be read in light of broader debates and discussions currently being had throughout HPS and STS, aspects of which can be found here www.narrative-science.org. In recent years historians, philosophers and sociologists of biology have, for various reasons, come to take engineering more seriously either as a professional group that interacts with and collaborates with biology, or as offering a distinctive epistemic approach to biological materials and questions. One way in which to push these discussions further, and better integrate them with mainstream histories and philosophies of science, is to consider what cases of biological engineering can teach us about narrative science. Some of the functions narrative has already been found to achieve in other sciences include ordering knowledge, classifying and categorizing it, offering additional tools of representation, and ways of drawing out explanations. Our panel builds on these kinds of entry point.

How the narrative of engineering in biology creates epistemic divides

Janella Baxter, University of Pittsburgh, USA

A longstanding narrative is that engineering biological phenomena is importantly distinct from the proper study of biology. On this view, the biological sciences seek to observe, study, and explain contingently evolved living system and processes. Engineering biological phenomena, by contrast, seeks to create novel, artificial living processes and systems for various applications (Loeb 1909; Deichman 2012; Campos 2010). The emerging discipline of synthetic biology fosters this narrative by adopting the attitude that significant advancements in biotechnology requires an engineering orientation to biology (Endy 2005; Purnick et al. 2009).

While this narrative highlights important differences between sub-disciplines of biology, I wish to argue that it can also encourage needless epistemic division among biologists. Focus on engineering novel commercial products can encourage synthetic biologists to be disinterested in the complex details of living organisms, while also justifying a disinterest in synthetic biology from researchers in more traditional areas of inquiry. Yet, some of successful research programs in synthetic biology employ methods, strategies, and materials very similar to the successful development and use of technologies in other areas of molecular biology. This means that development and use of synthetic technologies can illuminate naturally evolved phenomena similar to how more traditional molecular tools do. Consequently, researchers working in traditional areas of biology can learn some things about living organisms from synthetic biology. Moreover, synthetic biology can (and do!) benefit from the knowledge generated by traditional areas of biological research. A more nuanced narrative of how engineering and biology facilitate each other's success is therefore needed.

How do you get a project off the ground? Narrating and enacting value in synthetic biology

Robert Smith, University of Edinburgh, UK

In 2016, a largely North American team of biological engineers, lawyers and self-ascribed futurists announced a project that would aim to reduce the cost of synthesising DNA 1000-fold by attempting to design and synthesise a human genome. The proposal ricocheted around the world and has been met with excitement, concern, incredulity and apathy. In the years since the initial announcement, the proposal has morphed. For instance, the public goal has broadened from one that focuses exclusively on synthesis of human genomes to one focusing on synthetic genomes writ large. Based upon multi-sited ethnography and documentary analysis, I'll juxtapose a series of interlocking vignettes that trace how the visions circling – and helping to constitute – "Genome Project-write" are changing as different social groups try to get it off the ground. While sociologists have long-examined the making of promises and the creation of hype as ways to leverage the future to produce powerful narratives that can sustain scientific projects and fields, here I am concerned primarily with strategies that centre around imagination and dreaming, resistance and even cynicism that are playing active roles in attempts to actively create a cultural identity for the project and make it "doable" as it travels around the world. In particular, I will explore the ways in which the more promissory, forward-facing narratives are interfacing with longstanding largely historical bureaucratic visions, national identities and material infrastructure such as (largely public but also private) investments in centralised DNA synthesis facilities, BioFoundries.

Biotech as genre

Dominic Berry, London School of Economics and Political Sc., UK

Literary theorists have developed numerous accounts of genre. Where some are formal and normative, others maintain that genre is an ever-changing concept not confined to particular parts of text or its interpretation. These starting points stimulate a search for parallels, to find genre at work outside of the literary world. Drawing on key work from literary theorists including Frow, Herman and Ryan, I argue that phenomena in the history of science that we commonly describe in terms of “style” (as in styles of thought etc.) could be more productively thought of as genre. The switch to genre thinking adds value, because where style might be too easily reduced to a flourish, genre is instead constituted by many things only some of which are stylistic, others being formal, thematic, and enunciative. I make this argument through the example of the emergence of “biotech” in the second half of the twentieth century. One can certainly think of biotech as a style of biological science, and this can act as an evocative shorthand for dealing with some of the ways it has been defined by actors, their epistemic positions, biotech’s social and political meanings, and so on. But there is more to the making of biotech than style.

To build an account of biotech as genre I attend not only to the existing historiography, but also make use of the archive of New Scientist, which I have systematically searched from its first issue in 1956 up to the year 2000. This work assists in the making of new narratives of biological engineering by allowing us to be explicit about the features that are or are not shared with other areas of the biological sciences, some of which will be social, others epistemic, others aesthetic, and so on. We can thereby replace the question of whether or not biological engineering “is a thing”, with more productive questions about what goes into the making of any area of biological science or technology.

Let’s talk about sexual selection and gender relations

ORGANIZER

Marion Blute, University of Toronto, Canada

For example, is there a generally accepted evolutionary biological theory of sexual selection? Are relations between genders or kinds of gender functioning a matter of cooperation, of conflict or some of both, and if the latter, which came first or is more fundamental? How objective or politically biased are the theories? What about those who seem to think sexual selection if virtually all male mate or sperm competition, those who seem to think it is virtually all female mate choice or cryptic choice, and those who seem to think that the same variety of sexual orientations and identities present in humans including LGBTQ2 are present across all of life? What accounts for the diversity of marriage systems in human societies – polygamous, polyandrous and monogamous? Has our understanding of human gender relations been altered in the Me-Too Era? These are only some of the questions that could be discussed.

Why are men the criminal sex? Extended heredity and the gender gap in offending

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The gender gap in offending is probably the most significant empirical regularity in criminology: for almost all types of crime, in all cultures and all time periods, men are more likely to engage in criminal acts – especially those that inflict serious harm on others – than are women. Evolutionary psychologists have argued that gender differences in offending can be explained by drawing on the conceptual resources of sexual selection and parental investment theory. Lower male parental investment, higher potential reproductive rate, and greater variability in reproductive success has resulted in more intense sexual selection on male compared to female characteristics favouring traits that promote success in intra-sexual competition, including risk-taking, aggression, and status seeking. These differences manifest themselves in different rates of criminal offending. However, despite the explanatory value of this standard account, several key questions remain. First, what can account for the substantial variability in the magnitude of the gender gap cross-culturally and historically? Second, why do most men, like most women, not perpetrate serious criminal acts? And third, how is this explanation of the gender gap in offending consistent with contemporary accounts of sexual selection in humans which emphasize the role of mutual mate choice and the importance of intra and inter sexual selection processes? I argue that a framework that draws from recent work on the idea of "extended heredity" provides a more nuanced theoretical approach. Specifically, I argue that a more inclusive understanding of inheritance that includes four key mechanisms – genetic, epigenetic, ecological, and cultural inheritance (and their interaction) – can help us to better address the nature of the gender gap in offending and offers some specific suggestions for ultimately reducing the volume of crime in society. This framework also provides a perspective on the evolution of gender differences more generally, that might be relevant in a number of different domains.

From ape to (wo)man: Epistemological issues in the use of primatology for the study of human social evolution

Marie Lacomme, Paris Diderot French University, France

At the crossroads of evolutionary biology, primatology and anthropology, since the late 1970's, some researchers have been studying the behaviour of contemporary ape species in order to better understand the origin and evolution of human social behaviour. Since Bonobos (*Pan paniscus*) and common chimpanzees (*Pan troglodytes*) are phylogenetically the closest to modern humans (*Homo sapiens*), studies often focused on these two species. However, it turns out that bonobos and chimpanzees have very different social structures, especially with regard to the relations between males and females. For example, the dominance of males is much less in bonobos than in chimpanzees and female bonobos cooperate much more. Using data from the observation of these species, it is possible to formulate hypotheses about the evolution of social behaviours in the human lineage. How then do the theories produced in this field of research reflect our knowledge of bonobos and chimpanzees? What about the debate between the "chimp-like ancestor" and the "bonobo-like ancestor" which stirred the scientific world in the 1980s? To what extent do social representations of researchers play a role in their work? What influence does the gender of researchers have on their theories? With these types of questions and examples, I will discuss the biases that may come into play in this field of research. The presentation therefore will address epistemological issues related to gender relations that are at stake in the study of the evolution of human social behaviour based on data from primatology.

The puzzle of what compensates for the two-fold cost of sex solved: The advantages of specialization

Marion Blute, University of Toronto, Canada

It has long been said that there is a two-fold cost of sex – variously termed the cost of meiosis, of producing sons, or of sexual competition and selection. The answer proposed here is the advantages of specialization. Specialists are commonly more efficient in the segment of a niche that they specialize in than are generalists in that segment. If different sexes, kinds of sexual functioning in hermaphrodites, or mating types are specialists, and if specialists in these cases are slightly more than twice as efficient in the segment of a niche that they specialize in than are generalists in that segment, then the two-fold cost of sex would be compensated for. What kinds of specializations could be involved? These may be infinitely varied in different taxa. However, there are three broad kinds of specializations which can be considered. They may

a. both be ecologically i.e. naturally selected to be different;
b. one more ecologically i.e. naturally selected and the other more socially i.e. sexually selected to be different; or
c. both may be socially i.e. sexually selected to be different.

Somewhat counter-intuitively it will be suggested that males and females are commonly the first, that male and female functions in hermaphrodites are commonly the second, and that mating types are commonly the third. These will be explained. I emphasize that if there is a little more than a two-fold advantage to specialization, that does not favour any particular one of the many theories of the advantages of genetic recombination – instead it simply removes the major obstacle to all of them. However, for what it is worth I will opine that it is conceivable that rather than genetic recombination being the function of sex and gene conversion, commonly reciprocal, sometimes a side effect, gene conversion may be the function of sex and recombination a side effect.

On the origin of genes (by means of natural selection)

ORGANIZER

Zdenka Brzović, University of Rijeka, Croatia

There are two main groups of biological theories that answer one of the most significant questions at the interface between molecular and evolutionary biology, i.e., "how genes arise and become functional" (see Tautz 2014):

1. gene origin via duplication and divergence, and
2. de novo gene origin.

(1), which was until quite recently the only one accounting for the explanandum in question (see Ohno 2014), claims that a putative new gene arises from the gene ancestor by the duplication process or, as it is interchangeably labeled in the scientific literature, "mechanism" (see, e.g., Schmitz, Ulrich, and Bornberg-Bauer 2017). As the new gene duplicate is operating "in a shadow" of its gene ancestor, it can more readily diverge and end up:

i. as a pseudogene;
ii. sub-functionalize with respect to its ancestor's function; or
iii. neo-functionalize, that is, acquire a new function within the corresponding gene family.

Evolutionary genetics' theory (2), on the other hand, claims that a large portion of new genes arises from so-called "non-coding intergenic sequences" in the genome. We focus here on the details of the latter biological theory and its relationship to theory (1), having as our primary goal a determination of the explanatory strategy that (2) is, in fact, pursuing in accounting for de novo gene origin. In that regard, we proceed as follows: in the opening paper of the symposium proposal Mechanistic Explanation and the "Levels Problem", we examine which, if any, of the extant philosophical accounts of scientific explanation captures the role performed by biological theory (2) with respect to the target explanandum. More specifically, the paper examines the new mechanistic account, which, according to a self-proclaimed criterion of the closeness to scientific practice (see Darden (2008)) would make a perfect match with the case in question. We argue to the contrary, for the following reasons:

i. the term mechanism in both theories is only a stand-in for, more commonly, the term process;
ii. such a loose understanding of mechanisms results in an over-permissive account that cannot sanction problematic explanatory proposals without introducing further constraints (see Franklin-Hall 2016); and
iii. the theory of de novo gene origin is, in fact, more in tune with Salmon's idea of an etiological causal explanation, which we further develop in the paper Explanation in Molecular Biology: The Explanatory Force of the Details.

Finally, the paper Genes as Natural Kinds: Against Mind-Dependence and Contextualism assesses the criterion of the closeness to scientific practice itself by examining the concept of a gene in biological theory (2). Most notably, it argues that the new mechanists' and an overall tendency to equate closeness to scientific practice to mind-dependence, perspectivalism and contextualism, needs a careful reconsideration.

Mechanistic explanation and the "levels problem"

Predrag Šustar, University of Rijeka, Croatia

The new mechanistic (NM) account of scientific explanation has been acclaimed as especially suitable for molecular biology, because of its “closeness” to what actually is going on in the scientific practice in question. However, NM generally has been recently criticized for being overly permissive. In other words, it is unable to distinguish acceptable explanatory mechanistic models from those which, although meeting the corresponding NM basic criteria, are explanatorily unacceptable. That remains to be the case, even with the addition of three further explanatory standards or constraints: the “causal”, “carving”, and “levels” constraints on NM (see, in particular, Franklin-Hall 2016). With regard to that strand of the debate on the supposed matching between NM, both basic and upgraded, to the structure of explanations in the life sciences more generally, we examine two further issues that, in our view, follow from “levels” explanatory constraint itself. Hence, they also should be added to the challenges to which NM, in particular, in molecular biology should respond. The two issues are as follows:

1. the issue of the right-level, and
2. the issue of role ascription.

We argue, by referring in detail to the recent biological theory of de novo gene origin, against both the NM’s and its critics’ insistence on the “levels” constraint for an acceptable mechanistic explanation. Namely, as the scientific explanatory models of de novo gene emergence and functionality actually show is that the so-called “semi-reductive” strategy of descending a certain number of organizational levels below a mechanism related to the explanandum phenomenon is not a necessary condition for an acceptable NM type of a mechanistic explanation. Accordingly, we aim to show that the “old” mechanists’ (see, e.g., Salmon 1984) distinction between constitutive and etiological mechanistic explanations should be of help in clarifying the structure of explanation, such as those in the area of the origin of (new) genes. If NM, nevertheless, goes through a semi-reductive explanatory strategy of some kind and degree, then the identification of 1) levels themselves, and of 2) a component-part’s role(s) are both fixed by natural selection. This further strengthens the idea implicitly present, at least, in the recent biological theories of gene origin and functionality, that the term mechanism is, in fact, only a stand-in for, more commonly, the term process.

Explanation in molecular biology: The explanatory force of the details

Vito Balorda, University of Rijeka, Croatia

In this paper, we address the question of abstraction and specification in recent mechanistic debate. Namely, the role these procedures play in explaining biological phenomena, in particular, at the interface between molecular and evolutionary biology. Relatedly, we also address the issue of explanatory relevance, a key feature of the mechanistic accounts of explanation. We asses scientific abstraction, a procedure of ascending to a more general level in understanding target biological phenomena and having its main merits in providing a theoretical framework that allows us to filter and, then, fit into it explanatory relevant data. The explanatory power or force of a scientific explanation, however, consists in delineating the details.

We try to show that there are three basic steps in the delineating procedure, which, to their own degree, yield overall explanation in current molecular biology, and those steps are:

1. Formulation of an abstract scheme that can, at a very general level, capture the explanandum phenomenon;
2. Big data mining/collecting (for example, the ENCODE project's building a map of activities in different areas of the genome);
3. Extracting all the relevant data, i.e., the data that best fit the corresponding abstract scheme, which has been previously used in answering sufficiently similar biological questions.

We illustrate the steps in question through the case study of origination of new genes from non-coding regions that nicely instantiates explanations at the interface between molecular and evolutionary biology.

Furthermore, there is a related issue of the criterion for the explanatory relevant data, namely, the criterion by which one extracts relevant details to explain the phenomenon. The issue concerns the transition from step (2), in the overall 3-step procedure, to step (3). There are two main positions in that respect: (1) contextualism – there are many different criteria, which are used by scientists, especially biologists, to extract the relevant data and by that explain a certain phenomenon; (2) monism about criterion selection. Position (2), thus, refers to the situation in which biologists have a unified, single criterion. In that regard, we focus more specifically on Baetu's (2015) proposed criterion – mathematical modelling. In our view, however, mathematical modeling by itself cannot act as a criterion to that matter, but only as adequately embedded within the overall three-step explanatory process. Thus, we agree with Baetu's argument for a monistic approach, but we argue that the theoretical framework of evolutionary molecular biology indicates how this criterion might actually look like.

Genes as natural kinds: Against mind-dependence and contextualism

Zdenka Brzović, University of Rijeka, Croatia

There is a well-established trend in the debates in philosophy of biology to argue that our philosophical accounts need to stay close to actual scientific practice (see for instance Waters, forthcoming, Ankeny et al. (2011), Kendig (2016)). This approach, it is often argued, leads us to a more pluralistic and contextual approach that takes into consideration the complexity of the actual scientific practice and the fact that, depending on their interests, scientists might end up with different theories, concepts or even results. In this paper I examine this approach as it is applied in the case of biological classification, specifically classification into genes.

Thomas Reydon (2016) proposed that classifications into genes provide a good example how classifications in natural sciences, and not only in human ones, are embedded in matrices of investigative contexts, epistemic aims, institutions and other elements. Different ways in which genes are allocated to kinds, according to him, depend on investigative contexts and are thus fundamentally mind-dependent, even though there are still some natural boundaries that limit the delineation of gene kinds. I will argue that, even though classification into genes has proved to be especially problematic leading to different types of "gene skepticism", that Reydon's conclusion is overly pessimistic when it comes to the possibility of an objective classification of the genome.

I criticize the strategy of taking concepts that are in use in scientific practice, and equating them with natural kinds without establishing that such concepts fulfil some minimal conditions for natural kindness. The concept of gene was originally introduced as a vague notion for a unit of inheritance and it has changed substantially with development of molecular biology. Its "heterogeneous reference potential" (Kitcher 1982, p. 357) has led some to conclude that we should treat genes in a contextual, pluralist and pragmatic manner (see, for instance, Fogle 1990). The question, however, is why we should consider such a problematic concept to be a natural kind. I take it that there are two options available:

1. if the concept of gene is hopelessly problematic, then we should give up on it as a candidate for natural kind, and endorse, along with Kitcher (1982), that there is no molecular biology of the gene, but only of genetic material;
2. search for an improvement of the gene concept that has the potential of playing a role of natural kind in molecular biology (see Baetu 2010).

I argue that the second approach is more promising, and that regardless of the vast complexity of goings on at the molecular level there is a firm ground upon which to anchor the delineation of genes. That is, by referring to the fact that natural selection acts to fix important genomic segments and various additional molecular machinery involved in producing functional macromolecules.

Revisiting organ culture: History, concepts, technologies, part I

ORGANIZER

Silvia Caianiello, National Research Council & Stazione Zoologica Anton Dohrn, Italy

The focus of the panel is on the tradition of organ culture in vitro, as distinct from cell culture. In fact, while cell culture was committed to "observing the activities of cells when freed from the entanglements of the organism" (Harrison 1912) by means of an unprecedented act of disembodiment (Landecker 2007), involving the complete destruction of tissue architecture, the study of "controlled growth" (Thomson 1914) was rather aimed at identifying and reconstituting the suitable conditions for recapitulating in vitro morphogenetic processes and the maintenance of normal physiological functions (Willmer 1965). On one side, organ culture established new experimental settings for addressing the role of contextual factors in establishing, maintaining and switching cell specification and brought to light the lability of the differentiated state of cells (Harrison 1933; Grobstein 1963; Moscona 1964; Hay 1993). On the other side, these very settings also allowed highlighting the extent of the intrinsic self-organizational capacity of cells in collectively establishing functional higher order 3D structures such as tissues and organs. Organ culture's conceptual framework and technological innovations drove the shift from 2D to 3D culture systems, and can be seen as the common root of current 3D advanced microphysiological systems such as organoids and organs-on-a-chip. As to the first aspect, some contributions will focus on the role of scientists like Aron Moscona and Clifford Grobstein, and their respective insights into the biomechanics and biochemistry of the extracellular matrix in morphogenesis and their underlying philosophical commitments. Furthermore, an analysis on the contribution of Giuseppe Levi to organ culture will draw attention to the relevance of the Italian tradition of these studies. Characteristic of the early organ culture approach was the development of techniques for bridging the "unnatural divorce between morphology and physiology" (Fell 1956), and accounting for the role of the structures and forces emerging at tissue and organ level in setting the stage for specific biochemical and molecular changes. This "physiological morphology" ideal was implemented in a plurality of epistemically and experimentally diverging approaches in the 1980s, as the focus became the interaction between cytoskeleton and the extracellular environment. A comparison between the different approaches as they emerged at the 1987 Abercrombie Symposium will shed light on their respective influence on different specialized research fields, such as focal adhesion, mechanotransduction and tumor-microenvironment interactions. The second of the above-mentioned aspect, the emphasis on the self-organizational capacity of cells will be tackled at the case of the discovery of the unique morphogenetic potential of Madine-Darby canine kidney (MDCK) cells. Later experiments of 3D culture embedment of these cells allow evaluating the extent and limits of such potential, as well as reflecting on the trade-offs involved in mimicking morphogenetic events in vitro. Finally, an update to current debates on the notion of cell type identity and specification will be provided with reference to the latest developments of single-cell genomic analysis.

Envelope, mechanical support, microenvironment. The changing role of the extracellular matrix in Aron Moscona's research

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The contribution retraces the evolution of Aron Moscona's theory of tissue and organ development from the 1950s to the 1990s by focusing on the changing theoretical role accorded to the empirical object today known as extra-cellular matrix.

Moscona's research in developmental biology was devoted to explaining the emergence of specific tissue and organ architecture. He pursued this objective by making use of tissue and organ culture techniques, to whom he also contributed significant advances. We will distinguish three main clusters of papers whose chronological succession illustrate the evolution of Moscona's thought concerning the role of the extra-cellular matrix in tissue and organ development: a first cluster of papers dates back to 1950 when Moscona was about to finish his

PhD at the Hebrew University of Jerusalem. Here the extra-cellular matrix Moscona refers to is the inner layer of the egg coat of the insect *Bacillus libanicus,* the vitelline membrane. Its microscopical structure is only briefly mentioned by the author while its function is suggested to be that of an envelope. The second series goes from 1952 when Moscona entered the Strangeways Research Laboratory in Cambridge and became acquainted with tissue and organ culture technique, to the late 1960s. In these years, Moscona worked in many different institutes (Strangeways Research Laboratory, Rockefeller Medical Institute, Hebrew University of Jerusalem and University of Chicago, without mentioning many short research visits to Belgium, France, Italy and UK) and performed a huge amount of experimental work on in vitro tissues dissociation and re-aggregation and on the in vitro development of explants, by paying particular attention to the experimental variables affecting histotypic and organotypic development. We suggest that Moscona's hypothesis on the importance of the extra-cellular matrix in constraining tissue and organ normal development originated in this interval of years and shifted from a more traditional notion of the inter-cellular substance as a mechanical support for cells patterned proliferation to that of cellular microenvironment. We attempt to offer an epistemological analysis of the origin of this hypothesis, its experimental roots, and the coalescence of different epistemological drivers that influenced its formulation.

We will last focus on the third cluster of articles, from the late 1960s to 1992, the date of Moscona's retirement. Papers from this third cluster strongly advocate the critical importance of bridging (molecular) genetics and developmental biology and the urge for molecular mechanistic accounts of the interactions between the levels of genome expression, cell differentiation and tridimensional tissue organ structure. Despite the fact that Moscona never performed himself research on gene expression, he explicitly mentioned the genome and the molecular internal apparatus of the cell as missing links in his theoretical models (and graphical schemata) and encouraged research on tissue and organ development to look for molecular pathways bridging extra-cellular and genomic factors.

Clifford Grobstein and the “wisdom of the matrix”

Silvia Caianiello, National Research Council & Stazione Zoologica Anton Dohrn, Italy

Clifford Grobstein (1916–1998) was a bridging figure in the transition from classical experimental biology and developmental biology in the USA. As an academic leader in his later career at the Stanford University, he fostered the reorganization of biomedical education and the establishment of bioethical guidelines for fetal research.

His seminal work on the role epithelial-mesenchyme interactions in mammalian organogenesis in the 1950s was substantial in the shift, pioneered by Holtfreter, from an “instructive” notion of induction (organizer) to a fully relational one, as “developmentally significant interaction between closely associated but dissimilarly derived tissue masses” (1955). He employed organ culture methods, contributing with technical innovations, such as the transfilter system for studying the influence of diffusible agents in inductive processes.

My contribution will focus on the experimental basis and conceptual framework of Grobstein’s dynamic view of cell-microenvironment interactions, and particularly on the role of extracellular matrix in cytodifferentiation and in tissue integration, homeostasis and pathology. I will try to show that Grobstein can be seen as the systematizer of the tenets of what W. R. Gross labeled in 1956 as “the matrix theory of morphogenesis”, pioneered by P. A. Weiss and substantiated by a large body of organ-culture based experimental evidence.

Grobstein’s insight into the bidirectional communication between cell and extracellular matrix set the stage for the later work ECM biology, and in particular for the study of cytoskeleton-ECM mechanochemical interactions. It also prompted Grobstein to oppose in the 1960s to the extension of Monod’s and Jacob’s genetic regulatory model of differentiation to eukaryotes. He proposed an alternative theory of “cytodifferentiation as macromolecular synthesis", as the framework for a unified multilevel view of the "shells" of control layered upon and influencing the "switching of biosynthetic activity" (1963).

Giuseppe Levi and the question of growth and form

Ariane Dröscher, Università degli Studi di Trento, Italy

In the 1910s, the Italian neuroanatomist Giuseppe Levi (1872–1965) became one of the pioneers of cell culturing and from 1928 of microcinematography. Distinguishing himself from both dominating currents of cell research in Italy, the morphological as well as the emerging chemical and colloidal school, Levi advocated a dynamic and holistic cell concept. Throughout his scientific career, he aimed at finding a way to combine the concepts of form and function. For him, both were intimately linked with each other – physiology as the dynamic of form, and anatomy as the study of the interaction between the parts – and with a third field, the study of growth, considered as the dynamics of the change in form. The new technique of in vitro culturing seemed perfect to approach the question of the change of form and its underlying mechanisms experimentally. Levi's research project was especially successful. Between 1916 and 1957, he published more than sixty papers and two seminal treatises.

As one of the first to venture into this in the 1910s and 1920s still very controversial technique, Levi's work is particularly suited to investigate the initial hopes, promises and developments of the in vitro experiments. My talk will investigate how the basic questions of life, death, individuality, and the determining principles of growth influenced Levi's approach to cell culturing, and how his experimental strategies and ideas changed over the decades. Special attention will be directed to the aspects of differentiation, dedifferentiation, and the role of internal and external factors on these processes.

Revisiting organ culture: History, concepts, technologies, part II

Functional epithelial cells in culture

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In the 1950s Stewart H. Madin and Norman B. Darby developed several continuous (immortalized) cell lines for the study of viral infections from kidney tubules removed from a variety of species. In the 1970s, scientists recognized that at least one of these lines, Madin-Darby canine kidney (MDCK) cells, retained in culture certain characteristics of kidney tubular epithelial cells in vivo. When grown in typical culture dishes, confluent cultures develop “blisters” or “hemicysts” that break and reform over time, resembling “boiling oatmeal” in sped-up time lapse movies. These observations indicated that the cells not only formed tight seals between themselves, but also transported fluid vectorially from above the cells to under the cells, where it became trapped. In an effort to develop the MDCK cell line into an experimental system for the study of ion transport, scientists cultured them on permeable filters to mimic the Ussing chambers commonly used by transport physiologists. In 1978, Enrique Rodriguez-Boulan and David Sabatini extended the use of the MDCK cell line to cell biological studies of protein transport and sorting when they observed that certain viral proteins are directed only to the top (apical) surface or the bottom (basolateral) surface. By the mid-1980s, permeable culture supports were commercialized, and the MDCK cell line became the preferred model for the study of mammalian epithelial cell biology because they exhibit many essential differentiated features of normal epithelial cells. These include growth as a true simple epithelium one cell thick, a polarized distribution of membrane proteins and lipids, and formation of well-developed junctional complexes between the cells. Because MDCK cells are, in addition, immortalized but not tumorigenic when injected into mice, their characteristics remain stable and reproducible over time, in contrast to both primary cultures and cell lines derived from tumors that often have limited and unstable phenotypes. In a final development, MDCK cells were grown in three-dimensional gels of extracellular matrix proteins, extending the range of the culture system to the investigation of morphogenesis. The continuing story of MDCK cells illustrates how some characteristics of differentiated organs can be duplicated with a homogeneous cell line, as well as the trade-offs necessary to mimic complex differentiated events in culture.

Entangling morphology and physiology: The trajectory of simple and complex systems of cultured cells in 1980s research on cytoskeleton-environment interactions

Hanna Lucia Worliczek, University of Vienna, Alpen-Adria-Universität Klagenfurt, Austria & Marine Biological Laboratory, USA

In 1956 Honor B. Fell, a major contributor to cell/tissue/organ culture, presented her perspective on the future of tissue culture in relation to morphology. She described an "unnatural divorce between morphology and physiology", with the former describing the appearance and characteristics of cells and tissues grown in culture, and the latter investigating them biochemically. Fell attested that biochemical approaches had become more and more dominant but that a rapprochement between morphology and physiology has been on its ways in the field of tissue culture research – which she coined "physiological morphology". A requirement for scientists working with tissue culture to implement this rapprochement was in her view a thorough knowledge on form and structure as a basis for any physiological and biochemical studies. Taking Fell's remarks as a conceptual trajectory, I aim to investigate the interplay of morphology and physiology in a field of inquiry that has been strongly depended on various systems of cultured cells/tissues/organs: research on the interaction between the cytoskeleton and the extracellular environment in the 1980s.

In this context, I will:

i. compare how morphological and physiological aspects were brought together by representatives of different laboratories to explain cytoskeleton-environment interactions and phenomena associated with them;

ii. investigate the epistemic possibilities and technical/epistemic limitations of different models used to study cell-environment interactions, with a focus on visualizing morphological characteristics; and

iii. carve out further trajectories of different approaches to investigate cytoskeleton-environment interactions in increasingly specialized fields like focal adhesion-, mechanotransduction-, or tumor microenvironment-research.

I take four perspectives on interactions between the cytoskeleton and the extracellular environment as a starting point, which were presented in 1987 at the 2nd Abercrombie-symposium on "Cell behaviour: shape, adhesion and motility". In the proceedings of this meeting, two seemingly opposing approaches to these interactions can be identified in review papers from two different research groups: One came from the lab of Mina Bissell, who presented complex 3D systems of cultured cells as an imperative for modelling tissue environment, and who included visual evidence from gene expression studies, phase contrast and electron microscopy in contribution. The other approach came from the lab of Keith Burridge, who promoted a model of cultured fibroblasts monolayers for cell-substratum interactions, and who included micrographs of the cytoskeleton from immunofluorescence and interference reflection microscopy. However, these approaches were not conceived as mutually exclusive. The contributions by Avri Ben-Ze'ev and Benjamin Geiger to the 1987 symposium can be interpreted as a merging zone of these apparently opposing approaches, using methodologies and concepts from and referencing both directions.

By comparing these four positions on cytoskeleton-environment interactions from 1987, and by contrasting them with later published original work, reviews and personal recollections of the same actors, I aim to investigate the trajectory of qualitatively diverging "physiological morphologies" that led to the development of different specialized research fields.

From organs to single cell, and back

Denis Thieffry, IBENS, France

Since the deciphering of the human genome along with those of diverse model organisms at the turn of the 21st Century, high-throughput sequencing methods have been applied to characterise the polymorphism of genomes, gene transcription on a genome-wide scale, as well as various kinds of regulatory epigenetic mechanisms. However, one limit of these pan-genomic approaches lies in the necessity to process relatively large populations of cells, with inherent heterogeneity (e.g. regarding cell type or cell cycle stage). Hence, most results gathered with these techniques need to be considered as some kind of averaging over numerous and relatively diverse cells.

More recently, several groups have reported the development and the successful application of transcriptomic and epigenomic approaches at the single-cell level. Although of limited sensitivity and pretty noisy, these novel approaches provide new means to characterise genomic variation, gene expression and transcriptional regulatory processes at large scale for thousands of sorted individual cells.

In my contribution to this workshop, I will review some of these recent developments, focusing on results impacting on several key concepts in cell biology, in particular regarding the definition of cell types, the notion of cell fate commitment, and the evaluation of cell plasticity. Furthermore, I will present and discuss the conception of novel integrative representations to characterise and visualise molecular cell diversity, as well as ongoing attempts to redefine anatomical atlases at a single-cell level.

Rethinking transnationalism in the anthropological and genetic study of human populations: Methods of research, part I

ORGANIZER

Iris I. Clever, UCLA, USA

While historians have typically considered the history of physical anthropology in the context of the nation, more recently the global context of anthropological study has gained prominence in historical research. Indeed, the global study of human variation was fundamentally a transnational enterprise: unfolding the history of human evolution and the comparison of human types across the globe required the exchange of data and ideas beyond national borders. This panel considers the transnational travel and exchange of researchers, data, theories, and instruments in anthropological research throughout the twentieth century. Through a series of papers that explore individual, collective, and institutional efforts to construct and maintain transnational connections in the study of human variation, the panel shows how researchers strove to create knowledge that transcended political and geographic boundaries. The panel critically analyzes what transnationalism entailed in theory and practice. It highlights the manifold contexts of transnational concerns and exchanges and stresses the deeply interdisciplinary nature of anthropological research by reflecting on the practices of physical anthropologists, physicians, geneticists, biologists, physiologists, and state officials. The papers examine how these actors used transnational entanglements to their advantage, in the face of issues over nationalism, racial identity, colonization, and scientific internationalism. A particular strength of the panel is its geographical breadth, revealing the shared concerns of scientists from Portugal and Greece to Iran, India, and Japan in projecting their authority at home and abroad, and comparing the distinctive strategies and gestures they developed to navigate both national and international pressures. Moreover, the unstable and contested nature of transnational collaborations between North America and Western Europe with Asia and the Eastern Mediterranean often provoked controversy and conflict, requiring personal negotiations and professional adaptations. The papers assess these historical collaborations and conflicts by drawing on methodological and theoretical approaches from across the social sciences. Integrating archival research, oral histories, and ethnography, the authors address themes and questions posed by science studies, ethnic studies, and postcolonial studies. Changing colonial landscapes, for instance, made researching certain "vanishing" populations suddenly urgent, but also forced anthropological communities to provide international access to previously colonized spaces for fieldwork. Decolonization also prompted the rethinking of concepts such as race, tribe, and caste. Finally, the panel considers the remains of these transnational exchanges today. It reflects on the present-day use and re-use of historical anthropometric data and instruments collections, as well as the persistence of research methods that resulted from these historical transnational entanglements.

Researching and protecting a "race in fluid constancy": Narratives of physical anthropology in Greece, 1915–1950

Ageliki Lefkaditou, Norsk Teknisk Museum, Norway

Physical anthropology is an exemplary narrative science; it narrates the history of human origins and evolution, human migrations, and human biological differences and similarities. But unlike social or cultural anthropologists, physical anthropologists often eschewed first-person accounts and political statements. However, physical anthropological stories are far from straightforward descriptions of humans and anthropologists assume a role different than distanced explainers of situations. Their stories, which combine dispassionate descriptions of instruments and human bodies, statistical tables and models, photos and measurements, are politically potent. This paper explores the use of narrative in the work of the Greek physical anthropologist John Koumaris (1879–1970).

For the most part of the 20th century, he singlehandedly led an anthropological museum and society, and held the only dedicated university chair. Originally educated as a doctor, he took over the directorship of the museum after its French-schooled predecessor passed away unexpectedly. While the idea of a lineal continuity between ancient and modern Greeks – the constitutional myth of Greek national identity – remained at the heart of his investigations, Koumaris was closely associated with German physical anthropology, genetics and human heredity studies. This allegiance distanced him from the previous meticulous accumulation of anthropological body measurements and brought him closer to racial psychology and eugenics. His aim was to define and protect what he thought of as a “race in fluid constancy”. Koumaris developed understandings and practices that allowed him to survive scientific, institutional, political, and cultural transitions. The paper traces the network of scientific and popular writings, people, institutions, research tools and artefacts around Koumaris´s work and sketches out the narrative strategies he employed. The aim is to showcase the role played by narratives in the production of anthropological knowledge as a constant negotiation between national needs and transnational imperatives.

“Tiresome anthropometric affairs”: Standardization efforts in the history of physical anthropology, 1880–1950

Iris I. Clever, UCLA, USA

The global study of race required the aggregation of large amounts of data and thus international cooperation and comparison. At the dawn of the 20th century, however, there was hardly any national or international agreement on the methods of measuring bodies, skulls, and racial traits, and schools had largely developed their own approaches to physical anthropology. Many anthropologists from different countries considered this lack of unity to be a problem. Standardization of method, therefore, was a pressing concern within the discipline, a topic which has not been adequately addressed by historians thus far.

This paper focuses on the multiple attempts made to unify and standardize anthropometric techniques. It examines the international debates surrounding the Frankfurt Horizontal Plane before World War I and the efforts of the International Standardization Committee of Anthropometric Technique before World War II. The need to standardization seems obvious and one would assume that physical anthropologists should be able to agree on this. This was not the case: all sorts of political and scientific concerns and disputes surfaced when anthropologists attempted to negotiate anthropology across national borders. It is a story of resistance and controversy. Finally, the paper will reflect on the lack of standardization in early 20th-century physical anthropology in light of the current-day re-use of historic anthropometric data in studies on long-term standards of living.

Engaging with foreign science: Practicing transnationalism in late Portuguese colonial physical anthropology

Ricardo Roque, University of Lisbon, Portugal

This paper examines transnational practices and imaginaries in the context of a late form of colonial physical anthropology, so-called "anthropobiology". After World War II and until 1974, the Portuguese colonial empire stubbornly resisted international pressures for decolonization. Portugal's obstinacy in preserving and legitimating its imperial volition through visions of pluri-continental and "multi-racial" nationhood and a benign spiritual form of colonization was accompanied by an unprecedented investment in scientific research and fieldwork campaigns in anthropology or anthropobiology in the Portuguese colonies in Africa and Asia. Colonial anthropobiology then became dominated by a small but influential group of metropolitan scholars, who received official state support. In the 1950–1970s, however, trapped within the empire's geopolitical tension between isolationism and internationalism, the Centre of Anthropobiology in Lisbon struggled to keep up with the growingly international field of human biology. This paper explores how, in this historical context, Portuguese anthropobiologists managed transnationalism as an art of engagement with, and avoidance of, the threats and promises of what was foreign (estrangeiro) to the country. Anthropobiologists experienced a tension between remaining nationalistic and colonialist in character, and internationalist in their activities and networks simultaneously. Practicing transnationalism became an ambivalent gesture fed by connections as well as by segregations. Firstly, they struggled to exclude foreign physical anthropologists from direct access to fieldwork in the colonies. This aimed at building up an international authority based on monopolistic control of field data, and an exclusive sovereignty over Portuguese colonial terrains. Yet, secondly, they emulated foreign science, and eagerly sought connections and exchanges with foreign scientists. The latter, however, seemed above all as a way of capitalizing scientific authority within Portugal, less than a form of intervening in a wider international knowledge field. Hence the paper conceptualizes this mode of “transnationalism” as an inward-oriented form of engaging with foreign science as ambivalently powerful and threatening stranger.

Rethinking transnationalism in the anthropological and genetic study of human populations: Concepts of race, caste, and tribe, part II

ORGANIZER

Jaehwan Hyun, Max-Planck Institute for the History of Science, Germany

Transnational routes and knowledge transformation in the intersection of anthropology and genetics: “Race”, “caste” and “tribes” in German-Indian connections (1927–1970)

Thiago Pinto Barbosa, Leibniz-Zentrum Moderner Orient, Germany

Since the foundations of anthropology as a scientific discipline, the production of anthropological knowledge on human diversity has been done through an increasingly translocal and transnational network. The same applies to the emergence of genetics, which, in the 20th century, was very much entangled to anthropological research practices. Starting from the historical case of the Kaiser Wilhelm Institute for Anthropology, Human Heredity and Eugenics (KWI-A, 1927–1944) in Berlin-Dahlem (Germany), my current research project interrogates how knowledge in these intersecting fields, especially knowledge on human variation and with use of the notions of "race", "caste" and "tribe", has been scientifically produced and transformed through circulations in time and space. Specifically, I look at the case of Indian anthropologist Irawati Karvé (1905–1970), who initiated her scientific career through her PhD research stay (1928–1930) under supervision of German anthropologist and institute's director Eugen Fischer at the KWI-A. Later in Maharashtra, India, she undertook extensive research, among other topics, on "the racial" of different social groups such as castes and tribes, and contributed to the establishment of a biological anthropological school with a genetics-based approach. From an actor-network-theoretical understanding of science as a global network that is local at all points and shaped by human and non-human actors (e.g. Law 2006), my paper will explore the consequent key methodological and theoretical implications for the historical anthropological study of knowledge production on "race", "caste" and "tribe". My presentation draws from my current ethnographic and multi-archival in Germany and India in my attempt to follow the different actors that were central in Karvé's knowledge production (body measurement instruments, textbooks, human remains, supervisor, and Karvé herself) and their presence in today's knowledge practices in Pune. I argue that assessing the situatedness of such actors and their relationality is key to assess transnational entanglements in the production of anthropological knowledge.

From Konketsuji to Nisei: Human adaptability research and the making of Japanese Americans, 1945–1975

Jaehwan Hyun, Max-Planck Institute for the History of Science, Germany

It is alleged that the Human Adaptability arm of the International Biological Program (HA/IBP, 1964–1974) contributed to the maturation of human population biology and increased international scientific cooperation in the thematic field. Previous literature has revealed that the idea of "urgency" to preserve biological materials from and knowledge about vanishing "primitive people" was a driving force of human adaptability research. This paper adds to the literature with an analysis that focuses on anthropological and physiological research on Japanese Americans – a population that newly appeared in the twentieth century. Immediately after the end of the Pacific War (1941–1945), the "hybrid children" (Konketsu-ji) between Americans and Japanese in Japan and the second generation of Japanese immigrants (Nisei) in the US emerged as an "urgent" social and political problem in both countries. Since the 1930s, Japanese physiologists and anthropologists at Tokyo and Kyoto had defined the "hybrid children" as a threat to Japanese national integrity and a resource to test the biological improvement of Japanese's adaptation to different colonial environments through intermarriage with the colonized. By extension, they defined the Japanese-American "hybrid" as a national threat and measured their bodies to find their racial differences from the "pure" Japanese after the collapse of the Japanese empire in 1945. In contrast, American researchers, like Steven M. Horvath (1911–2007), carried out biological research on Japanese Americans within the framework of the cultural and biological adaptation of immigrants and were concerned about the physiological effect of stress caused by new environments. The paper illuminates that such different cultural interests and values were embedded in the anthropological research practices on the population in the two countries, and the US-Japanese cooperative HA/IBP program, entitled "Comparative Studies on Human Adaptability of Japanese, Caucasians, and Japanese Americans," was the place where the values and research practices were conflicted, negotiated, and entangled together.

Iran as ethnic homeland or racial crossroads: Indian and Japanese approaches to Iranian genetics

Elise Burton, University of Cambridge, UK

“The period between the early 1970s and late 1980s marked major logistical and conceptual shifts in Iranian anthropology and human population genetics. Previously, Iranian scientists collaborated primarily with European and North American anthropologists and medical researchers. Their own research interests were similarly westward-facing, dovetailing with the political concerns of the nationalist Pahlavi regime. Since the late nineteenth century, Iranian scholars had turned to the discourses of physical anthropology and Indo-European linguistics to emphasize their membership in a Caucasoid, European, and/or Aryan race. In the postwar period, Iranian geneticists preferred to collect and publish data on a homogenized “Iranian” national population to be compared to other nations, erasing or downplaying the remarkable ethnic, religious, and linguistic diversity in Iran.

This paper analyzes how these patterns changed in response to the emerging interests of Indian and Japanese geneticists in Iran as a site for anthropological research. Through close readings of scientific publications and doctoral theses, I show how educational networks and blood-sampling expeditions refashioned Iran as both a cradle of uniquely ancient, isolated ethnic groups and a “contact zone” of Caucasoid and Mongoloid races.

In the early 1970s, a team of Japanese medical geneticists traveled to northern Iran to study specific ethnic groups (Mazandarani and Gilaki) living along the Caspian Sea, with the support of Iranian colleagues from the University of Tehran. For the Japanese, this expedition was part of a large-scale research program that sampled population groups across Asia and the Pacific islands in order to identify the geographical extent of “Mongoloid” genetic traits. Their understanding of Mazandaranis and Gilakis as racially mixed ethnic groups with primarily “Mongoloid” genes clashed with the beliefs of their Iranian colleagues that these ethnicities represented “Aryan” Caucasoids.

Meanwhile, Indian anthropologists and geneticists, who studied racial and ethnic diversity in terms of endogamous groups defined by religion, caste, or tribe, initiated comparative studies in Iran, which they regarded as the ethnic homeland of groups like the Parsis of Bombay. I focus on the career of Mohammad Sharif Kamali, an Iranian anthropologist trained at the University of Pune in India. Throughout the 1980s, he worked with Iranian medical and anthropological geneticists to apply Indian approaches toward studying Iran's population, which he characterized as a conglomerate of many "ethnically distinct" endogamous groups. Today, Iranian geneticists continue to use this "ethnic" methodology of group sampling, and capitalize on the concepts highlighted by both Indian and Japanese approaches – the country's internal ethnic diversity, and its geographic location as a racial crossroads – to describe the transnational value of their research."

Moving past the naturalism-normativism dichotomy in philosophy of medicine

ORGANIZER

Brandon Conley, Virginia Commonwealth University, USA

What, exactly, is it to be ill or healthy? The question is one about which strong intuitions abound, largely convergent, but in important cases disputed; is ADHD really a medical matter, or are these simply unruly children? Are Deaf people disabled, or a linguistic minority like any other? Between 1952 and 1973, the Diagnostic and Statistical Manual of the American Psychiatric Association classified homosexuality as a mental disorder. The effort to define the concept "disease" is therefore of philosophical and clinical interest in its own right; but insofar as it affects when and where people seek or are offered medical treatment, it is also of significant moral and social importance. Francois Jacob supposedly described teleology as "as a mistress whom biologists could not do without, but did not care to be seen with in public"; in biomedicine and psychiatry, this tension between descriptive science and a sense there is some way organisms ought to be comes to the foreground. The debate over the disease concept has therefore traditionally split between normativists, who think the concept is inherently evaluative, and naturalists who think it is purely empirical. Organised around this dichotomy, however, the debate has in recent decades largely ossified into the familiar stalemate typical of "mature" philosophical disputes, characterised by increasingly complicated and qualified restatements of the major positions, and a lively trade in counter-examples and problem cases between their partisans (Griffiths & Matthewson 2016). For a philosophical debate of such genuine importance to the lives of so many, this is a most regrettable state of affairs. There is urgent need, therefore, of fresh approaches to the question, which can move past this stale dichotomy and reinvigorate the debate. Several previous attempts have been made to do so in recent years (e.g. Ereshefsky 2009, Simon 2007, Kingma 2014, and Broadbent 2018). The papers in this symposium build on these attempts in order to explore new ways of framing and understanding the debate, as well as to propose new philosophical accounts of key medical concepts which fly the nets of the old dichotomy, whether by embracing both its naturalist and normativist sides (Conley & Glackin) or by unpicking the assumptions and semantic relations that underpin them, thereby avoiding both (Fairbairn). Our exploration here will also allow us to investigate the idea that the nature-norm dichotomy, at least as it currently exists, further entrenches a variety of pernicious stereotypes about health, disease, and mental illness. In particular, a discussion of the notion of "coding groups" (Fairbairn) will prompt structured investigation into the ways in which the vocabulary of the naturalism debate is ethically, as well as analytically, problematic.

Coding groups in the mental illness literature

Francis Fairbairn, Cornell University, USA

The question "what is mental illness?" has generally been taken to have two possible answers: either it is a socially constructed phenomenon, or it is a natural one. In this literature, the term "natural" is taken to code for a group of concepts including "natural", "fundamental", "real", and "non-normative". Similarly, the term "socially constructed" is taken to code for concepts such as "social", “non-fundamental”, and “reducible”. My claim is that these “coding relationships” (or “coding groups” in my language) are such that:

1. They are especially invisible or hard to track.
2. They are often inherited from previous assumptions or views.
3. They inhibit research programs by foreclosing discussion in certain areas.
4. They perpetuate real social and epistemological harms.

On my picture, concepts within coding groups code for each other so subtly and so strongly that we tend to use them interchangeably without realizing. And yet, when we do interchange them in this way, it changes the flavor of the dialectic, sometimes radically. For example, if we end up thinking that:

1. In order to be “natural” (as opposed to socially constructed) mental illnesses must be value-free, objective, non-social … etc and
2. The natural is more robustly “real” than socially constructed

and we also think that:

1. It is ethically important to reify mental illnesses so that they are appreciated as genuine, sometimes debilitating, conditions …

… then one’s desire to reify mental illness as part of a project to make mental illnesses less stigmatized will lead one to argue that (e.g.) mental illnesses are non-social.

The upshot of my account is that mental illness should not be assessed against the categories “natural” vs “social” because these categories represent problematic coding groups. To establish this, I tie together historical analysis and conceptual analysis; the history of the debate shows the effect of social and political ideology on the requirements of success for analyses and even on the meaning of the question at stake. In this way, the debate has not just “switched” via a clean break but rather the underlying inferences/inferential ideologies are still there. Our dialectics inherit the sins of their fathers.

How to be a naturalist and a social constructivist about disease, part I

Brandon Conley, Virginia Commonwealth University, USA

The apparent conceptual connection between disease and dysfunction has been used to develop naturalistic accounts of disease, as opposed to social-constructivist and normative accounts, by serving as a tool for providing explications of the disease concept which are either non-normative, or normative in a reductive sense. However, this strategy presumes that normative judgements, including social ones, are not already part of the scientific practice of making dysfunction attributions.

I present an independently attractive framework, and some simple formal machinery, for understanding the role dysfunction attributions play in scientific practice. On this view, any arbitrary norm can serve as a descriptive point of reference for expressing causally relevant information about the system under scrutiny; however, the goals of a given discipline or research program will make some norms especially useful for doing scientific work. Given that the scientific work could, in principle, be done by any arbitrary norm, it is possible that the norm arises from social judgments. Beyond mere possibility, I argue that the goal of some sciences, including medicine, to control and manipulate, in addition to describing and explaining, is in fact best served by the kinds of social-normative judgments emphasized by normativist and social-constructivist accounts of disease. Importantly, a social constructivist account developed along the lines I suggest would count as naturalistic in the broad sense in which the label "naturalist" is used in philosophy more generally, and which motivates naturalistic accounts of disease, namely that the account is methodologically, ontologically, and epistemically continuous with the natural sciences, and the disease concept does not reduce to simply "that to which we apply the term 'disease'." For an account of disease to be naturalistic in the important sense, does not imply the concept is non-normative or non-socially grounded.

Demonstrating the full potential of this brand of naturalistic social-constructivism requires developing specific proposals about the normative judgements underlying attributions of disease, a task Shane Glackin will undertake in a companion presentation. However, I close by outlining one argument that Shane will develop in more detail, and which will serve as a base for addressing various problem cases in the literature: Our brand of naturalistic social-constructivism enjoys an advantage over rival views because it can capture the apparent explanatory power of both the selected-effect (Griffiths and Matthewson 2016) and biostatistical (Boorse 1975) accounts, but has additional explanatory resources because it includes a role for social-normative judgements. The intuitions supporting rival views can be explained by conceptions of innateness facilitating a move from knowledge about evolutionary history or statistical norms to judgements of social acceptability, or at least non-manipulability. However, showcasing the additional explanatory work social norms can do will require a concrete proposal about the relevant norms of the kind Shane provides.

How to be a naturalist and a social constructivist about disease, part II

Shane Glackin, University of Exeter, UK

By way of a "proof of concept" for the claim that a broadly naturalistic account of dysfunction not only makes space for, but positively encourages, a role for social norms, I start by outlining a simple set of socially evaluative criteria for the attribution of disease-status: a biological or behavioural state is judged to be a disease, briefly, just in case it is regarded:

1. as not representing a tolerable state of affairs; but
2. neither as representing a moral failing of the individual concerned.
3. as not being worth reorganising society so as to fully neutralise the relative impairment caused by the state; but
4. as being nevertheless worthwhile to divert resources to "correct" and/or ameliorate it.

This allows us to supplement the naturalistic account of dysfunction given by Brandon Conley in the preceding talk with a set of normative social grounds for selecting the particular subset of the broad class thus defined which are to count as diseases, in a way that accords with common intuitions about the disease-concept's extension.

This demonstrates the compatibility of naturalism and social constructivism. To show that this is not merely a coherent position, however, but an attractive one, we need to go further. I therefore elaborate and extend Brandon's closing argument. Canonical accounts of the disease concept such as Boorse's (1975) Biostatistical Theory, Griffiths & Matthewson's (2016) Selected Effect Account, and Wakefield's (1992) Harmful Dysfunction account look particularly plausible as applied to veterinary diseases, which are only rarely as controversial as human cases can be; conversely, social constructivist accounts can be difficult to apply outside the context of human societies. Our approach explains the social evaluative judgements that underlie intuitions about disease-attributions, as well as how evaluative differences underlie the clash of intuitions in problem cases. We can therefore go beyond Boorse, Wakefield, and Griffiths & Matthewson by explaining in terms of our own theory why those accounts produce intuitively plausible results, especially in "natural" and non-socialised or pre-social cases; the evolutionary and statistical phenomena they invoke do not themselves directly play a role in a proper account of the disease concept, but they do influence the way the social evaluative judgements which play a central role in our theory are made. We can also go beyond them in another way; by explaining the disease-status of conditions affecting non-functional body-parts, such as appendicitis, in the same way as other diseases, rather than by extension or disjunctive courtesy.

Regeneration across the scales of complex living systems

ORGANIZER

Frederick R. Davis, Purdue University, USA

How has regeneration been understood, defined, and utilized in scientific research at different scales of living systems, both now and in the past? This session will begin with the premise that all complex living systems maintain some capacity to repair and to maintain themselves in the face of events that cause disturbances or damage. For example, microbial communities can regenerate to achieve the same function even as species composition changes, spinal neurons in the lamprey can regenerate function even though their cellular wiring changes, and ecosystems can maintain a level of resiliency in the face of changing conditions. In all instances, while these biological systems undergo stress and damage, their parts can coordinate responses to provide repair. But do we mean the same thing by regeneration in each case? How do the regenerating parts "know" how to cooperate to make the individuals and systems healthy and whole again? How does an understanding of one level of regeneration inform the others? Is there an underlying logic of regeneration across complex living systems? These are the main questions that our speakers will address. Specifically, Jane Maienschein, introduces regeneration studies in the broad sense. She interrogates regeneration and multiple levels of biological organization: the organism, the cell, the organ, the ecosystem, and the microbiome. Xan Sarah Chacko explores the concept of seed banking as the regenerative capacity of seeds. How scientists view dormant seeds in freezers as "natural" or "artificial" shapes their notion of the role of seed banks in addressing mass extinctions, ensuring food security, and staving off loss of biodiversity. Carlos Santana examines the idea of the novel ecosystem, an ecosystem established by natural processes in the wake of anthropogenic disturbance. Finally, Frederick Davis considers the shifting baseline hypothesis, which calls for application of historical datasets to better understand population declines and ecosystem change. A better grasp of shifting baselines facilitates conservation efforts as ecologists work to re-establish species and foster ecosystem regeneration. In this session, we will present an overview and four cases that challenge and expand our thinking about regeneration – how it is perceived and what it means – across the different scales of complex living systems. This session is a part of the

McDonnell Initiative at the Marine Biological Laboratory, which seeks to bring philosophers, historians, and scientists together in order to transform the way we understand shared problems. The McDonnell Initiative is supported by the James S. McDonnell Foundation.

How images shape the concept of regeneration in microbial communities

Anna Clemencia Guerrero, Arizona State University, USA

Historians and philosophers of biology have demonstrated that images can shape what scientists think, what scientists know, and what scientists choose to study about natural phenomena. The ways that images participate in concept generation are particularly evident and consequential when scientists depend on images, and the technologies that create those images, to make any observations at all. For example, a single conceptual diagram about protein signaling determined cellular research efforts for several decades, x-ray crystallography was pivotal for cracking the structure of DNA, and electron micrographs of mitochondria inspired the first theories and experiments about oxidative phosphorylation. In creating both data and concepts about the microscopic world, scientists are often bound to the imaging technologies available. The evolution of imaging technologies, and therefore the kinds and styles of images created, likely influence the development of scientific concepts about the microscopic world.

In order to study regeneration in microbial communities, scientists rely on microscopes and the diverse images that those microscopes create. Images provide information about the state of and changes in spatial composition and gene activity of microbial species within a community. Scientists must use those images to generate concepts about the establishment, decay, and repair of microbial community structure and function. Images are simultaneously the medium through which scientists can document the processes of regeneration, as well as the lens through which they develop understanding and make theories about those processes. The kinds of information that images provide can vary greatly depending on practical factors like sample choice, sample preparation, and the type of technology used to create an image. Visual factors like scale, color, and composition are also variable carriers of information. The evolution of imaging technologies and the images created have likely have influenced and continue to affect the development of scientific concepts about regeneration in microbial communities. Since images can represent, inform, and reflect how scientists think about regeneration in microbial communities, one way to study the development, adoption, and transformation of the concept of regeneration is by examining the images that scientists used to introduce, develop, and share their concepts. This kind of analysis aims to reveal how visualization has canalized or inspired our understanding of regeneration in microbial communities, and will explore the ways that modes of visualization may affect our general understanding of the concept of regeneration in complex living systems.

Let it go: Exploring the assumptions of regeneration in frozen seed vaults

Xan Sarah Chacko, University of Queensland, Australia

The basic assumption that undergirds the concept of seed banking is the regenerative capacity of seeds. This paper interrogates the assumption that a seed frozen in a vault can be pulled out of stasis and into its lively plant form through thawing, germination, and propagation. I show that the science of seed regeneration, viability, and degeneration is contested. Scientists in seed banks around the world do not agree on the best temperature, duration, method, materials, or protocols for preparing, storing and the subsequent testing of seeds in freezers. This paper reflects on data collected during two years of archival and ethnographic fieldwork where I examined and participated in the processes that render seeds viable for storage, legible within a system of information at the bank, and valuable based on their promise of regeneration from stasis in the future. Moreover, I learned that how seed scientists conceptualise the dormancy of seeds in freezers as “natural” or “artificial” affects how they perceive and adjudicate on the seeds ability to protect and repair themselves during and after storage.

A second assumption about regeneration, or rather the lack thereof, frames the creation of seed banks as a solution to combat climate change and the ravages of biodiversity loss. The assumption is that ecosystems have been damaged past the point of regeneration and that only through salvage projects such as seed banking can the future of life, food, and plants, be guaranteed. The rise of seed banks as the solution to mass extinctions, food security, and loss of biodiversity, requires a taken-for-grantedness that the ecosystems will not regenerate on their own; Human intervention is required. Interested in why scientists were motivated to bank seeds, I studied how threats to biosecurity and ecosystemic imbalances scaffolded state and private gains by rebranding plants as genetic resources.

Restoration, regeneration, and novel ecosystems

Carlos Santana, University of Utah, USA

The famous wolf population on Isle Royale is about to die off; should we replenish it by transporting wolves from elsewhere? Most residential lots in Detroit are abandoned; should we allow nature to reclaim that land? Shipwrecks serve as habitat for marine organisms; should this discourage recovery efforts? Ecologists aiming to contribute their expertise to these sorts of questions have come up with a conceptual toolkit to sort out different types of ecosystems which have been affected by global change (Mascaro et al. 2013). A key concept in this toolkit is that of the novel ecosystem, which is an ecosystem established by natural processes in the wake of anthropogenic disturbance. Whether this concept is useful, or even coherent, is controversial (Hobbs et al. 2006; Murcia et al. 2014).

Standardly understood, a novel ecosystem can't form by restoration, because restoration is anthropogenic, and a restored ecosystem is engineered. Nor can a novel ecosystem form by regeneration, because regeneration is a return to the historical ecosystem, not a transition to a novel one.

I challenge this understanding by showing how it relies on excessively narrow interpretations of restoration and regeneration.

The first major issue is that responses to perturbances typically involve a mix of recovery of historical communities, natural adaptation, and intentional human design. Moreover, these factors aren't separable into distinct processes of regeneration, transformation, and restoration. For example, regeneration is something which can be "encouraged" (Hobbs et al. 2009) or "assisted" (Murcia et al. 2014) by intentional human activity. The process of recovery can thus be neither fully restoration nor fully regeneration but possess aspects of both. Similarly, it can be difficult or impossible to distinguish between regeneration and transformation, since whether we want to consider a system moving from one basin of attraction to another a transformation to an alternative system or merely regeneration to an alternate state of the extant system is often arbitrary.

A second issue is that talk of "regeneration" often trades on ambiguity in whether it is the community or functional processes which are regenerating. It is possible to have one without the other, as when an invader drives out historical community members but replaces them in functional networks. Potentially novel ecosystems may have regenerated in one sense but not the other, and it again becomes a matter of discretion whether we want to call the recovered system "novel."

Both of the first two issues point towards a third: whether an ecosystem is novel supervenes not only on facts internal to the system in question, but also on normative considerations. This means that arguments for conservation strategies which appeal to the concept of a novel ecosystem are at risk of being circular. For example, some argue that we shouldn't replenish that wolf population on Isle Royale, and instead let the novel ecosystem develop on its own (Mihell 2018). But since what sorts of potential states count as novel ecosystems will depend on how we think the system should be managed, this argument begs the question.

Implications of shifting baselines for species recovery and ecosystem regeneration

Frederick R. Davis, Purdue University, USA

Marine ecologists have drawn upon historical sources to examine the state of species and ecosystems. Pauly (1995) introduced the concept of shifting baselines to explain each generation of ecologists tends to accept as a baseline the stock size and species as it existed at the beginning of their careers and use that general sense to evaluate changes. By the time the next generation begins its career, populations have declined further, but the new generation of ecologists uses those numbers as the basis to evaluate further change. Shifting baselines across generations of ecologists can obscure gradual disappearance of resource species. Lack of historical perspective has deeper implications, however. Historical ecologists interpret a range of historical data using a diversity of records including paleoecological, archaeological, historical, and ecological. Such data have yielded insights into the past and present states of a variety of marine ecosystems such as kelp forests.

Regeneration across the scales of complex living systems

Jane Maienschein, Arizona State University & Marine Biological Laboratory, USA

History, Philosophy, and Regeneration Research Around 1900, studying regeneration in biology meant removing parts of individual whole organisms and watching them regrow. Sometimes the structure looked about the same and the organism seemed to function normally, and at other times, they looked quite different and functioned, but maybe in different ways. What was the process of regenerating an individual organism? What was being regenerated? Thomas Hunt Morgan, Jacques Loeb, Ross Granville Harrison, and others asked how they could study regeneration in order to understand normal development. As the twentieth century progressed and two world wars led to many injuries, the search was on to use regeneration biology to develop methods for wound repair. For this purpose, regeneration is equated with restoring function, even if the form looks different. Underlying this work are assumptions about what we mean by “generation” in the first place, and whether the “re-generation” follows the same processes, produces the same structure, and/or restores function. As details change, to what extent is the organism the same individual? What is healthy or injured; what is repair? In the twenty-first century, regenerative medicine seeks to recover spinal cord function, neural function, and other damaged function with stem cell or other therapies. What is happening biologically in each case? Then looking at a different level, what about ecosystems? Do they have a healthy form and function as individual wholes that undergo damage, perhaps from climate change, and then restoration? Is this regeneration the same kind of process as with individual organisms? What is an individual ecosystem? And what about microbial communities, whether in the ocean or making up our microbiome: is this an individual living “organism” that undergoes damage or injury and also regeneration to wholeness? Again, do we mean the same thing? This paper will explore the underlying questions and assumptions, asking how philosophical reflection and historical perspective inform and are informed by life science research.

Averages, templates and types in past and present biosciences

ORGANIZER

Abigail Nieves Delgado, Ruhr University Bochum, Germany

It is a common practice in the biosciences to develop methods that allow producing generalizations such as types, averages and templates to make sense of complex phenomena. These generalizations are an allegedly successful way to obtain a good representation of a certain group. Additionally, these artifacts are important elements in the production of scientific knowledge as they make comparisons and inferences possible. Philosophers of biology have theorized extensively on types and typological thinking in the last century, but mostly from a metaphysical point of view. In addition, the normal/abnormal dichotomy usually linked to this topic has stimulated discussions on disease, gender, race, and disability studies. This session aims to revisit these philosophical problems but from a different angle. It focuses on the methods, practices, assumptions, and consequences of making averages, and constructing templates and reference types in past and present biosciences. To do this, this session brings together scholars from different backgrounds and case studies from the history of physiology, comparative genomics and past and contemporary facial recognition techniques. The papers give special attention to

i. the different scientific practices (and their consequences) of producing averages, templates and types,
ii. the ontological presumptions and epistemological challenges of this particular way of constructing knowledge, and
iii. the construction of what is consider normal, expected and ordinary (instead of the pathological or abnormal, as done in many previous debates).

By doing so, the session seeks to illustrate the relevance of practices of producing averages, templates and types in the history of the biosciences. Additionally, the cases presented analyze whether there is a correspondence between the (unconscious or not) philosophical standpoints of scientists and the methodologies and models used in their research. Lastly, the contemporary case studies show that current developments in genomics and biometrics face long-standing challenges regarding the possibilities of producing knowledge from these particular kinds of scientific generalizations.

What is "normal"? Frederik Buytendijks reflections on 1920s animal psychology

Julia Gruevska, Ruhr-University Bochum & Friedrich-Schillller-University Jena, Germany

Frederik J. J. Buytendijk (1887–1974) was the director of the renowned physiological institute in Groningen, the Netherlands, from 1925 to 1946. In this period, he tried to establish a theory in animal psychology that methodologically pays tribute to phenomenology, hermeneutics as well as gestalt-theoretical holistic concepts yet does not abandon quantitative data collection to examine the behavior of animals. Starting from the bio-theoretical thesis that animal and environment form an organic unit (see Jakob v. Uexküll), Buytendijk set out not only to carry out explanatory quantitative analyses of living beings, but also to take into account an "understanding" perspective on their behavior given that, according to Buytendijk, living processes had to be interpreted as wholes (Ganzheit).

Considering these questions, the Dutch physiologist opened up his experimental arrangements and tried to give the animals as much freedom as possible so that they could reveal their natural behavior. In a T-maze, Buytendijk critically remarks, the animals can only move left and right; however, he considers such a situation very unusual for animals, which is why the behavior they exhibit in the experiment must also be unnatural. Therefore, phenomenological and hermeneutical methods must be regarded to be of equal value in experimental investigations. Only then can categories such as "normal" be constituted and finally serve for comparison with the "deviant".

Taking recourse to a rat experiment that Buytendijk conducted on brain-operated and non-operated rats in a critical examination of Karl S. Lashley's 1929 study "Brain mechanisms and intelligence: A quantitative study of injuries to the brain", I explore to what extent Buytendijk understands behaviorism as unreflected research that leads to misinterpretation of terms such as "normality" or "intelligence". If one does not reflect on what constitutes "normality", how can one even say what is "not normal" in the first place? According to Buytendijk, the problem of behaviorists thus is that they don't question their experimental procedures but consider animals to be merely mechanical material rather than living beings.

By looking at Buytendijk's research we get to know a very significant case in history of physiology that constantly wanted to draw attention to the fact that if we want to gain real insights, a reductionist view will not be sufficient. Buytendijk offers an alternative research program that makes this case even more interesting if we also take into consideration that we are still confronted with these questions in research today.

Cascades of comparability: “Trans-species shuttling strategies” in genomics research

James Lowe, University of Edinburgh, UK

As the human genome project drew to a close, the National Human Genome Research Institute decided to conduct sequencing of non-human mammals and primates. They intended to use data from this to assist in the ongoing annotation of the human genome. This comparative genomics approach was not new, however: it had dominated the agenda of researchers and collaborations working on the genomics of non-human animal species since the late 1980s.

I will detail how and why researchers conducting genomics research on the domesticated pig, *Sus scrofa,* made use of the more comprehensively developed data and resources available on the human, and to a lesser extent, the mouse. These “trans-species shuttling strategies”, to use a term coined by two livestock geneticists, consisted of the development of models of correspondence between the respective genomes of pig and human.

These models, which included the construction and use of comparative maps, structured the inferential relations that pig geneticists used to: identify and make use of particular primers and probes derived from human genomic research; hypothesise the existence and/or function of particular genes; and work out how to adapt particular methods to appropriately be applied to pig genomics. In the period before the availability of standard reference genomes, pig researchers were reliant on consensus maps, sequence data uploaded to databases such as GenBank, materials from institutions such as the UK Medical Research Council’s Human Genome Mapping Project Resource Centre, and mapping assignments in the literature. Once reference genomes were available, these could serve as anchors of comparability.

The use of such strategies enabled the researchers to improve the resolution and accuracy of the models mediating between the genomes of the two species, in some cases by establishing new biological knowledge structuring which inferences could be made, and which were invalid.

This was not only a one-way process. Experiments could, after all, be conducted on pigs that would not be allowed on humans, and this could generate data and knowledge that could then, through the very means of inference developed to make use of the resources of human genomics, be used to inform human geneticists and genomics researchers.

Moving beyond the discussion of the discernment of the relations between the genomes of two species, I conclude by elucidating what I term “cascades of comparability” – networks of inferences between the genomes of multiple species, which allow data, resources and knowledge to cascade from better-characterised species, down to progressively less well-characterised species. This was able to occur despite reference genomes for different species being constructed differently, representing different aspects of the variation and variety within given species, and even having different meanings for the communities that work on these organisms.

Understanding genomics in the light of the centrality of shuttling and cascading practices for non-human animals suggests that scholars cannot capture the research processes that result in the construction of genomes, and therefore the products of that, if research into an individual species is taken in isolation.

From Galton to Facebook: Producing facial types in the study of human variation and identification

Abigail Nieves Delgado, Ruhr University Bochum, Germany

The introduction of anthropometric techniques to anthropology and criminal identification in the late 19th century led to the production of types and averages that, since then, have become central in the study of human variation and individual identification. These generalizations are usually generated from a group of individuals that are assumed to share relevant characteristics. The ways to produce these generalizations as well as the objectives and consequences of their use are quite diverse. Equally varied are the ontological assumptions underlying the production of specific types, averages, and templates. Among the facial types that are long lasting in the history of anthropology and identification are those related to racial and gender belonging. In these cases, different ways of defining normality are at play. Recent examples of these practices are algorithms that allegedly can predict the sexual orientation, origin, or aggressive behavior from the facial traits of a person.

This paper explores three cases in the history of identification techniques in which different methodologies of producing types and averages from faces are used:

1. The composite portraits produce by Galton to identify the typical traits of a group of persons. Galton devised a methodology to produce an average face from the exposure of a group of photographs. To him, this process was analogue to the perceptual processes of the mind.
2. The "face space" theory of perception proposed by Valentine in 1991. Similar to Galton's averages, the "face space" theory argues that the mind perceives faces by creating a "space" where all the faces seeing during a person's life are organized. In this space, the most common face, the norm, is located at the center of the space, while the rarest faces are at the edges. And
3. norm-based and exemplar-based facial recognition algorithms, such as DeepFace (Facebook), whose development is influenced by the "face space" perception theory.

Despite the temporal distance and differences among these three cases, they allow to understand the role the construction of types has played in the history of facial recognition. Moreover, facial types and their implicit normality parameters have a direct effect on the knowledge produced about humans and the ways we categorize ourselves. Finally, the cases presented here help understanding why (and in which way) traditional and often problematic categories such as race, gender and the normal are still relevant to contemporary identification practices.

Natural selection: Revisiting its explanatory role in the development of evolutionary biology, part I

ORGANIZER

Richard G. Delisle, University of Lethbridge, Canada

It is an entrenched belief that the 1930–1960 period saw the rise of the Evolutionary Synthesis, an event E. Mayr (1980) and S.J. Gould (1980) characterized as organized around two main explanatory components:

1. gradual evolution is explained by small genetic changes (variations) oriented by natural selection, a process leading to adaptation;
2. evolutionary trends and speciational events are macroevolutionary phenomena merely explained by the extension of processes and mechanisms occurring at the previous microevolutionary level.

On this view, natural selection holds a central explanatory role in evolutionary theory, one that apparently reaches back to Charles Darwin's *The Origin of Species.* This understanding gave rise to a historiography focused on a "mechanism-centered" view of the development of evolutionary biology, excluding other important explanatory components and relations. The contributions presented in these sessions constitute an invitation to consider an alternative historiography which favours a more complete and multidimensional interpretation. Although most evolutionists incorporated natural selection into their explanations, its function varied greatly from one scholar to another, even among so-called Darwinians and neo-Darwinians. For instance, Richard Delisle argues that working our way through Charles Darwin's rhetoric in *The Origin of Species* shows natural selection to be secondary in terms of its explanatory role. For her part, Emily Herring holds that the explanatory role of natural selection was sometimes exploited by Darwinians (J. Huxley, Th. Dobzhansky, R. Fisher) and non-Darwinian alike through the common mediation of Henri Bergson's understanding of "creative evolution", thus revealing the philosophical underpinnings of evolutionary views which extend beyond a narrow view of science. In a similar spirit, David Ceccarelli focuses on Henry Fairfield Osborn's efforts at generating an evolutionary synthesis that recasts natural selection in a broad synthesis, one which blurs the historiographical lines between the so-called "Eclipse of Darwinism" and so-called "Evolutionary Synthesis." In Alex Aylward's contribution, Ronald Fisher's understanding of natural selection is expanded to encompass an idea of "selection" that goes beyond evolution itself, thus highlighting the narrowness of our current presentist view of Fisher. Georgy Levit looks into Bernhard Rensch's "selectionism", one that makes sense only as an outer explanatory level whose core is to be found in the universal worldview proposed by Theodor Ziegen.

Natural selection as a (mere) auxiliary hypothesis in Charles Darwin's *The Origin of Species*

Richard G. Delisle, University of Lethbridge, Canada

The notion of "natural selection" appears in *The Origin of Species* (1859), implicitly or explicitly, on nearly every page. This fact seems to convey definitive support for the received view that Darwin placed it at the explanatory core of a theory of evolution. This paper will contest this assumption, which is inherited from a "mechanism-centered" view of science. As much as Darwin attributed an important role to natural selecction, he could not but mitigate its explanatory function, by applying it against a series of different and contradictory factual and conceptual backgrounds, thus depriving it of a central position.

In order to build our case, it will be necessary to work our way through the three main explanatory layers contained in *The Origin of Species,* two of which are direct contributions to Darwin's rhetoric.

Layer 1: A somewhat superficial reading presents a theory of biological evolution organized around a causal explanatory core, giving meaning and unity to apparently unrelated disciplines. This theory leaves the reader with the impression that it is devoted to explaining a unified tree of life fully open to all evolutionary manifestations under the conceptual tool of the strong contingency thesis.

Layer 2: A more careful reading shows a theory designed to put evolution in a pan-divergent straitjacket, with the dual principle of divergence-gradation at its irrefutable explanatory core, one that is surrounded by a protective belt of flexible and auxiliary explanatory variables composed of geographical distance, geological time, taxonomic level, and amount of selective pressure. This argumentative layer jettisons any pretence of explaining universal evolutionism in all its manifestations with the help of the strong contingency thesis, except under a rhetorical guise. Rather, the evolutionary process is simplified to fit a segmented tree of life organized around nearly permanent and stable classes and phyla.

Layer 3: A more careful analysis still sees Darwin as overwhelmed from all sides with a wide array of evolutionary phenomena, often described by himself, and which his evolutionary theory is powerless to synthesize. At that particular explanatory level, Darwin fails to give meaning to evolutionary complexities such as: packed reproductive networks, sustained directional and progressive trends, the rise of analogical forms, reticulate evolution, random evolutionary walks, ancestors without apparent descendants, and the exhaustion of the evolutionary drive implicit in his theory. For Darwin as for others, evolutionary biology proves to be an area too complex to be reducible to a mere mechanism-centered theory.

Creative evolution and natural selection: Darwinian and Anti-Darwinian Bergsonisms in 20th-century biology

Emily Herring, University of Leeds, UK

In 1907, French philosopher Henri Bergson weighed in on one of the burning issues of the day, biological evolution. With *Creative Evolution,* Bergson, who was already well known among philosophers, was propelled to international fame and his philosophical ideas about life were discussed in most intellectual and scientific circles. In this book, Bergson argued that evolution was creative, that is, non-deterministic and non-teleological. In other words, he saw evolution as producing absolute, unpredictable novelty. He also argued that mechanistic theories of life misrepresented life. Among these mechanistic theories Bergson counted Darwinian natural selection. It is therefore unsurprising, given Bergson's popularity and his anti-Darwinism, that several anti-Darwinian biologists integrated some of Bergson's ideas about evolution in their own arguments against natural selection. Among these thinkers were British geneticist Arthur Darbishire and botanist Agnes Arber, as well as the fiercely anti-Darwinian French neo-Lamarckian zoologists Pierre-Paul Grassé and Albert Vandel. More surprisingly perhaps, Bergson's nondirectional vision of evolution provided several neo-Darwinians of the early 20th century, such as Julian Huxley, Theodosius Dobzhansky and Ronald Fisher, with theoretical tools allowing them to counter the teleological ladder model and drive home Darwin's original message. Evolution by natural selection, according to these thinkers, was creative in a Bergsonian sense, meaning that it brought about absolute novelties and did not follow a predetermined plan nor result from deterministic causation.

In this paper I will present and compare the different ways in which Bergson's notion of creative evolution was used by 20th-century biologists to both attack and defend Darwinian natural selection. I will challenge the common misconception that 20th-century neo-Darwinism was a purely mechanistic and reductionist enterprise. To adhere to the theory of natural selection did not mean to adhere to a materialistic vision of the universe. The aforementioned neo-Darwinian biologists and their anti-Darwinian opponents shared similar metaphysical premises such as a hierarchized vision of the cosmos and the Bergsonian notion of creative evolution. Therefore, by taking the biological appropriations of Bergson's ideas seriously, I will shed new light on some of the philosophical motivations of 20th-century biologists and, more widely, on the complex interplay between science and philosophy.

Recasting natural selection: Osborn and the orthogenetic view of life

David Ceccarelli, University of Rome Tor Vergata, Italy

Historians have almost overwhelmingly considered Henry Fairfield Osborn (1857–1935) an authority of twentieth-century American science. As the foremost paleontologist at Columbia University and President of the American Museum of Natural History of New York, Osborn was, historian Brian Regal stated, "second only to Albert Einstein as the most popular and well-known scientist in America." Behind his political and institutional clout is the parabola of a scientist whose work embodied the complexity of the debate in evolutionary biology at the turn of the century. Considered to be the leading proposer of orthogenesis in American vertebrate paleontology, throughout his career Osborn denied natural selection the power of producing fossils "trends", and rather explained evolution as the result of the use-inheritance theory, organic selection and internally-directed variations. In many ways, Osborn's theoretical shifts reflected all the disputes that characterized the so-called "Eclipse of Darwinism". At the same time, his late-career effort towards a synthesis among different evolutionary factors and approaches seems a noteworthy aspect of his work too often minimized. In this regard, this paper will explore the research agenda in evolutionary biology that Osborn outlined between the 1910s and the 1920s. In particular, we will consider how Osborn aimed at

a. overcoming the specialization of biological studies at the turn of the century through a renewed holistic approach in life sciences;
b. outlining a synthesis (the theory of Tetraplasy) among all the evolutionary factors proposed in the years of the so-called eclipse of Darwinism;

c. recasting the role of natural selection within an orthogenetic view of life.

We expect this analysis could help us rethink the contribution of non-Darwinian traditions as well as question the narratives of the pre-Synthetic evolutionary studies advanced by the architects of Evolutionary Synthesis. Far from dismissing Osborn's ideological refusal of Darwin's view of evolutionary contingency, we will try to highlight how many historiographical accounts have lost sight of the complexity of Osborn's research agenda, as well as of the fact that orthogenesists tried to provide solutions to the outstanding issues raised by the neo-Darwinian paradigm between the two centuries.

Natural selection: Revisiting its explanatory role in the development of evolutionary biology, part II

Was R. A. Fisher a selectionist?

Alex Aylward, University of Leeds, UK

For many, the question serving as my title will appear to have an obvious answer: Yes! Indeed, for several writers, R. A. Fisher (1890–1962) was not simply a selectionist; he was the arch-selectionist of last century. In this talk, however, I will suggest that things aren't so simple. When historians label Fisher as a "selectionist", they assume that he was attempting to provide an account of evolution (in general), and that his account was one in which selection dominated, to the exclusion of other evolutionary causes. I will argue that this is a mistake. If so, it is a long-standing one. Sewall Wright remarked in his 1931 review of *The Genetical Theory of Natural Selection* that "Dr. Fisher's conception of evolution is pure Darwinian selection." In saying so, Wright was misconceiving the task Fisher had set himself. Fisher began his book with the words, "Natural Selection is not Evolution." I will suggest that this sentiment was true for Fisher in at least two ways. Selection was both narrower and broader than

Evolution. The former is likely a more familiar notion. "Evolution" includes organic change brought about by a host of causes besides selection, which is but one aspect of the evolutionary process. His correspondence and lesser-known writings demonstrate that he was wise to the diversity of causes of biological change.

This leaves us with the question of why he devoted so much effort to studying selection, to the neglect of other putative evolutionary causes. The answer is not, as the traditional thinking goes, that Fisher thought selection was the only cause of evolutionary change. My suggestion as to why Fisher was so enthused by Natural Selection relates to the second sense in which "Natural Selection is not Evolution"; namely, that Natural Selection is broader than Evolution. Selection was, for Fisher, more general than the historical fact of Evolution. He saw selection not as "merely" a biological process; because of its generality, selection could be understood independently of the particular material upon which it happened to work in any one case; something which Fisher viewed as a great strength. Fisher thought about selection as distinct from the issue of evolution in general. In studying him historically, we must endeavour to do the same. As well as providing an illuminating perspective on Fisher's thinking, this approach also highlights the way in which historians tend to project present understandings of the nature of – and relations between – natural selection and evolutionary biology onto past thinkers, including those who pre-dated such configurations.

Theodor Ziehen's (1862–1950) philosophy for Bernhard Rensch's (1900–1990) modern synthesis

Georgy S. Levit, Kassel University, Germany

Theodor Ziehen was a prominent German psychiatrist and psychologist and a marginal philosopher of the first half of the 20th century, who developed an exotic subjective-idealistic theory based on quasi-empirical psychological arguments. Nevertheless, Ziehen's philosophy became influential in German biology, first of all, due to his direct and very strong impact on Bernhard Rensch. Towards the end of the 1930s, Bernhard Rensch turned from Lamarckism and orthogenesis to selectionism and became one of the key figures within the Modern Synthesis. Being a Darwinian selectionist at the purely empirical-descriptive level, Rensch became a controversial philosopher, whose claims went far beyond the conventional Darwinian "biophilosphies". Moreover, Rensch's "philosophy" wasn't a Sunday-occupation of a "scientist", but became an integral part of his theoretical system as a framework and foundation for his applied scientific methodology. Both parts developed tightly interconnected and interdependent. I demonstrate the role of Ziehen's philosophy within Rensch's theory and argue that Rensch's selectionist turn would be impossible without metatheoretical presumptions underlying his biological theory. In other words, his biological selectionism represents the outer level of his theoretical system at the core of which was a universal worldview constructed under the influence of Theodor Ziegen.

Is organismic agency a mere heuristic?

ORGANIZERS

Hugh Desmond, KU Leuven, Belgium
Philippe Huneman, CNRS, France

Stags lock antlers to gain access to mates. Arctic poppies rotate and track the sun in order to maximize solar exposure. Bacteria swim up a sucrose gradient in order to get better access to the source of sucrose. Upon detection of predators, a vervet monkey may give an alarm call, in order to help others (and at potential cost to itself). Such "agential explanations", where organismic behavior is explained as purposefully produced by an agent, are habitually used across ethology and other biological sciences. Yet, the received view on organismic agency has long been that it is a mere heuristic: organisms are only represented as agents because of explanatory expedience, and instead are bundles of traits shaped by natural selection (cf. Lewens 2007). The view finds powerful expression in behavioral ecology, which explicitly operates with what is called the "maximizing agent analogy" (Grafen 1984), where the behavior exhibited by organisms is assumed to be explainable by means of a process of natural selection, maximizing inclusive fitness. Consequently, a lot of philosophical work on the concept of organismic agency has focused on issues concerning the received view, especially on the structural parallel between evolution by natural selection and rational deliberation (cf. Martens 2016). In recent decades a more robust approach to organismic agency has become increasingly influential. Some ethologists have explicitly called for a focus on whole organisms (Bateson 2005). A deepened understanding of gene-regulatory networks has undercut the view of organisms as bundles of traits (e.g. Müller 2017). The niche construction perspective holds that organisms do not simply passively undergo evolutionary processes, but are themselves a cause of adaptive evolutionary change (e.g. Odling-Smee et al. 2003). Finally, philosophers have developed accounts of agency and have explored the wider consequences for how we understand evolution (e.g. Walsh 2015). In this symposium, we focus on the fault line between these two views on organismic agency, and seek to enquire into the reasons, if any, why organismic agency should not be considered an explanatory heuristic. Some questions we consider are: What precisely is to be gained by viewing organisms as agents? Under what conditions may agency be indispensable for explaining an organism's behavior? Can agential explanations always be replaced by mechanical and/or selectionist explanations?

Agency and environmental novelty

Hugh Desmond, KU Leuven, Belgium

Can explanations of organismic behavior dispense with agency, in favor of explanations referring only to physiological mechanisms shaped by natural selection? The importance of the environment is often overlooked in this question. Explaining a behavior as selected for certain effects assumes a selective environment that was both common to all individuals in the population and to successive generations (cf. Brandon 1990). Yet, organisms encounter environmental novelty all the time: how does this fit in?

In this paper, I argue that it does not: if an organism produces an adaptive behavior in a novel selective environment, then this must be explained as an agential behavior. Novelty here means different selection pressures, and I argue that if an organism **O**'s behavior **B** was selected for in selective environment **E**, but that **O** produces an adaptive behavior **B*** in a novel selective environment **E***, then this must be explained as agential. This is a conceptual criterion for the indispensability of agency.

I then develop this argument further through an objection, namely that it is difficult to establish environmental novelty in a way that is not dependent on how the environment is described. For instance, if **O** produces an adaptive behavior in **E***, one could object that this is due to some cue **C** that is common to both **E** and **E***. Behavior **B** was not selected for because cue **C** was present in **E**, and thus **E*** does not represent a novel selective environment. While I argue that this objection does not threaten the core proposal, it has interesting consequences for the separate question of whether agency can be considered robustly real, because the objection suggests that the presence of agency depends on the grain at which environments are described. I finish by discussing whether there are privileged grains of description.

A matter of priorities: Evolution, biology, and agency

Denis Walsh, University of Toronto, Canada

Evolutionary biologists typically treat agency as a dispensable heuristic device. Evolutionary models of behavior, for example, often seek to demonstrate that the strategies that evolve are those that would be chosen by a rational agent whose objective was to maximize inclusive fitness. In these contexts, organismal agency plays no ineliminable explanatory role (indeed, I argue, no explanatory role at all). It simply serves as a comparator, intended to show that evolutionary processes can produce outcomes that rational fitness maximisers would choose. As such, the strategy carries no ineliminable commitments to organismal agency. Innocuous as it appears, this strategy depends upon certain metaphysical assumptions about the relation between what I shall call “evolutionary” and “biological” processes. The assumption is evidenced most clearly in the so-called “phenotypic gambit”. In particular, the strategy presupposes a causal and explanatory priority of evolutionary processes over biological processes. I argue that recent empirical and philosophical work in evolution suggests that the presumptive primacy of evolution over biology is mistaken. I argue, instead, for the primacy of biology over evolution – that is to say that biology is metaphysically and explanatorily prior to evolution. It is in this context that the indispensable role of organismal agency becomes apparent. It is not the case, contrary to the received view, that organisms are ersatz agents because adaptive evolution is optimizing, rather, it is the case that adaptive evolution is “optimizing” because organisms are real agents.

Agency, selection and adaptation: Finding a middle way

Tim Lewens, University of Cambridge, UK

What is the relationship between adaptation, selection and agency? Some say selection is the only explanation of adaptation, some say it is never the explanation of adaptation, and some suggest it is sometimes the explanation of adaptation. For example, Futuyma (2017) has recently re-asserted an old adage of synthesis biology: “Directional or positive natural selection is the only known cause of adaptive change”. Charlesworth et al (2017) have made a similar claim: “allele frequency change caused by natural selection is the only credible process underlying the evolution of adaptive organismal traits”. They are reacting to a more pluralist suggestion from proponents of the extended evolutionary synthesis, who insist that: “the burden of creativity in evolution (i.e. the generation of adaptation) does not rest on selection alone” (Laland et al 2015). Meanwhile, Denis Walsh (2000) has hinted that perhaps selection does not explain adaptation at all: "The source of adaptation is the generic properties of self-organisation of individual organisms."

In this talk, I use the comparatively uncontroversial example of cultural evolution to show what it means to say that agency can explain adaptation in way that is not pre-empted by selection. I then move on to suggest ways in which other exploratory developmental processes can explain adaptation in analogous ways. While this shows that selection does not always explain adaptation, it leaves open the question of whether selection sometimes explains adaptation. In the final section of the talk I argue that Godfrey-Smith's (2013) account of how selection achieves this – which involves an appeal to Malthusian struggle – needs to be re-worked.

Cultures of care in animal research

ORGANIZER

Michael R. Dietrich, University of Pittsburgh, USA

The presentations in this session draw on a range of cases from historical and contemporary research to consider how cultures of care are and have been constituted in scientific research involving animals. Greenhough and Roe's enthographic investigation of animal technicians in UK universities contextualize the interplay between animal and human welfare. Burns' analysis of transparency in Australian animal research committees considers the effectiveness of animal regulation in university contexts. Dietrich and Crow's historical analysis of research on developmental chimeras locates the conditions under which chimeras became ethically objectionable.

Culturing care: Insights from the laboratory animal house

Beth Greenhough, University of Oxford, UK
Emma Roe, University of Southampton, UK

Laboratory animal science offers arguably one of the most challenging and certainly controversial forms of human-animal relations in the Anthropocene, and as such has formed the focus of intense moral concern and regulation within the UK. This paper draws on longitudinal ethnographic research and in-depth interviews undertaken with junior laboratory animal technicians in UK universities between 2013 and 2015, as well as insights from interviews with key stakeholders in laboratory animal welfare. We consider how within and through the space of the animal house, different notions of care are enacted alongside practices which inflict animal harm and suffering as permitted within the limitations of research protocols. These notions of care range from the pervasive and enduring influence of Russell and Burch's (1959) 3Rs (reduction, refinement and replacement) for animal welfare, to a growing emphasis on professionalism and standards framed as a "culture of care", to concerns over the emotional labour and burden carried by laboratory animal technicians, to the individual response-abilities (after Haraway 2008) enacted by animal technicians in the course of their day-to-day care work, to the challenges presented by anti-vivisectionist activism. In contrast to existing discourses within both geography and critical animal studies, which juxtapose the instrumental labour of caring for and the ethico-political will to care about, we offer a more expanded and multiple understanding of care. We argue that practices of care and responsibility that seek to address both animal and human welfare needs' within the laboratory animal house emerge in multiple forms (after Mol 2002); sometimes with interspecies complementarity (where human and animal wellbeing coincide) at other times contradictory (where the goods of animals, humans and scientific practices diverge), and always with implications for how we might conceptualise and practice human and laboratory animal welfare in the future.

Keeping animal research practices in Australia honest: A discussion of transparency, translation and replacement in animal research

Karina Burns, University of Adelaide, Australia

This paper aims to draw together a number of themes that have emerged from my research, centring around the future of animal research in Australia. The concept of transparency within animal research practices is a hotly debated and contentious issue both within Australia and internationally. Transparency in research refers to the flow of information from the scientific community to the broader public. This may include the availability of information on practices used in animal research, the species and number of animals used, the husbandry and housing practices, or the aims and anticipated value of the research. There is also debate in the literature around the translation of findings from animal research to human clinical outcomes. Shanks and Greek (2009) and Knight (2011) have critically evaluated, and in the case of Andrew Knight, conducted quantitative research addressing the issue of translation, articulating in detail the problems associated with using animals as models for human disease and for carcinogenicity and toxicology testing. Finally, the framework of "the 3Rs" (Russell & Burch, 1959) within the setting of modern animal research raises new questions. The construct of "replacement" has given rise to debate, both in how this principle is applied within a regulatory setting, and its connection to the development of non-animal models in research. While the structure of animal research regulation aims to protect the welfare of research animals, it has been suggested that these systems in fact enforce the instrumental use of animals. There is an interplay between these discussions when appraising the current state of animal research in Australia and considering future directions. These discussions raise the questions of whether current practice of animal research is valid, and, even if it is, how to continue to improve welfare standards by communicating practices and outcomes.

Creating chimeras: Ethics and monster-making in developmental biology

Michael R. Dietrich, University of Pittsburgh, USA
Nathan Crowe, University of North Carolina, USA

Early twentieth century developmental biologists were captivated by the intricate and complex process of transformations that led from a fertilized egg to an adult animal. Their research faced a severe problem though: how to see the details of this process in embryos that reveal internal differences to outside observers. To visualize development, biologist, such as Hans Spemann and later Nicole Le Douarin, created trans species chimeras first in amphibians and then in birds. These chimeric monsters exploited the plasticity of early development to create visual difference that make the observation of development possible. As fantastic as these chimeras were, they did not become the subject of ethical controversy until nuclear transplantation became feasible and human-animal chimeras became a consideration. The transition from chimera as fantastic creation to worrisome monster seems to hinge on both ideals of human control and the animal-human boundary. I this paper we will trace the trajectory of developmental chimeras from epistemic objects to ethical objects.

Articulating ancestors in the molecular age, part I

ORGANIZER
Michael R. Dietrich, University of Pittsburgh, USA

This double session will explore ways in which the articulation of ancestors in an evolutionary context have changed with the introduction of molecular data. Blending historical, philosophical, and sociological forms of analysis, the papers in this session will critically engage with the processes of inferring ancestry, the challenges of visually representing ancestry relationships, and the historical and conceptual changes wrought by the molecularization of ancestry.

Visualisation, inference and extending the meaning of "genetic" from "related by heredity" to "related to genes and genomes" in medicine

William Leeming, Ontario College of Art and Design University, Canada

The number of diseases identified as being “genetic” climbed steadily through the second half of the 20th century in relation to the increasing number of visualisation strategies being used to diagnose “genetic diseases”. In this paper I examine how medico-scientific reporting of genetic diseases permitted scientists in a wide range of fields to manipulate and extend the meaning of “genetic” in medicine from “related by heredity” to “related to genes and genomes”. Broadly speaking, it is important to understand that there are a number of different visualisation strategies that have been utilised to diagnose genetic diseases. It is also important to understand that rather than overtaking or replacing one another the strategies accumulated over time and have complemented one another. Variations of the graphic depiction of family histories used in the first half of the 20th century for the drawing of pedigrees, for example, continued to be used alongside a variety of new visualisation strategies in the second half for representing chromosomal anomalies and genetic metabolic disease and, subsequently, “new genetics” methods of analysis and large-scale automated genomic sequencing. Nonetheless each strategy has involved independent rendering practices which attempt to integrate the individual and aggregate properties of laboratory data. In this paper I trace how scientists devised new typological systems of thinking built on monosemic meanings attributed to sets of graphemes. These have been used to construct process models for framing the approximate regularity and uniformity of something proximal in the sense of presenting genetic/genomic reconstructions of situated loci for genes on chromosomes and points of origin of disease causality. At the same time, in the context of the growth of “medical genetics” as a service specialism, these process models have involved levels of amalgamation and unity among scientists working in a wide range of fields.

Depicting simultaneously similarity, diversity, ancestry, and admixture?

Peter J. Taylor, University of Massachusetts, USA

Can any depiction of genetic relationships among humans allow simultaneously for similarity, diversity, ancestry, and admixture (i.e., groups that had split mixing again)? I asked this question while puzzling over the messages conveyed by diagrams from the work of Tishkoff and collaborators on genetic variation among humans in and out of Africa. In this talk I present explorations of alternative depictions of human genetic variation keeping my initial question in mind. By the end I will have prepared the ground for an assertion that the very methodology of generating and depicting human ancestry privileges a racialized view of human diversity.

Dynamic homology and circularity

Ariel Roffé, University of Buenos Aires & Universidad Nacional de Quilmes, Argentina

A classical problem in the philosophy of systematics is the alleged circularity in the determination of homologies. It is held that not every trait is useful or informative for recognizing phylogenetic relationships, but only traits that are homologous are. Thus, homologies have to be identified prior to the beginning of phylogenetic analysis itself (i.e. detection of homologies is implicit in the construction of the data matrix that functions as input to phylogenetic analysis). On the other hand, homologies are usually defined as traits that are derived from a trait in a common ancestor, which implies that phylogenetic relationships (and thus phylogenetic analysis) have to be established before homology recognition can take place.

An also classical (by now) solution to this problem consists in distinguishing between two concepts of homology. Primary/topographical/hypothetical homologies are traits that are similar in their structural (topographical or compositional) features, and are recognized prior to phylogenetic analysis by using the classical Owenian criteria (or by multiple sequence alignment for molecular traits). Secondary/phylogenetic homologies or homogenies are traits that are derived from a trait in a common ancestor and are recognized via phylogenetic analysis. These analyses will typically reveal that not every primary homology is a secondary homology, since they usually result in some convergence among structurally similar traits being present (i.e. primary and secondary homology concepts tend to have different extensions).

Beginning in the mid-1990s, a new methodological framework for the detection of homologies has emerged, called the “dynamic homology” approach. It initially came about for molecular traits (although it has now been extended to morphological traits as well). The novelty consists in the fact that sequence alignment takes place during tree search and not prior to it, resulting in different alignments for different trees. This blurs the line between primary and secondary homology concepts, and proponents have indeed suggested that we should get rid of this distinction.

Although these techniques have potentially groundbreaking consequences for the circularity debate and its standard solution, their philosophical significance for this debate has been mostly overlooked (especially by philosophers). This presentation is an attempt to examine the consequences of the dynamic homology approach for the circularity debate. I will hold two theses. First, that even if the proponents were right and the distinction between primary and secondary homologies had to be discarded, there would be no reason to worry about circularity within their approach. And second, that the idea that this distinction makes no sense is incorrect, because dynamic analyses still require a data matrix that is generated by applying criteria that are prior and external to the analyses themselves.

Articulating ancestors in the molecular age, part II

The “microbialization” of ancestry: Culture collections and the chemotaxonomically modified “tree of life”

Alexander Waszynski, Technische Universität Braunschweig, Germany
Nicole C. Karafyllis, Technische Universität Braunschweig, Germany

This paper explores

1. fundamental mid-20th century shift in the understanding of ancestry on the microbial-global scale, and
2. the role of microbial collections as material preconditions for this process, exemplified by the history of the West-German microbe bank DSM and its changing knowledge orders and techniques.

The shift is signified by the debated terms prokaryote, archaebacterium and, latest, proteobacterium, all of which denote origins of life in the microbial world, though different ones. The endosymbiont hypothesis (Margulis 1967; 1970) and the introduction of the "urkingdom" of archaebacteria (today: Archaea) by means of chemotaxonomy, i.e. sequencing and comparing the 16S-RNA of ribosomes for genealogical purposes (Woese/Fox 1977; Woese 1981), suggested a bacterial origin of life on Earth. A third line of thought roots in earlier photosynthesis research by means of purple sulfur bacteria. In consequence, the concept of a "general microbiology", promoted by biochemists and microbial photosynthesis-researchers C. B. van Niel and R. Stanier, turned up as a new fundament for biology; specifically for a biology aiming to integrate systematics, ecology and physiology into a narrative that started from the very beginning of life on the planet. At the same time, microbial culture collections turned into world models as material reference systems.

Within the deeper layers of these universalization processes, frictions occurred (and still occur) that can be related to the specifity of the chosen model organism and the techniques used for its analysis and cultivation. While Margulis' hypothesis aimed at explaining the genesis of higher eukaryotes (that is: "us"), Woese's methodology loosened this link: archaebacteria, astonishingly resembling eukaryotes more than prokaryotes on the molecular genetic level, were suggested as potential precursors of every form of life. Noteworthy on the level of material objects: Margulis linked the eukaryogenesis to the cells of oxygenic organisms and their organelles capable of photosynthesis, thereby mainly relying on ultrastructural analysis by electron microscopy. By contrast, Woese and Fox used ribosomal

RNA sequencing, mainly of the smaller subunit (16S). Proclaiming this RNA as evolutionary conservative, they found methanogenic bacteria to be a probable “common ancestor” (Woese/Fox 1977, 5090). At close look, both approaches do not unveil the origin of “us”. They rather grounded the academic battlefield regarding the question, if (chemo) lithotrophy or (photo)autotrophy was the original mode of survival.

Going back to origins implied covering all forms of life in their prehistoric depths, including geological shifts in atmospheres, light conditions and nutrient availability. The microbiology of the 1950/60s saw a planetary framed interest in microbes able to metabolize H_2S and CH_4, in general: to survive under anaerobic life conditions. For microbial collections, not only taxonomical frictions but also technical challenges of isolation and cultivation – from sulfur bacteria to extremophiles – were on the agenda. Around 1970, collecting microbes (incl. microalgae) was not for medical, agricultural or biotechnological purposes only anymore, but also meant to gather potential witnesses of the archaic past. It profited from ambitions to centralize and crosslink culture collections all over the world (cf. Iizuka/Hasegawa 1970). One of the hubs became the newly founded West-German Deutsche Sammlung von Mikroorganismen (DSM; German Collection of Microorganisms) and its two professoral actors: microbiologist Hans Günter Schlegel (author of *Allgemeine Mikrobiologie,* 1969ff.), an expert in methanogens and “hydrogen bacteria”, and botanist Otto Kandler, a cell-wall specialist. The latter established, together with Carl Woese and others, the concept of archaebacterium, leading to the idea of a Three-domain phylogenetic system.

(Re)producing mtEve: Recognition work in the Wilson Lab

Marina DiMarco, University of Pittsburgh, USA

In their 1987 *Nature* publication, “Mitochondrial DNA and Human Evolution,” Rebecca Cann, Mark Stoneking, and Allan C. Wilson established a new reconstruction of human evolution on the basis of differences in mitochondrial DNA among contemporary human populations. The phylogeny they established supported an account of human origins that posited an African common mitochondrial ancestor for all human mitochondrial DNA (mtDNA) lineages, and Cann et al.'s reconstruction became known as the "Out of Africa" hypothesis. Since mtDNA is inherited exclusively through the maternal line, the common ancestor who was first branded African Eve later became known as Mitochondrial Eve (mtEve, for short). mtEve came to figure prominently in establishing both the primacy of mtDNA and the reliability of molecular anthropological inference more broadly in competition with archaeological explanations. She became a celebrity in the popular imagination of human origins.

How did Cann, Stoneking, and Wilson come to know mtEve? How did social, material, and epistemic work align to produce and reproduce ways of knowing mtEve not only in the material world, but also the deep past? In this paper, I offer an account of the scientific collaboration that produced mtEve, with particular attention to the epistemic, material, and social elements of scientific change. This analysis highlights the importance of recognition work in the Wilson laboratory: the work of aligning social, material, and epistemic conditions to identify and solve what Fujimura (1987) calls the "do-able problems" of scientific knowledge production. I argue that recognition work resists discretization: we should not consider these kinds of work in addition to epistemic or intellectual labor, but rather ought to recognize the relationships among these ways of working in virtue of their integration and alignment. Attention to the alignment (rather than the inventory) of these elements in the Wilson laboratory helps us to understand the production and reproduction of mtEve as an ancestor, as a scientific object in our deep past, and as a popular figure in our contemporary social imagination.

The genetization of "the Khazar controversy"

Snait B. Gissis, Tel Aviv University, Israel

This talk will contextualize the recent genetization of the controversy on the possible origins of Ashkenazi Jews, "the Khazar controversy", within a longue durée discussion of the genetic make-up of Jews. Thus, I shall first look into notions of "Jewish biological difference" and "Jewish biological commonalities" since the end of 2nd world war, the roles of the concept of isolates, the significance of genetic /genomic research technologies, and of non-genetic components within genetic research. Then I shall deploy these discussions to explicate the Khazar Controversy and to analyze the diverse meanings of its recent process of genetization within communities of both Israeli and non-Israeli, Jewish and non-Jewish human population geneticists.

From gene regulatory networks to dynamic mechanistic explanations

ORGANIZER

James DiFrisco, KU Leuven, Belgium

Static (graph) representations of gene regulatory network have become the standard for mechanistic explanation in cell and (evolutionary) developmental biology. They are a powerful way to summarize the genetic components and interactions that underlie a given cellular, developmental, or reproductive phenomenon or phenotype. This session intends to highlight some important problems with this type of explanation. They are all rooted in the central fact that structure does not imply function. The main shortcoming of network-based static explanations is their lack of diachronicity. Beyond the simplest networks, it is not possible to infer network dynamics from the qualitative structure of the network. This session unites three contributions that highlight how processual explanations are essential to explain developmental phenomena, and how such explanations relate to mechanistic explanation in biology.

Beyond networks: Dynamical explanations in evo-devo

James DiFrisco, KU Leuven, Belgium

Modern developmental genetics explains developmental phenomena almost entirely in terms of gene regulatory networks (GRNs).

While this represents a clear improvement over models in early genetics that focused on individual gene-trait correlations, the newer explanatory mode faces persistent and principled limitations. In this talk, I will argue that explanations based on GRNs often fail to provide a robust, mechanistic and dynamic understanding of the developmental processes underlying the evolving genotype-phenotype map of organisms.

Explanations based exclusively on GRNs suffer from three main issues. First, they are committed to an implausibly strong form of genetic determinism. The deterministic stance neglects non-genetic causes, non-genetic inheritance, and typically introduces misleading computational metaphors such as "programs" and "hardware/software."

Second, these explanations do not account for the dissociability of network structure and function. The same network can correspond to different epigenetic and morphogenetic processes depending on interaction strengths, timing, and cellular context.

Third, network explanations neglect diachronicity, or the unfolding of causal processes over time. Static networks do not explain or predict the trajectory of a developmental system through time nor are they informative about the states a system could access under various changes in initial and boundary conditions.

To overcome these problems, we require dynamic explanations, relying not only on mechanistic decomposition, but also on dynamic modeling to reconstitute the causal chain of events underlying the process of development. I illustrate the power and potential of this type of explanation using a number of biological case studies that integrate empirical investigations with mathematical modeling. I conclude by examining how these ideas relate to earlier views on mechanism and process in evo-devo.

Dynamical modularity of the genotype-phenotype map

Johannes Jaeger, Complexity Science Hub, Austria

The phenotype of an organism can be thought of as consisting of a set of discrete traits, able to evolve relatively independently of each other. This implies that the underlying developmental processes generating these traits – the genotype-phenotype map – must also be functionally organised in a modular manner. The genotype-phenotype map lies at the heart of evolutionary systems biology. Recently, it has become popular to define developmental modules in terms of the structure of gene regulatory networks. This approach is inherently limited: many developmental gene networks do not show any obvious structural modularity. More generally, the connection between structure and function is quite loose. In this chapter, I will discuss an alternative approach based on the concept of dynamical modularity, which allows us to transcend many of the limitations of structural modules. A dynamical module consists of a set of genes and their interactions that generate a specific dynamic behaviour (or dynamic regime). These modules can be identified and characterised by phase-space analysis in data-driven dynamical models. I showcase the power and the promise of this new approach using empirical and theoretical case studies as examples. Based on the available evidence, I propose a new framework for the study of modularity in developmental evolution. Dynamical modularity forms an important component of a broader, more general, theory of the evolution of dynamical regulatory systems and the genotype-phenotype map they define.

Developmental mechanisms beyond the embryo: Reproduction and evolvability in mammals

Silvia Basanta Martínez, Complutense University of Madrid, Spain

Evolvability is generally defined as the capacity of a lineage to generate heritable and selectable variation. Evo-devo conceptualizes evolvability as depending on developmental mechanisms, such as robustness and modularity, that constrain lethal mutation and facilitate adaptive change. However, the connection between evolvability and reproduction, involving developmental mechanisms that transcend embryonic structures, has tended to be neglected. At the same time, the evolution of reproduction has been commonly identified with changes in the way genetic transmission is achieved. In contrast, I argue that looking at reproduction from a developmental perspective might lead us to understand critical evolutionary innovations involved in the disparities of potential evolutionary change found among metazoan. To this aim, I will take mammalian pregnancy as an example of how the evolution of mother/embryo developmental relations might have had a crucial impact on eutherian evolvability. Rather than focusing on their different reproductive strategies, the marsupial/eutherian split is our case study to hypothesize how distinct developmental relations during reproduction may underlie variational properties. Compared to eutherians, marsupials only display 5 % of the taxonomic diversity, which seems to indicate lower evolvability. In the literature on the evolution of placental mammals, heterochrony and developmental modularity are the most invoked developmental mechanisms responsible for this disparity. However, these variational properties, influenced by the respective particularities characterizing organogenesis, are usually seen as causally restricted to intraembryonic structures. Instead, new empirical evidence supports the view that the distinct mother/embryo developmental interactions underlying each type of pregnancy might have played a significant role in accounting for this dissimilarity in morphological burst. The evolution of eutherian extra-embryonic membranes, associated with ancestrally invasive placentation, as well as the origin of a new cell type (the decidual cell) resulting from an extensive interaction between trophoblast and endometrial cells, are some of the developmental innovations typical of eutherian reproduction. These new relational innovations may have resulted in a modularisation of the reproductive relation between mothers and embryos that enabled higher freedom in the exploration of morphospace. More generally, I argue that this particular case illustrates that we should consider the co- developmental mechanisms involved in the evolution of reproduction if we aim a thorough knowledge on how developmental mechanisms shape evolution.

Stability and migration of research strategies within and across different levels of scientific organization, part I

ORGANIZERS
Steve Elliott, Arizona State University, USA
William Bausman, University of Geneva, Switzerland
Caterina Schürch, Ludwig-Maximilians-Universität München, Germany

Scholars of science have long sought to understand why some research endeavors thrive and persist while others struggle and perish. Historically, many scholars have focused on the dynamics of large social and epistemic units such as paradigms or disciplines and asked how those units structure and explain the success of theories. Increasingly, philosophers, historians, and sociologists study more local contexts like particular laboratories and investigate how researchers evaluate and export practices and data (Rheinberger 2010; Boumans and Leonelli 2013; Ankeny and Leonelli 2016). In the study of science, dichotomies between theories and models, on the one hand, and practices and data on the other, are heuristics that focus investigations of science on neglected topics. In science, however, theories, practices, and data often form closely connected parcels that are exported together as parts of research strategies. As connected parcels, how do theories, practices, and data move between research contexts, and why sometimes do they not? We propose a double symposium of five papers that address aspects of that overarching question, followed by commentary from Hans-Jörg Rheinberger. In the first paper, Niccolò Tempini discusses health sciences and introduces an account of data-curation research as projects designed to develop and evaluate reusable data practices and infrastructures. Next, Steve Elliott proposes a general account of research projects and their attendant rationales as tools by which to judge a given theory, practice, or strategy as successful and exportable. He illustrates these tools with a case from evolutionary genetics. Third, Caterina Schürch examines how researchers decide what problems to work on and argues, based on case studies from early twentieth century biology, that theories migrate easier from one disciplinary field to another in combination with realizable practices. Fourth, Katharina Steiner discusses how the organizational structure of the Naples Zoological Station enabled its early researchers to develop novel research and communicate it across many disciplines. Finally, William Bausman focuses on two research programs in community ecology, and he discusses how specific modelling and experimental strategies are coupled together and why methodological decisions constrain the movement of strategies between the two programs and beyond. As commentator, Rheinberger places the five papers into more general contexts of history, philosophy, and sociology of science. He poses a series of questions to the presenters, and time permitting, he leads an extended question and answer session between all five speakers and the audience. Ultimately, this session offers a range of analyses and conceptual tools for further studying how practices and theories function together in research strategies. As those who study science increasingly focus on local contexts and on the export of practices and strategies, they will look for tools to help them conduct their research, and for exemplar studies to guide their own work. This symposium provides both.

Making health big data research possible: On “data curation-research” and the development of new digital data re-use practices

Niccolò Tempini, University of Exeter, UK

Health big data research aims at leveraging the flexibility that digital technology allows in storing, organising, configuring, and processing increasingly complex assemblages of data and data structures. One of its distinctive promises is to render descriptions of the world (entities, processes, procedures, therapeutic strategies) more easily manipulable, so at to be transferred across contexts and scales in ways that were not possible before. Digital systems can allow patients to log comprehensive accounts of their symptoms and experience at very specific levels of description, and researchers to aggregate disparate sets of national statistics, health care, social and genomics data. With data so comprehensive it should become possible to discover razor-sharp causal relations and correlations that can be exploited or targeted through new therapeutic solutions or prevention policies.

As Leonelli has shown (2016), in most cases big data research requires for data to be "labelled" and "packaged" with various kinds of metadata as a precondition for their successful reuse in new situations of research. In this paper I extend this account, and argue that making health big data research possible increasingly requires data infrastructure managers to analyse and conduct research on the data so as to successfully translate them across conceptual and evaluative scales, and to bridge the gap between their current epistemic status and new research situations the data could be employed in. This translation moves away from the resolution at which health big data sources are generated, and towards scales that are appropriate to the kinds of problem spaces that different users are working in.

Indeed, data infrastructure developers and managers often embark in full-fledged research projects that explore new uses of the data and create new research resources, practices, and evidential claims. I call these efforts "data curation-research". These practices are set apart from labelling and packaging processes, which sit in an intermediary space in respect to research processes traditionally defined. Data curation-research is centred around research projects and on data re-use "pathfinding". It includes a broad set of practices that are at the same time aimed at

1. addressing a specific research question, and
2. creating new "paths" along which data might be used in new ways repeatedly and consistently by developing a legacy of technologies, methods, derived data, and practices that will be more easily employed by subsequent internal and external users of the data.

The paper builds on case studies of health big data infrastructures: the cancer genomics platform COSMIC, and the participatory self-reporting platform called PatientsLikeMe. The paper identifies issues that are key to the successful adoption of the research infrastructures by the research communities they try to cater to, and the data reused by them.

Research projects and rationales

Steve Elliott, Arizona State University, USA

Scientists ubiquitously describe their work as that of conducting research projects, a practice that partly leads to, and then is partly reinforced by, a general cognitive structure for research funding in which agencies solicit and review proposed projects and fund the ones they prefer. Philosophers of science increasingly aim to understand science as it's practiced in local contexts, but they've yet to detail a framework that captures both the social and the epistemic aspects of research projects. To address that issue, I propose an account of research projects as socio-epistemic units of local science. Key to the account is a description of rationales, which provide epistemic structures by which researchers evaluate the success or failure of projects and the exportability of the theories, models, data, results, practices, and strategies used in the project. I illustrate the account with an example of a project in molecular evolutionary genetics from Greg Wray's lab at Duke University. I also indicate how the account of research projects and of rationales complements related notions of research laboratories, repertoires, and project knowledge. The account provides a historiographical, sociological, and epistemological construct with which those who study science can describe especially contemporary science, and they can study how it is particularized in university and funding contexts.

Making theories work

Caterina Schürch, Ludwig-Maximilians-Universität München, Germany

In support of a colleague's application for funding, plant physiologist Frits Went wrote in 1935: "he has the right feeling for problems and the material and methods with which to attack them." According to Went, good investigators are able to consolidate their theoretical understanding and practical skills, to work out methods suited for solving particular problems. Having a feeling for problems entails realizing what questions could be readily answered with the resources available, i.e. the instruments and material at hand as well as the technical and theoretical competences of the researchers.

To learn more about scientists' evaluation of research problems and the strategies they adopted to solve them, I will examine three cases from early twentieth century biology. In each of these cases, researchers used concepts developed in the physical sciences to investigate biological phenomena. My first example is plant physiologists' adoption of the concept of hormone specificity in their study of plant growth. Secondly, I will outline how zoologists Selig Hecht and William Crozier drew on physical chemistry to identify chemical processes in living matter. Thirdly, I will introduce Prague's "biological-physical working group" and its attempt to determine the electric potential of living cells to eventually learn more about digestion and other physiological phenomena.

The three research projects were destined to rather different fates. The migration of the hormone concept into plant physiology, on the one hand, was highly successful: While the term "plant hormone" was rarely used among botanists in 1930, the new line of research was picked up by many researchers on both sides of the Atlantic and several facilities suited for plant hormone research were built in a short tim. On the other hand, biologists were moderately critical of the methods promoted by Hecht and Crozier; and fairly critical of the work of Prague's working group.

I will argue that researchers' evaluations of theoretical concepts depended to a considerable extent on practical consequences. A theoretical concept was potentially attractive if it promised to solve a research problem in an acceptable way. However, in order to be actually appealing, the concept needed to suggest research actions that researchers could, in fact, realize with the resources at their disposal. In other words: A concept's successful migration into another field hinged upon practitioners who realized how to make the theory work in the new research context.

Stability and migration of research strategies within and across different levels of scientific organization, part II

Investigating marine invertebrates: The Naples Zoological Station and its research program 1873–1913

Katharina Steiner, University of Zurich, Switzerland

Founded in 1873 by Anton Dohrn, the Naples Zoological Station was a pioneering non-university-based marine biological research institute that served as a model for many later marine stations. Historians of science have emphasized the institute's modern lab research structures in the framework of experimental biology. These histories focus on the guest researcher's perception and approach the work life and research practices at the Naples Station from the outside. In recent historiographical discussion we continue to read that field research was not carried out there. My paper offers an alternative perspective on the Naples Zoological Station. Focusing on its employees, I render the institute's research program visible, which centered on a then little-studied research object, the marine invertebrate. I illuminate the institute's social organization and working culture against the backdrop of both the institutional structures developing between 1873 and 1913 and the unique social and ecological environment of Naples. Addressing daily research routines being carried out by a heterogeneous group of employees, this paper foregrounds first, the co-production of knowledge between employees from different social milieus, educational statuses and trainings, and national backgrounds; and second, the program's multidisciplinary approach (including ecology, embryology, physiology, and systematics) encapsulated in the concept of the "scientific fishery" forming the connection and interaction between laboratory and field research in both a spatial and practical sense. I show how the employees, tools, and disciplines come together in the Station's monographic series Fauna and Flora in the Gulf of Naples and the Adjacent Marine Regions (German originally). I argue that the employment of individuals from a wide range of backgrounds and areas of expertise provided the basis for the institute's innovative and diverse methodological marine biological research. My present remarks are thus meant to introduce the Station as a local example within the history of oceanography.

Why do biologists use the methodologies that they do?

William Bausman, University of Geneva, Switzerland

The biological sciences are home to many research programs, each investigating different domains in different ways. Why don't all biologists study the same domain in the same way? The first hints at an answer begins by breaking down the methodologies used in research programs into their component activities. Research programs answer questions about a domain by theorizing and turning experimentation into evidence for hypotheses. This means that theoretical strategy, experimental strategy, domain investigated, and purpose are all potentially make a difference to research programs. Biologists and philosophers have characterized the tradeoffs within modeling strategies and experimental strategies. My talk expands this work on tradeoffs to understand the choices across modeling strategies and experimental strategies. I argue that some combinations of strategies fit together better than others for certain domains and purposes. I aim to characterize these groupings and to understand why they fit together well. I support my argument through a comparative analysis of programs across biology. My case study for the comparative analysis is two families of research programs – Neutralists and Selectionists – spanning in evolution, paleobiology, and ecology. Each family starts with similar modeling assumptions and modeling strategies, but then must deal with the differences in access to data and control of experimental system. This case study then shows the differences that domains and questions make on experimental and modeling strategies.

Extended commentary on all papers from the double session

Hans-Jörg Rheinberger, Max Planck Institute for the History of Science, Germany

Rheinberger places the five papers into more general contexts of history, philosophy, and sociology of science. He poses a series of questions to the presenters, and time permitting, he leads an extended question and answer session between all five speakers and the audience.

Tackling bioinvasions 60 years on: Lessons from the trenches, part I

ORGANIZER
Alkistis Elliott-Graves, University of Helsinki, Finland

Sixty years ago, Charles Elton published *The Ecology of Invasions by Animals and Plants,* spearheading the discipline of invasion biology. Since then, the field has made rapid progress, in uncovering the causes of bioinvasions, devising ways of managing them and formulating policy recommendations to extra-academic stakeholders. Notable successes notwithstanding, there remain important gaps in our knowledge of bioinvasions, especially regarding the accurate and timely predictions of successful invasions and the unforeseen negative consequences of interventions. In addition, controlling invasive species is expensive, and we must constantly weigh investment in control against other possible actions. This has led to the emergence of several lines of scepticism towards invasion biology; some moral, some conceptual, and some epistemic. Why do consistent predictions of invasions remain elusive? How much should we invest in the control of invasive species if the effects of interventions are not certain and the target outcomes not sufficiently well defined? The aim of this symposium is to bring together an interdisciplinary group of researchers to address the most important difficulties currently manifesting in the study of bioinvasions, to overcome some of the skeptical criticisms and to point to new directions for the future of invasion biology. In part 1 of the double session, we will address new and unresolved conceptual issues in the study and management of invasions, and in part 2, we will focus, in more detail, on one of the most important "hard problems" of invasion research: prediction. Part 1, we focus on three important theoretical issues in invasion research: how invasive species, the process of invasion and the policy framework for managing invasions are conceptualized. More specifically, Chris Lean, a philosopher of ecology and conservation biology uses the notion of "biodiversity realism" to argue against the idea that invasive species are positive forces for ecological systems as they create "novel ecosystems". Alexis Synodinos, an applied mathematician working on theoretical ecology, will critique the "stability paradigm", popular in invasion biology, by adapting the general ecological notion of "rate induced transitions" to invasion biology, and explicating how invasive species can exploit windows of opportunity through rapid response rates. James Maclaurin, a philosopher of science, and Elizabeth Ellis, a political theorist, who have both worked on the "Predator Free New Zealand" project, examine the notion of "conservation moonshots", i.e. large scale, multi-decade conservation projects. They argue that such projects are increasingly necessary to combat threats from harmful invasive organisms and engender distinctive and serious problems which can nonetheless be overcome by a mix of scientific and policy strategies.

Biodiversity realism and invasive species

Christopher Lean, University of Sydney, Australia

"Invasion ecologists are xenophobes" some critics have declared. They argue there is no sound reason to control invasive species or even prefer native species over non-natives. Such preferences are just prejudice, a prejudice not always held by the layperson (Peace

2015). The public often shows affection to the alien compatriots; for example, the public support for Brumbies in Snowy Mountains. Ecologists critical of invasion biology have argued that invasive species do not destroy ecosystems but instead create “novel ecosystems” (Hobbs et al. 2006; Hobbs et al. 2013). These novel ecosystems are claimed to be more biodiverse than extant ecosystems and across the globe most local ecosystem patches have increased in biodiversity! These more biodiverse ecosystems will provide more ecosystem services than extant ecosystems and therefore are more valuable. This position is only possible with the following assumptions about how we justify conservation. First, public interest or opinion should determine our stance towards the control of species. Second, the direct monetary value of ecosystem services is the only justification for conservation past public interest. Third, biodiversity can be flexibly defined. I reject all these assumptions. Once we see that there is more to conservation then opinion and immediate monetary gains, we can see that such slippery stances defending invasive species are not justified. I utilise biodiversity realism to reject the permissive stance towards invasive species. Biodiversity realism conceives of biodiversity as a natural quantity in the world which is measurable, valuable to prudent agents, and causally salient to ecological systems (Lean 2017). Once we take a realist position towards biodiversity, we can analyse the impact of invasive species in a way which does not rest of personal preferences and immediate economic value. This will not vindicate controlling all invasive species, which in practice no one has ever done, but will vindicate the control of many invasive species.

Transitions caused by the rate of change: The special case of invasions

Alexis Synodinos, Potsdam University, Germany

Traditionally in ecology, the long-term behaviour of populations, communities, and ecosystems has been assumed to converge to a stable steady state. This model of nature’s functioning, or “stability paradigm", has dominated the discourse in theoretical ecology. So far, the stability paradigm and the related notion of alternative states has helped us conceptualise how gradual change in external conditions can cause a non-linear response, known as a regime shift, when crossing a tipping point. However, the stability paradigm has eclipsed the importance of valid and useful alternative theories. Transient dynamics theory, for instance, points to certain ecosystems whose complex or even chaotic behaviour cannot be explained through the prism of stability. Rather it postulates that the repeating pattern of complex phenomena, which emerge as the result of species interactions, prevents the convergence to a steady state. The study of non-linear transitions represents another case in point.

The theory of regime shifts provides an explanation for non-linear transitions between steady states along a gradient of changing external conditions, by implicitly assuming steady state convergence for all external conditions. Transient dynamics theory also treats external conditions as constant over the time of development of the ecological entity's dynamics. Not considering the temporal properties of the driver of the transition has left a gap in the theory of transitions, one which has caught up with us due to the current rate of environmental and climatic change. Particularly problematic for the special case of invasions, however, is the notion of external conditions which assumes an independence between transition driver and the ecological entity undergoing the transition.

Our work aims to highlight these issues and to provide the first building blocks for the development of a theoretical framework of transitions which are caused by the rate of change both in physical conditions and in the biotic components of the ecological entity. To this end, we transferred the theoretical notion of rate-induced transitions to a broad ecological context, and made the first steps towards a predictive framework by defining the types of drivers, the properties which make ecological entities vulnerable to these transitions and the buffering mechanisms which can be affected by rates of change. In this talk I will focus on a specific type of driver, the rate of biotic change, and a special case thereof, ecosystem-altering invasions. Successful exotic species will often first appear and establish a small population, before rapidly expanding once physical conditions provide such a “window of opportunity”. Thus, once dominant, they will form an altered ecosystem in terms of the species interactions, and the functions and structure of the resulting community. By identifying the mechanisms or ecological entities most in need of management and protection against such invasions or rate-induced transitions in general, our ultimate objective is to facilitate conservation efforts against the current unprecedented rates of ecological catastrophe. We believe our efforts will help a more complete body of theory gradually – or rapidly – emerge.

Conservation moonshots

James Maclaurin, University of Otago, New Zealand
Elisabeth Ellis, University of Otago, New Zealand

Understanding and controlling harmful invasive species is both contentious and difficult, though there have been great successes particularly at small scales. The mainstay of successful control efforts has been based on the eradication of harmful invasives on small islands, However, in many other regions the chance to eradicate or control a newly-introduced invasive species has long since passed. Moreover even small island conservation efforts are now coming under threat from climate change, as once secure populations find themselves in increasingly inhospitable environments. This paper explores the options for countries facing extremely well-established and very widespread populations of harmful invasive species.

Conservation moonshots are large scale, high cost, high value, multi-decade projects designed to reset the ailing ecosystems of large regions and whole countries. In 2016 the New Zealand government proposed such a moonshot aimed directly at eradicating invasive mammalian predators (rats, mustelids and possums) nationwide. Predator Free New Zealand 2050 would take more than two decades and cost a non-trivial proportion of the country’s gross domestic product. It also offers a unique opportunity for philosophers and social scientists to research the viability and sustainability of such massive conservation efforts which raise many distinctive issues. Moonshot projects may not be able to meet normal success criteria such as eradicating all members of target species. In fact one critical issue for conservation moonshots is the difficulty of setting defensible targets when seemingly simple candidates like returning to pre-human conditions are not practicable or even desirable. Furthermore, the very high costs involved might well necessitate the development and deployment of new technologies such as gene drives for species eradication. These are likely to be poorly understood by the general public. Most importantly, the financial and social risks of any moonshot are very high. Conservation moonshots in particular run serious risk of catastrophic failure in the event that the project is abandoned (for political or perhaps economic reasons) after many years of very high expenditure and effort. These risks as well as the potential rewards of such projects will impact on future generations who do not get a vote in whether or not such projects should be undertaken.

We argue both that conservation moonshots are likely to be necessary in the 21st century and that their social, political and scientific challenges can be addressed. We analyse a series of practical strategies for conservationists and policy makers.

Tackling bioinvasions 60 years on: Lessons from the trenches, part II

Why are biological invasions uncertain, and what can trait-based predictions tell us?

Andrew Latimer, University of California, Davis, USA

Predicting whether a particular exotic species will successfully invade a particular biological community has resisted general solution for several kinds of reasons. Nonetheless, there have been some successes at identifying high-risk species, and screening potential new plant introductions has been operationalized into law in some jurisdictions. In this talk, I first discuss the major reasons why predicting biological invasions is a hard problem, focusing especially on the implications of small initial population size. I describe and review one major way in which ecologists have approached the problem – trait-based invasion risk prediction. Finally, I evaluate what the results of this approach tell us about prospects for the field.

Predicting invasion outcomes is hard because of causal heterogeneity: there are different kinds of reasons why invasions succeed or fail (Elliott-Graves 2016). Further, predictions of interactions among several or more species are generally very difficult to make, and typically require complex, parameter-rich models (Grimm et al. 2005). Third, invading species generally start at low population density, strengthening the effects of demographic and environmental stochasticity and increasing the probability of extinction (Koontz et al. 2018). Finally, target communities are typically in transition due to disturbance and climate change, limiting the usefulness of equilibrium-based predictions of species interactions for these systems (Hastings et al. 2018). Faced with such complexity, ecologists often simplify the problem by characterizing invasion risk as a feature of the introduced species, and use species traits to try to predict invasion risk. This approach has yielded some moderate successes (e.g. Van Kleunen et al. 2010), but tends to have high error rates when generalized. Nonetheless, some consistent results emerge from this approach. Traits associated with high "r" or rapid intrinsic population growth rate often have some predictive value, and "invasive elsewhere" is often a relatively strong predictor of invasion risk (e.g. Herron et al. 2006). I discuss the implications of these patterns, tying them to population dynamics and the importance of "priority effects," and to the importance of competitive advantage in successful invasions.

Can the hierarchy-of-hypotheses (HoH) approach facilitate explanation and prediction in invasion ecology?

Tina Heger, Potsdam University, Germany

The hierarchy-of-hypotheses (HoH) approach has been introduced as a tool for synthesis in invasion ecology (Heger et al. 2013). Its basic conception is that complexity in many cases can be mastered by structuring the topic under study in a hierarchical way. In an HoH, an overarching, major hypothesis branches into several more specific formulations, i.e. sub-hypotheses, which branch again and so forth, until the desired level of specificity is reached. This nestedness allows to structure and display relationships of different ideas.

In previous work (Jeschke & Heger 2018), the HoH approach has been used to synthesize the results of empirical studies on twelve major invasion hypotheses, i.e. twelve potential explanations for biological invasions (for a summary of results see hi-knowledge.org, Jeschke et al. 2018). The studies reveal an enormous complexity: even on the lowest hierarchical levels, i.e. even for the most precise formulation of the respective hypothesis analyzed in the HoH, empirical studies are rarely in agreement.

The presentation will offer ideas on how the nested representation of empirical evidence may be used to assess the range of applicability of general ideas on how invasions work. It will be explored how the HoH approach may help to develop novel ways for explanation and prediction, aiming not so much at broad generalizations, but rather at the identification of classes of cases in which similar mechanisms apply. To reach this aim, on each level of the hierarchy it could be analyzed what it is that distinguishes tests supporting the respective sub-hypothesis from those that question it. Potentially, there is causal heterogeneity (Elliott-Graves 2016) separating classes of cases e.g. according to taxonomic or functional groups of organisms, or ecosystem types. Ideally, such a procedure would allow to state in which empirical cases a certain major hypothesis is highly likely to apply.

Meta-analysis as a predictive tool for invasion biology

Alkistis Elliott-Graves, University of Helsinki, Finland

Meta-analysis is a statistical tool for analysing and synthesising the results of large numbers of individual studies (Gurevitch et al., 2018). The primary aim of a meta-analysis is to identify causal relationships from different types of evidence (Stegenga, 2011). In some disciplines (such as ecology), meta-analyses are also used as a means for generating generalizations (Gurevitch et al., 2018). However, the status and role of meta-analysis remains a controversial and divisive issue, as its adversaries have condemned it as irrevocably biased (Ioannidis, 2016; Stegenga, 2011). A second criticism is that the studies within a meta-analysis are often too heterogeneous to yield useful generalisations, which is thought to explain why different meta-analyses of the same studies can yield contradictory results (Whittaker, 2010).

While I agree with the critics that the quality of many meta-analyses is quite low, I believe that in some contexts where meta-analysis is used to generate generalisations, heterogeneity can be a feature rather than a bug. Predictions in invasion biology often fail because systems are causally heterogeneous (i.e. causes of invasions differ across systems) so generalisations have a very limited scope (Elliott-Graves, 2016). Meta-analyses can identify generalizations that support predictions but can also reveal the upper limits of a generalization's scope, thus providing invasion biologists with a safeguard against predictive failure. I will present two examples of meta-analyses which served as tools for successful prediction in invasion biology. The first is the identification of invasive in species of the Pinus genus, which was instrumental in preventing an invasion of Pinus contorta in Sweden (Rejmánek & Richardson, 2004). Importantly, the study showed that the predictive power of the theory lessened as it was applied more widely (i.e. conifers, woody angiosperms). The second meta-analysis showed that because of methodological variation associated with the application of the theory to different taxa, only some sub-hypotheses of the enemy release hypothesis have predictive power (Heger & Jeschke, 2014). This explains why previous studies of the hypothesis have generated contradictory results and demonstrates a second way that restricting the scope of a generalization can increase predictive accuracy in invasion biology.

The role of non-epistemic values in scientific classification, part I

ORGANIZER

Marc Ereshefsky, University of Calgary, Canada

When studying scientific classifications, philosophers tend to focus on the metaphysical and epistemological aspects of classifications. On the metaphysical side, philosophers worry about whether scientific classifications reflect the causal structure of the world, whether they highlight stable property clusters, whether they involve essences, and so on. On the epistemological side, philosophers worry about whether such classifications support inductive and explanatory practices. Little attention, however, has been paid to how non-epistemic values (social, moral, and political values) affect scientific classifications. In other parts of philosophy of science, there is a burgeoning field of philosophers investigating how non-epistemic values generally affect scientific inquiry. But little work has been done studying the specific connection between non-epistemic values and scientific classifications. This session aims to rectify that lacuna by investigating how non-epistemic values affect scientific classifications. This session will explore a number of issues concerning values and scientific classification. One is to provide case studies that illustrate how non-epistemic values affect classificatory practices. This is a descriptive project, and its aim is to investigate how epistemic and non-epistemic values are actually related to each other when scientific classifications are constructed. For example, do non-epistemic values set the agenda for a classificatory investigation (such as picking out domains and properties of study), and then epistemic concerns come into play once that agenda is set? Or is the interplay between epistemic and non-epistemic values more complex than that? Besides such descriptive questions, the session will consider more normative questions. How, for example, should epistemic and non-epistemic concerns be balanced in a classificatory project? Perhaps there are cases where there is no conflict between them and how they should be balanced is not an issue. But in cases where there is a conflict, how should the two types of values be integrated? These and other questions will be pursued in this session. More generally, the focus of this session is this: if epistemic and non-epistemic values are intertwined in the construction of classifications, then a proper understanding of scientific classification should study and reflect on that interconnection. This session will consist of five presentations and a panel discussion. It will span two 90 minute sessions.

The role of non-epistemic values for psychiatric classification and biomedical kinds

Ingo Brigandt, University of Alberta, Canada

While the intersection of science and values (including a role for non-epistemic values) has been addressed, this talk more specifically looks at classification and scientific kinds. I start with a brief look at race and biological sex, to underscore the relevance for social-political values for categories that are not just social kinds but have a clear biological aspect. Longstanding debates in the metaphysics of race illustrate how any account of the nature of race and how to classify persons into races answers not just to empirical considerations but also non-epistemic values. This case already highlights my point that some of these values, while all legitimate, may pull in different directions. Biological research has moved toward the view that biological sex in humans is not just a set of distinct categories (e.g., male and female), but due the presence of a variety of intersex conditions and the complexity of sex development, sex is better seen as a spectrum. At the same time, persons are assigned a sex at birth and decisions are made about how to treat persons with intersex conditions; and I argue that such decisions of how to classify persons into sex categories and how to theoretically construe nature of biological sex must have social-political concerns in view. The main part of my talk deals with classification of psychiatric disorders, in particular personality disorders. The formulation of psychiatric categories and the classification of symptoms into disorders needs to pay attention to several non-epistemic aims, including a person's the right to effective treatment (upon genuine need), the need to protect others from anti-social behaviour, the need to avoid the stigmatization of persons diagnostically classified, and the relevance of avoiding the reinforcement of gender and racial inequities by the design of diagnostic categories.

While a detailed argument is beyond the scope of a short presentation, the position that these case studies support is that non-epistemic values do not just play a subordinate role to epistemic values (e.g., being used once empirical considerations cannot adjudicate between two possible classifications). Instead, the more fruitful strategy is to use a combination of epistemic, practical, moral, and political interests. Although there are cases where different legitimate interests and values may pull in opposite directions (different values tending to favour different classifications), this actually reinforces the need to not eschew some values, but to jointly consider them and assess how to best address a given set of values. I conclude by pointing out that this position always has implications for the topic of scientific kinds. Kinds answer to diverse human interests and have to be philosophically investigated in terms of a combination of epistemic and non-epistemic aims – a position on scientific kinds at clear variance with Khalidi's, who wants to keep out non-epistemic aims altogether. (I avoid the label "natural kind" precisely because scientific kinds answer to human interests and can be based on contingent social processes subject to human responsibility.)

Joint necessity of values and epistemic considerations: The case of paraoxonase

Stijn Conix, KU Leuven, Belgium

There is growing agreement among philosophers of science that many scientific decisions, even those concerning justification and data interpretation, should sometimes be influenced by value-judgments. There is no similar consensus, however, about when such influences are legitimate and when they should be avoided. The main answers to this question can be divided into two broad positions, namely, an "epistemic priority view" and a "joint necessity view". The former view holds that non-epistemic values can play a legitimate role as long as they do not trump epistemic considerations in scientific decisions. The latter view rejects this epistemic priority thesis and holds that, at least sometimes, value-judgments and epistemic considerations should stand on equal footing.

Arguments for and against both views have focused almost exclusively on the role of values in theory choice, inference, and modelling. In this paper, I try to shed light on this debate by looking into an aspect of science that has remained mostly undiscussed in this context, namely, scientific classification.

I do this by means of a case study of the Enzyme Commission classification of paraoxonase. First, I show how value-judgments and epistemic considerations were deeply and inevitably entangled in the decisions that led to the establishment of this and related categories of the Enzyme Commission classification system. This suggests that the current shape of this classification is as much determined by these value-judgments as it is by epistemic considerations. I then argue that this entanglement poses a problem for the epistemic priority view, as this view assumes that epistemic considerations and value-judgments can be separated to allow prioritization of the former over the latter. Thus, I argue, the case of paraoxonase provides indirect support for the joint necessity view. I end the paper by briefly considering the broader implications of my argument for any general framework for thinking about the appropriate role for values in science.

How non-epistemic values can be epistemically beneficial in scientific classification

Soohyun Ahn, University of Calgary, Canada

Griffiths (2004) and Khalidi (2013) argue that some social and psychological kinds fail to be natural kinds due to their value-laden aspects. Their concern about value-modified categories arises from observing that many social and psychological kinds serve two different aims – epistemic and normative. On the one hand, natural kinds are revised to conform to new empirical evidence with the aim of increasing predictive and explanatory power. On the other hand, many social and psychological kinds serve the aim of social reform, thus their modification reflects the change in our normative attitudes towards certain phenomena. Griffiths and Khalidi's overall concern is that when a clash between these two aims occurs, the epistemic aim of discovering natural kinds is compromised by non-epistemic aims.

I will argue that is not always the case by using the example of infantile autism. I examine the early history of the case of infantile autism where non-epistemic value considerations, such as "welfare of autistic children and their families is important," drove the modification of the category's boundary. As I will argue, non-epistemic value considerations facilitated the process of knowledge production by opening up a new research area and contributing to creating diagnostic checklists.

Although the concern over value-driven modifications of scientific categories does have initial appeal, if we view it through the lens of the value-free ideal (VFI) of science it becomes clearer that the concern is part and parcel of the VFI. Motivated by the concern, it has been suggested that the only way to secure the pursuit of natural kinds is to be exclusively guided by epistemic purposes and not to be deflected by non-epistemic interests. However, I argue that such a prescription does not offer a priori criteria to distinguish natural kinds from arbitrary categories. One merit of identifying the concern over value-driven modifications of scientific categories as part of the VFI is that various arguments against the VFI can be appealed to in order to demonstrate how the concern is overstated.

The role of non-epistemic values in scientific classification, part II

Human values do and should shape all scientific classifications

Matthew H. Slater, Bucknell University, USA
Matthew Barker, Concordia University, Canada

We specify and argue for both the factual thesis and the normative thesis stated in our title. To start we distinguish between operational concepts and theoretical concepts used in scientific classifications, then focus on the theoretical concepts – those that are supposed to get at the very nature of things. The definitions of the theoretical concepts FLUORINE, PLANET, and MELANOMA, for example, are supposed to summarize theories about the conditions in virtue of which a thing is an example of fluorine, a planet, or melanoma, respectively. Surveying relevant scientific literature on such concepts, we next build on recent work that identifies the operation of pragmatic classificatory norms. These are norms to which scientists implicitly appeal, for what amounts to pragmatic support, when making classification claims that involve theoretical concepts. We show how these norms are essentially based partly in human values. We then argue, first, that all justifications for scientific classification claims involving theoretical concepts in fact appeal (at least implicitly) to pragmatic classificatory norms and hence values, and, second, that in each instance some values but not others should play this role. We close by discussing how scientific classification could improve by making such appeals to values, and arguments featuring them, more explicit.

How to balance contextual and epistemic values in scientific classification

Marc Ereshefsky, University of Calgary, Canada
Thomas Reydon, Leibniz Universitat Hannover, Germany

Philosophical accounts of scientific kinds and classification tend to implicitly assume that the construction of scientific classifications should only be guided by epistemic values. In particular, the usefulness of such classifications in explanation and prediction is usually taken as the principal criterion of success. When it comes to contextual values (such as moral, social, and political values) the standard philosophical view is that scientific classifications should be as free of the influence of such values as much as possible. However, recent work in the philosophy of science acknowledges that the effects of contextual values on scientific classification are more widespread and persistent than generally recognized by philosophers. We concur that contextual values often play a role in scientific classification. We highlight a case

concerning species concepts and environmental conservation to show the effect of contextual values on classification.

Our main concern, however, is not to show that contextual values affect the choice of classifications. Our main concern is what to do about it. We assume that in some cases the effect of contextual values is unavoidable. Moreover, we believe that contextual values play a legitimate role in classificatory practice. The question we focus on is how to balance the promotion of contextual values with the promotion of epistemic values when selecting a classification. We believe that fruitful guidance for answering this question comes from work in feminist philosophy of science, particularly in the work of Helen Longino and Elizabeth Anderson. Using their work, we offer some suggestions on how to balance epistemic and contextual values when selecting scientific classifications.

Fidelity in cultural evolution

ORGANIZER

Chiara Elettra Ferrario, University of Münster, Germany

The study of cultural evolution is a deeply interdisciplinary field of research, spanning over evolutionary biology, anthropology, archaeology, cognitive science, and linguistics, inter alia. Since its onset in the second half of the 1970s, the field has been developing steadily, with the last decade witnessing a burst in the number of research groups, publications, reviews of the field, novel experimental and modelling methods, and the foundation of the "Cultural Evolution Society" in 2015. It is safe to say that the field is reaching a stage of maturity and becoming increasingly productive. Yet there are central disagreements about the key mechanisms involved in the transmission and evolution of cultures, and several conceptual issues pertaining to the foundations of cultural evolutionary theory need to be seriously addressed, especially if the field is to bring together experts from many different scientific backgrounds. Cultural fidelity – or simply "fidelity" – is one such problematic theoretical concept. Fidelity is used to explain why cultural traditions – lineages of cultural traits such as social norms, rituals, tales, artefacts, etc. – can last for long periods of time while remaining relatively stable in the face of disruptive factors. As individuals learn from one another, there is a constant risk that the transmitted knowledge gets altered, either by being miscopied to some degree or through a loss of the information necessary to sustain the tradition. The high-fidelity of human cultural transmission would act as a safeguard against the transformation and the loss of cultural information, thus ensuring both the stability and longevity of cultural traditions. Fidelity also serves to explain the human-specific capacity for an open-ended, cumulative cultural evolutionary process, that is, our capacity to cumulate innovations leading to evermore complex and sophisticated cultural and technological traditions. Fidelity would thus serve as the key difference-maker between human cumulative cultures and non-human non-cumulative traditions, explaining why only us humans, with our uniquely high-fidelity transmission capabilities, are able of evolving and sustaining complex traditions Perhaps surprisingly in the light of fidelity's explanatory centrality, there seems to be no clearly agreed-upon understanding of the concept. The notion is used very liberally, its significance often debated, yet systematic definitions are virtually nonexistent. Working with one's own intuitions opens the door for cultural evolutionists to talk past one another, interpret the same results in different, conflicting ways, and yet fail to realize that they do so. Moreover, fidelity is often operationalized in incongruent ways in laboratory experiments, in field studies, and in evolutionary modelling, leading to more potential equivocation. Considering the centrality of fidelity to cultural evolution studies, it seems legitimate to avoid idiosyncratic interpretations as much as possible, and instead set the notion on more solid ground, both conceptually and operationally. This symposium aims to address the many different meanings of cultural fidelity, examine their varying uses in the contributions of the several fields involved in cultural evolution research, and assess their explanatory import with the hope of shedding some conceptual clarity on the notion.

Understanding cultural fidelity

Mathieu Charbonneau, Central European University, Hungary

A leading idea of cultural evolutionary theory is that for human cultures to undergo evolutionary change, cultural transmission must generally serve as a high-fidelity copying process. The high-fidelity of human cultural transmission would act as a safeguard against the transformation and loss of cultural information, thus ensuring both the stability and longevity of cultural traditions. Cultural fidelity would also serve as the key difference-maker between human cumulative cultures and non-human non-cumulative traditions, explaining why only us humans, with our uniquely high-fidelity transmission capabilities, are capable of evolving and sustaining complex traditions through the so-called "ratchet effect". But just what does it mean for cultural transmission to be more or less faithful?

Based on its explanatory importance alone, one would expect cultural fidelity to be a clearly defined, unified concept. However, the literature shows no consensual understanding of what cultural fidelity amounts to, yet alone any principled way to operationalize the concept such that it can serve its two main explanatory roles. Instead, cultural evolutionists have used largely uninformative and epistemologically problematic characterizations of the notion.

In this presentation, I first argue that cultural evolutionists in fact use several fidelity concepts, concepts which I set to define and clarify. I argue that cultural fidelity is typically construed as a property ascribed either

1. to episodes of cultural transmission (episodic-fidelity) – where a cultural trait is acquired more or less faithfully –,
2. to the mechanisms involved in the cultural transmission of specific cultural traits (propensity-fidelity) – where some transmission mechanism is more or less faithful than another in perpetuating some tradition –, or
3. to the ensemble of social learning mechanisms possessed by a species (generalized-fidelity).

For each notion, I offer a definition and illustrate their use by cultural evolutionists.

Second, I set to clarify how each of these concepts serve their different explanatory roles. I argue that episodic-fidelity and propensity-fidelity are adequate concepts when used to explain cultural stability. However, I offer a more critical argument concerning the explanatory import of a general notion of cultural fidelity (generalized-fidelity) by arguing that the concept, in its current form, relies on problematic assumptions. I first identify three conditions underlying the generalized-fidelity concept as it is currently used in the literature:

1. a mechanism of cultural transmission possesses one and only one degree of fidelity,
2. the degree of fidelity of all transmission mechanisms should be quantifiable using a common metric, and
3. fidelity is an intrinsic property of a transmission mechanism.

I then argue that each condition suffers from problems that makes the concept of generalized-fidelity inoperative and deprives it of explanatory power. I conclude that if generalized-fidelity is to serve as an explanation of the key differences between human cumulative cultures and non-human non-cumulative traditions, then the concept will have to be redesigned and rely on different assumptions.

Cultural fidelity: More food for thoughts

Chiara Elettra Ferrario, University of Münster, Germany

In a much-needed piece of exploratory work, Charbonneau (2018) sets out to delineate the conceptual space of "cultural fidelity". In this talk, I take Charbonneau's work as starting point and develop a few more ideas to advance the debate on fidelity.

Here's where I fully agree with the author. For a start, I fully endorse Charbonneau's way of delineating the issue. Fidelity has indeed received remarkably scant press to date: it suffers from underdetermination and lacks a clear-cut operational definition. This state of affairs is undesirable, for fidelity is explanatorily central to at least two important projects in cultural evolution studies (it is thought to ensures the stability and longevity of cultural traditions; it purportedly explains the cumulative nature of human traditions, as opposed to nonhuman ones – typically within "ratchet argument" analyses).

Here's instead where my views differ from Charbonneau's. The author distinguishes three notions of cultural fidelity: episodic-fidelity, propensity-fidelity, and generalized-fidelity (for the sake of clarity, I maintain his terminology). While the distinction is generally valid and appropriately captures part of the diverse and often implicit construal of the notion, I believe that

i. generalized-fidelity is not as problematic as the author thinks;
ii. fidelity may conceal further conceptual hurdles, which are not captured by the present analysis.

As for (i), I suggest Charbonneau's three notions of fidelity can be understood hierarchically. Episodic-fidelity is the fundamental notion: propensity-fidelity and generalized-fidelity can be derived from it (indeed, they must). I show how this can be done, and how it takes care of some of Charbonneau's worries about generalized-fidelity.

Moving on to (ii), I focus first on episodic-fidelity. As correctly noted, episodic-fidelity revolves around the notion of trait similarity, thereby inheriting the critical "relevance problem" (roughly, the idea that any two items can be both similar and dissimilar in an indefinite number of ways. We need to determine a "relevant perspective" in order to meaningfully compare them – but which perspective is correct?). I argue that the relevance problem is deeper than envisaged, for it cannot be solved, but only reined in. One way to do this, as Charbonneau suggests, is by appealing to the explanatory interests of cultural traditions' investigators. But the perspective of those who sustain cultural traditions (cultural actors) must also be taken into account on a case by case, contextual basis. This approach will show that cultural traditions cannot be fruitfully investigated as a unitary phenomenon, but should rather be parsed into different domains, or areas of cultural expression (e.g. material technology, rituals, art, etc.), which are governed by heterogenous transmission and stabilization dynamics. Finally, I explain why expecting a solution to the relevance problem from a better understanding of private mental representation is a misplaced hope.

I conclude by sketching two further thoughts. Firstly, the notions of cultural fidelity, stability and longevity are at present often confused, and should be distinguished more sharply. Second, the notion of fidelity may reveal further undetected and theoretically important distinctions in the context of so-called "ratcheting" explanations.

Culture without high-fidelity copying

Alberto Acerbi, Eindhoven University of Technology, Netherlands

A key question for cultural evolutionists is: what are the causes of cultural stability? Many distinct research traditions, across evolution, psychology, and anthropology, have either argued or assumed that cultural stability, whether over shorter or longer timespans, necessarily requires psychological mechanisms capable of copying (imitating) cultural items -- such as recipes, nursery rhymes, specialised skills, etc. -- with some high degree of fidelity. In other words, faithful transmission at the level of the individual is necessary to explain population-level cultural stability.

However, another possibility exists: cultural stability at the level of the population could also be explained by convergent transformations at the level of the individuals. Even if transmission at individual level is characterized by low fidelity, if cultural traits are transformed in non-random, convergent ways, we may observe at population level stable cultural traditions. Verbal arguments have been developed in support of this latter possibility, especially in a framework known as "Cultural Attraction Theory", but formal models are lacking, making unpractical the comparison with the rich modelling literature in cultural evolution.

In my talk, I present such a model. The results show that: (i) cultural stability can emerge and be maintained for both short and long periods of time by virtue of convergent transformations alone (i.e., in the absence of any form of hi-fi copying or selection process);
(ii) convergent transformation and (unbiased) high-fidelity copying, when both present in a population, can have complementary effects,

with high-fidelity copying increasing the strength of the process of convergence; and, finally, (iii) while high-fidelity copying and convergent transformation can both end up in stabilizing cultural traditions, we can empirically distinguish them through different evolutionary signatures and recognize the relative contribution of each.

The politics of Lamarckism

ORGANIZERS

Snait Gissis, Tel Aviv University, Israel
Eva Jablonka, Tel Aviv University, Israel

There has been a growing interest in the contextual history of Lamarckism and its entanglement with issues political and social that goes far beyond the older interest in the Politics of Lamarckism in the Soviet version. The session will reflect these wider interests: presenting three different snapshots of nineteenth and twentieth/twenty-first centuries multifaceted effects of Lamarckism on political thinking and practices in Europe and the US.

Lamarckism in the West, or the ambiguous politics of biological plasticity

Maurizio Meloni, Deakin University, Australia

Lamarckian ideas, and in general notions of biological plasticity, are often associated with views of social reform, if not true political radicalism and socialism. They have been traditionally seen as the support for benign ideas of social change unlike the more crude aspects of biologism usually associated with hard heredity and Mendelism. In my paper I focus on some bleak aspects of the politics of Lamarckism in Europe and the US in the nineteenth and early twentieth century, particular the way in which notions of corporeal plasticity, theories of uses and disuse, and inheritance of characters have been connected with discourses of race and class differences. I discuss the way in which theories of racial and corporeal plasticity have been used to map, reproduce and strengthen social hierarchies through biological distinctions, particularly by considering some bodies as softer, more vulnerable, and more subject to external influences than others: in a word more "impressionable" (Meloni, 2019). This often forgotten history may help problematize contemporary identifications of genomic plasticity – driven by research in molecular epigenetics – with openness, unlimited potentialities and social change.

The short "Lamarckian period" in the German Democratic Republic after the Second World War

Martin Battran, Independent scholar, Germany

Lamarckian ideas flourished in Germany continuously between 1890 and 1940, gaining an increasingly political dimension after the turn of the 20th century. Lamarckian thinking emphasized the *active* individual in contrast to neo-Darwinism, where the individual was seen as more *passive,* subordinate to selection. The notion of the active individual, who explores the environment, determines its own niche, and guides its own development, led to an appreciation and acceptance of transgenerational effects. Therefore German Lamarckists criticized genetic determinism and advocated environment- and development-centered approaches. After 1933, when the National Socialists came into power, Lamarckian concepts were rejected due to their allegedly Marxist character. During the first decade after World War II therewas practically no renowned biologist in West-Germany who proposed any form of Lamarckian ideas of inheritance and evolution. The situation in the eastern part of Germany (GDR) was, on the other hand, very different. Partly because of political guidelines from the Soviet Union and "Soviet genetics", and partly because of their own antagonism to the Nazi regime and its Social-Darwinist ideology, several biologists in the GDR between 1948 and 1960 were engaged in basic and applied research based on Lamarckian and/or Lysenkoist premises. The biological research done in the GDR during this period shows a complex mix of ideas about the "inheritance of acquired characteristics" that cannot be easily assigned to standard Lamarckian thinking.

The politics of Lamarckism in Fin de Siècle Vienna

Johannes Feichtinger, Austrian Academy of Sciences, Austria

This lecture explores how specific local scientific, social and cultural contexts formed a particular understanding of Lamarckism, and how the prevalent Lamarckian biology shaped the politics of early twentieth-century Vienna. Studying how evolutionary change worked, Vienna's leading biologists rejected the exclusively selectionist understanding of Darwinism completely, considering it unable to explain the undeniable increase of complexity in organic life. Within the framework of Darwinian thought, and against a liberal-bourgeois background, they developed and promoted particular Lamarckian concepts. They built the basis of the comprehensive research undertakings at the Vienna Vivarium, and they laid the foundation of ambivalent forms of Social Lamarckism. It is the goal of this presentation to elucidate the specific manifestations of Lamarckism in Fin de siècle Vienna, and to show how they shaped the emergence both of ambiguous forms of racist thought and of the most extensive program of communal welfare policy that has yet existed.

Fidelity in cultural evolution

ORGANIZER

Ivan Gonzalez-Cabrera, Konrad Lorenz Institute for Evolution and Cognition Research, Austria

Recently, scholars working on the field of cultural evolution have realized that parameters of cumulative cultural evolution are broader than previously thought. Concepts of "imitation" seem poorly suited for explaining the kind of complex multilevel transmission that is lumped into the category of "social learning." The present session builds upon some theoretical insights and conceptual tools previously discussed by Charbonneau, Ferrario, Acerbi in the first part of this double organized session. The main focus of this debate concerns the role of fidelity in the evolution of cumulative culture – in particular, the idea that the kind of complex cumulative culture displayed by humans relies on some form of high-fidelity social learning such as imitation (Ferrario, 2018). In this second session, we further explore the application of these theoretical tools in the context of the evolutionary dynamics of specific cultural traits such as social norms, music, and language. In the first talk, Gonzalez-Cabrera argues that the faithful transmission of social norms depends not only on the transmission of normative contents (i.e., what the norm is about) but also the transmission of a certain attitude towards them when the norm is said to be "sincerely endorsed" by other agents (i.e., when we want others to follow a norm for a particular kind of reasons or motives). He argues that human-unique capacities for shared intentionality led to the emergence of a distinctive capacity for sharing (otherwise private) normative standards involved in instrumental action in a way that is both intrinsically motivating and socially self-reinforcing. In the second talk of the session, Villanueva shows how musical practices are sometimes clustered by social norms that coalesce rituals, music, and dance, creating several forms of co-dependent entrenchment. These are mechanisms of propensity-fidelity (Charbonneau, 2018) that are "embodied in practices." Such mechanisms are beautifully exemplified by the Villanueva's own ethnographic work on the "Danza de Negritos" performed by the Totonac indigenous community in the Municipality of Huehuetla. Once a certain musical practice is transmitted, Villanueva argues, the co-dependent entrenchment of cultural practices that these norms coalesce constrains the range of variation of musical traits. Finally, in the last talk of the session, de Vladar uses a modified version of the Naming Game (Steels and McIntyre, 1999) to show that different evolutionary outcomes are possible depending on the way individuals reinforce their knowledge, rather than population-level mechanisms such as social norms. When agents have idiosyncratic preferences on which cultural traits to adopt that are subject to reinforcement (Hebbian) learning, sharp linguistic divides can be largely stable, despite continuous social interaction. But under a certain set of parameters, the same reinforcement dynamic can lead individuals to achieve some degree of cultural integration. Incorporating these reinforcement mechanisms into models of cultural evolution can help us to understand the role of the rewarding system in the fate of the faithful transmission as well as how the complexity of the cultural traits affects their fate.

High-fidelity transmission of social norms

Ivan Gonzalez-Cabrera, Konrad Lorenz Institute for Evolution and Cognition Research, Austria

Social norms are mechanisms that support cultural fidelity, but they are themselves cultural traits that must be transmitted faithfully. The faithful transmission of social norms depends not only on transferring the contents of a norm but also the right kind of attitude, for we often want others to hold these norms sincerely. We not only want others to blindly follow rules but also to comply with them for the right sort of reasons and motives. In this talk, I argue that the faithful transmission of norms depends on the coevolution of phylogenetically old mechanisms for instrumental reasoning and relatively recent ability to share intentional mental states – a capacity known as "shared intentionality". This coevolutionary process was driven in the hominin lineage by ecological challenges that selected for increased cooperation in foraging. I speculate about how this could have happened in the context of the hominin transition towards big-game hunting. The coevolution of these cognitive traits led to the emergence of a new disposition for sharing private normative standards involved in instrumental action in a way that is intrinsically motivating for others as well as socially self-reinforcing. To the extent that these norms are intrinsically motivating and socially self-reinforcing, the resulting disposition supports the sincere endorsement of social norms, and thus their faithful transmission. I conclude by making some predictions about the conditions we under which the reliable transmission of social norms might fail and by drawing some implications of this view for the accurate transmission of cultural traits that are supported by social norms.

Mechanisms of propensity fidelity embodied in musical practices

Alejandro Villanueva, National Autonomous University of Mexico, Mexico & Konrad Lorenz Institute for Evolution and Cognition Research, Austria

Fidelity has been used to explain why cultural traditions – lineages of cultural traits such as social norms, rituals, tales, artifacts, etc. – can last for long periods of time while remaining relatively stable. One particular family of mechanisms explaining patterns of cultural transmission and stability are mechanisms of propensity-fidelity (Charbonneau, 2018). In order to expand and complement the explanatory scope of this concept, I will propose the notion of "propensity-fidelity embodied in practices". First, I will argue that this notion can shed important light on the relevance problem discussed by Ferrario in this symposium, especially in the context of the transmission of musical practices. I agree with Ferrario that cultural traditions should not be conceived as a unitary and homogenous phenomenon stored in an individual mind. Accordingly, I will argue that they are better understood as a cluster of social practices (e.g. rituals, music, dance, etc.) transmitted co-dependently through heterogeneous mechanisms of varied, but complementary, stabilization dynamics. These practices are often clustered as a result of (implicit or explicit) social norms that coalesce sets of cultural practices (Gonzalez-Cabrera, in preparation), which in turn are transmitted through, and alongside, these social practices. Second, I will show that once a certain musical practice is transmitted, the co-dependent entrenchment of cultural practices that these "coalescing" norms produce constrains the range of the variability of certain musical traits. This allows the maintenance of a socially acceptable degree of fidelity of a cultural tradition over time, providing a partial solution to the relevance problem – the problem of determining the relevant aspects that must be copied by an agent (or group of agents) in order to adequately reproduce a cultural trait. In order to show how this conceptual framework can be applied to explain concrete cases of cultural transmission, I will refer to my ethnomusicological work conducted over several years in Mexico (Villanueva 2012). I will specifically focus on the music of the "Danza de Negritos" performed by a Totonac indigenous community of the Municipality of Huehuetla, Puebla.

Stability and dynamics of multicultures

Harold P. de Vladar, Konrad Lorenz Institute for Evolution and Cognition Research, Austria; Hungarian Academy of Sciences, Hungary & Parmenides Foundation, Germany
Eörs Szathmáry, Center for the Conceptual Foundations of Science, Germany

The fate of multi-cultures is a question of pressing relevance. Cultural evolution has largely been addressed through derivative models from evolutionary biology, but to an extent has left aside the question of cultural mixing. I present a computational framework based on Language Games to address the question of cultural mixability.

The Language Games are a class of Artificial Intelligence platforms designed to study language evolution. These models rely on horizontal exchange of information amongst agents by means of digital, acoustic, visual or other transmission channels. Although the naming games account for certain features of language, such as conventionalisation, these do not allow the maintenance of variability of cultural traits.

The framework hereby introduced is a particular modification of Language Games where

i. there are two (or more) types of individuals that have different cognate traits and
ii. each individual has idiosyncratic preferences on which cultural traits to adopt that are subject to reinforcement (Hebbian) mechanisms.

Individuals interact in pairs with one taking the role of a speaker and the other of a hearer. The speaker transmits the information it prefers and the hearer either learns for the first time or reinforces it if it already knows it. Although the interaction is pairwise, populations of agents are modelled and in each round the agents and their roles are randomly chosen.

In general, we find that there are different possible outcomes, depending on the way agents reinforce their knowledge: in some parameter combinations, it is found that a state of “contention” is maintained where, despite continuous interaction, a sharp separation is stable, where individuals preserve their cognate culture. However, we also find that some individuals switch cultures, thereby achieving a certain degree of integration. With this framework, several other questions are studied, such as the role of the rewarding system in the fate of the transmission, how the complexity of the cultural traits affect their fate and also spatial dynamics of the game. Finally, we draw a precise analog between this framework and replicator equations of coordination games, providing a precise evolutionary interpretation of “memetic” horizontal transmission.

Revisited & undone: Fresh perspectives on molecules and life in the 20th century, part I

ORGANIZERS
Mathias Grote, Humboldt University, Germany
Lisa Onaga, Max Planck Institute for the History of Science, Germany

The history of molecular genetics from the discovery of DNA to the human genome project appears as a distinct and somewhat distant part of the historiography of science nowadays, but many of the broader historical and philosophical questions related to molecular biologies are still pertinent, or beg for re-questioning in the light of recent developments in the life sciences. This session attempts to take stock of molecular studies writ large, through foci upon objects such as fibers and membranes, organelles and pathways. Our aim is to sketch a more inclusive historical picture of the molecularization of life as an ongoing process driven by philosophical questions at the beginning of the turn of the twentieth century about the relationship of molecules to life, and practical questions about techniques to visualize proteins and their dynamics. A longue durée view of molecularization situates the molecular gene as part of a broader endeavor and sheds light on the historiographic absences that prompt historical research alongside genealogies of contemporary philosophical questions about tinkering with life in the age of synthetic biologies and new investigative technologies of structural biology, or in silico approaches. Starting with a discussion of 1850s plant physiology, Dan Liu examines the history of cell wall and membrane research, as well as the micellar theory of molecular structure in order to suggest an earlier periodization for the establishment of key features characteristic of molecular biology research methods. Through analysis of biochemist Fritz Albert Lipmann's work on phosphate compounds, Gina Surita shows how the bioenergetic metaphor of the "cellular economy" shaped the development of modern biology and how biologists asked questions about the "essence of life" during the first half of the twentieth century. Soraya de Chadarevian contemplates the notion of molecularization by revisiting the tensions between cytogeneticists and molecular biologists and focusing upon the significance of digitally supported microscopes, that today define molecular biological working practices. Mathias Grote discusses the 1970s and 1980s synthesis of biological molecules and structures and the piecemeal advancement of knowledge and practices through the reassembly of life from organic, colloid, and biochemistry, that prefigured synthetic biology. In a reconsideration of silk as protein, Lisa Onaga examines how and why various molecular biological research interests came together in the development of artificial silkworm food and polyphagous silkworms in wartime and postwar Japan when mulberry acreage shrank. Sarah E. Tracy redraws the history of monosodium glutamate used in studies of metabolic disorders, and makes an important case about the changing assumptions about the relationship between dose rate and toxicity, and ultimately the workings of epigenetics. These papers revisit the molecularization of life at different moments in time and recast assumptions of what topics can contribute to the history of molecular biology. Studying these diverse facets together--from the study of cellular membranes and structures to histories of metabolism and diet, to the practices of laboratory work--may help open up the horizon to question neglected aspects, such as about the relationship of life and matter, or chemistry and biology.

Where does the history of molecular biology begin? Configuring continuity vs. discontinuity in the historiographies of plant physiology, cell biology, and biochemistry

Daniel Liu, Berlin Institute for Cultural Inquiry, Germany

Compared to the history of molecular genetics, the molecular anatomy of the cell has a much longer and more continuous history, whose core concepts date back to the mid-nineteenth century, and possibly earlier. We usually understand the origin of molecular biology as the revolutionary synthesis of genetics with biochemistry, culminating in the cracking of the genetic code in the 1960s. If origin stories are ways for historians to frame and understand issues in the present, then how should we reconfigure the history of molecular biology in an era when the Central Dogma of molecular biology is becoming less "central," and making way for epigenetic and other cellular dynamics? In this paper I will argue that we should understand the early and pre-history of molecular biology as a synthesis of three, rather than only two distinct scientific traditions:

1. the history of the genetic code;
2. the history of macromolecular biochemistry, centered on the isolation and analysis of complex biomolecules; and
3. the molecularization of "living matter," centered on the molecular anatomy of cell and tissue structure.

By examining the history of cell wall and membrane research, as well as the micellar theory of molecular structure that arose endogenously within plant physiology, I will show how many of the central concepts of molecular cell biology were in place as early as the 1850s – at least, in plant physiology, if not in other domains of biology. These include a willingness to speculate about corpuscular mechanics, the use of polarization microscopy, an emphasis on physico-chemical forces, and the use of a visual language as an aid to abstraction. Finally, I will also suggest that this durée plus longue view of molecular biology rearranges some of our assumptions about the social-conceptual division of structure and function in the historiography of biology as a whole.

The power of phosphate: Energy and the "cellular economy" in twentieth-century biochemistry

Gina Surita, Princeton University, USA

This paper will examine an oft-overlooked development in the history of twentieth-century biology: the rise of bioenergetics, or the study of energy transformations in living organisms. Through a case study of the work of biochemist Fritz Albert Lipmann and his associates, this paper will describe the changing role of the molecule adenosine triphosphate (ATP) in bioenergetic research from the 1920s through the 1950s. In the course of his work on phosphate metabolism, Lipmann developed the notion of the "high-energy" or "energy-rich" phosphate bond, which he symbolized by the "squiggle" notation, or "~P". According to Lipmann, ~P's stored large amounts of energy that could be released when these bonds were broken; for example, in a molecule of ATP, which has three phosphate groups next to each other. Lipmann's definition of bond energy was not popular with organic and physical chemists, who were used to thinking of bond energy as the energy required to form a bond, not the energy that is released when a bond is broken. This paper will describe the work that led to Lipmann's redefinition of bond energy, and the ways in which Lipmann and his colleagues linked carbohydrate oxidation to phosphate uptake and ATP formation. The energy from carbohydrate breakdown, they argued, was "captured" in the phosphoanhydride bonds of ATP, which biochemists increasingly began to refer to as the universal "energy currency" of the cell. The "currency" of ATP circulated within a metaphorical "cellular economy," in which energy-requiring metabolic reactions were often linked to energy-releasing metabolic reactions. Building upon recent work on the history of metabolism, this paper aims to articulate a new interpretation of twentieth-century biology by arguing that the bioenergetic metaphor of the "cellular economy" shaped the development of modern biology – and the ways in which biologists asked questions about the "essence of life" – in ways distinct from the metaphor of "genetic information," which has received a great deal of historiographical attention.

Of microscopes and molecules

Soraya de Chadarevian, UCLA, USA

For much of the 20th century chromosomes were the province of researchers peering down the microscope. Molecular biologists regarded the object of fascination of cytogeneticists as the "dullest form of chromosome: an inert package needed to make orderly mitosis possible", while only recognizing a molecular approach to genetic information (Crick 1977). Pitted against each other for much of their history, cytogenetics and molecular biology – not unlike the process described by Peter Galison for the analytic and imaging traditions in microphysics – are sometimes presented as eventually "fusing" with the advent of fluorescent in situ hybridization or FISH techniques. The technique uses fluorescent molecular probes, produced by recombinant DNA techniques, to locate and highlight specific chromosomal sites. The result can be viewed under a fluorescent microscope and in practice allows for a molecular resolution of the chromosome image. Yet if FISH and other techniques using fluorescent labeling has allowed chromosome researchers to "go molecular", the same techniques in conjunction with vastly refined and digitally supported microscopes have been changing the working practices and research objects of molecular biologists. As chromosome researchers all along, now also molecular biologists study microscope images, while fractionation techniques, analytical centrifuges and scintillation counters that dominated molecular research in the 1950s to 1980 have moved out of favor. Looking at these developments in more detail makes it possible to untangle and historicize the notion of “molecularization”.

Revisited & undone: Fresh perspectives on molecules and life in the 20th century, part II

Synthesizing molecules, assembling cells – toward a “plug-and-play” life science, 1970–1980s

Mathias Grote, Humboldt-Universität zu Berlin, Germany

This paper analyzes practices of (re-)making biological molecules and cell models throughout the 1970s and 1980s within a broader inquiry of syntheses in between chemistry and the life sciences. The production and use of liposomes (membrane-ensheathed vesicles) as models of cell membranes was pioneered by British biochemist Alec D. Bangham and transferred into bioenergetics by Austrian-American colleague Efraim Racker around 1970. Later, methods of recombinant DNA, but also organic chemical synthesis added to modifying life’s material inventory. Har Gobind Khorana, an Indian-American chemically-minded molecular biologist inspired by syntheses, set out to gradually remake life’s components, producing not least the first functional synthetic gene, before transferring his making approach to membranes and proteins. Khorana’s research illustrates how molecular mechanisms have been spelled out since the 1980s by taking apart, modifying and remaking life’s components in what I call a “plug-and-play” mode. Historiographically, this paper’s focus on practices of making biological molecules and structures suggests a change of perspective on the development of synthetic biology: While this field’s history has often been understood by looking at landmark events such individuals, research programs or conceptual innovation, the present approach takes into view a genealogy of synthetic biology, that is, a bottom-up perspective of this

field as shaped by piecemeal advance through practices to reassemble life from organic, colloid and biological chemistry.

On apples and omnivores: Molecular recipes for silkworm food in 20th century Japan

Lisa Onaga, Max Planck Institute for the History of Science, Germany

It is largely understood and assumed that the silkworm, Bombyx mori, eats the leaves of the mulberry plant exclusively. By applying the adage "you are what you eat" to silkworms, one is tempted to think of silkworms as machines that convert mulberry into luxurious silk. In practice, many silkworms reared in industrial, laboratory, and hobbyist conditions today can also eat artificial food. Mulberry is still cultivated in Japan and elsewhere to maintain silkworm genebanks, university stocks, and to cultivate artisanal silk, but expensive artificial food is used in some instances that view the silkworm as a source of protein, including as reptile food, or more practically, where mulberry plants are absent. Artificial silkworm food, a green mash with a consistency resembling Play-doh, is compounded from powdered mulberry, starch binders, and nutritional substances such as soybean extract or purified amino acids, among other things. This material opens up two veins of questioning about how humans came to accept feeding silkworms with artificial food. The first follows the specifics of why silkworm scientists were interested in the biology of silkworm mutants that strayed from the strict mulberry diet to eat apples. Artificial silkworm food also prompts inquiries into changing mulberry acreage in wartime and postwar Japan.

A deliberate reconsideration of silk as protein allows an alternative perspective toward the intellectual and practical reasons that underwrote scientific studies of silkworm diet in the late twentieth century. This paper examines the historical motivations and contingencies leading to research in artificial silkworm food and polyphagous silkworms in postwar Japan, thereby expanding the understanding of how molecular biological concerns arose in various types of studies that contributed to making artificial food. A focus on substituting mulberry leaves with proteins provides a means to comprehend the re-scaling of sericulture in the face of urbanization and industrial diversification. Analysis of silkworm artificial food highlights the material consequences of re-scaling life in a post-imperial nation forced to reconfigure itself. The situation fosters the conditions for a vastly different range of biological questions to surface that do not seem obviously justified by the raw silk industry alone. In such a light, the postwar conversion of mulberry acreage into parking lots, apartments, and other infrastructure is at once a consequence of postwar development, a prompt for silkworm experimentation sans the labor of moriculture, and a means to understand the relationship between diet quality and silk quality.

Fat mice: Revisiting umami, monosodium glutamate, and the molecular gut

Sarah E. Tracy, The New School University, USA
Hannah Landecker, UCLA, USA

In the early twentieth century, Japanese chemists theorized a fifth basic human taste sensation associated with the amino acid glutamate, commercialized as flavor enhancer monosodium glutamate (MSG). They called it umami (translated as savoury deliciousness) and proclaimed its centrality to the modernization of nutrition in Japan. Nearly a century later, molecular techniques of mapping chemosensory reception (taste and smell perception in the oral cavity and viscera) validated umami as a basic taste sensation. Many food and sensory scientists have since enrolled umami in an evolutionary narrative, portraying the taste as a beneficial adaptation that incentivizes protein consumption. However, recent toxicological research has also investigated additive dietary glutamate as a possible endocrine disruptor.

This paper addresses a historiographical gap: a consideration of the uses of MSG not in taste or food science research itself, but in research on metabolic disorder (defined as a cluster of risk factors including diabetes, impaired glucose tolerance, dyslipidaemia, insulin resistance, obesity, high cholesterol, and high blood pressure).

Since the 1970s, diabetes research protocols (e.g. Bunyan, Murrell, and Shah, 1976) have relied upon the obesogenic effect of large doses of MSG administered intravenously to neonatal mice. These dosings bypass the oral cavity, and are not used to enhance the palatability and, thus intake, of rodent feed. Their effect is not to "add umami," or conscious pleasure in eating.

The cause of MSG-induced obesity in rodent neonates has itself gone unstudied, even though dietary additive glutamate has been thoroughly investigated in relation to potential neurotoxicity and the formation of mass lesions in the retina and hypothalamus. This paper demonstrates how study of the effects of MSG administration in young rodents is dependent upon a molecular ontology of sensation. It narrates the historical transition from a linear dose, acute toxicology, dominant in the postwar decades, to one focused on the low-dose, developmentally-specific exposures of epigenetics research that emerged at the close of the twentieth century.

Pain, care and killing in animal research

ORGANIZER

Tarquin Holmes, London School of Economics, UK

Most controversies in animal research, where not motivated by human-centred ethical and epistemic concerns (e.g. translation, replication, fraud), relate in one way or another to perceived problems of animal pain or diminished wellbeing and welfare. Historical controversies over practices perceived as producing high levels of individual or collective physical and mental pain, e.g. vivisection, deprivation studies, and toxicity testing, have led to the development of both informal and official frameworks, including government legislation, for minimising unnecessary animal pain and improving wellbeing. There is, however, considerable heterogeneity in international standards, and continuing debate about whether such measures are effective in preventing cruelty and in helping internalise a “culture of care” among lab scientists and animal techs. There are also international differences of practice in the employment of euthanasia in animal labs, which partly reflect outstanding disagreements as to the compatibility of killing with care and welfare. These differences of practice and opinion are further complicated by the difficulties of measuring animal pain and comparing pain across individuals, strains and species. This session will see contributors from history, philosophy and sociology of biology discuss how pain, welfare and death are perceived and conceived in and outside the laboratory, how such perceptions have developed over time and in different places, and whether better criteria for assessing pain and promoting welfare can be developed.

The sleep of reason? The contested role of anaesthetics as a technology of care at the 1875 Royal Commission on Vivisection

Tarquin Holmes, London School of Economics, UK
Carrie Friese, London School of Economics, UK

The Cruelty to Animals Act of 1876 marked a turning point in British animal science in that this legislation brought animal experimentation under government regulation through a stringent licensing system. Among the restrictions to which experimental biologists became subject was that “The animal must during the whole of the experiment be under the influence of some anaesthetic of sufficient power to prevent the animal feeling pain” and “The animal must, if the pain is likely to continue after the effect of the anaesthetic has ceased, or if any serious injury has been inflicted on the animal, be killed before it recovers from the influence of the anaesthetic which has been administered”. I will argue that at the 1875 Royal Commission on Vivisection, on whose findings the Act was based, prominent members of the British scientific community, with the support of moderate antivivisectionists, sought to present anaesthetics as a technology of care that, in removing animal pain, could ensure the humanity of experimental medical research. But this came in the face of accusations from radical antivivisectionists that anaesthetics were being used not to mitigate animal pain but rather "with the view of rendering the animals helpless" (Jesse), and that they were "more efficacious in lulling public feeling towards the vivisectors than pain in the vivisected" (Hoggan). These allegations appeared to receive corroboration when the histologist Emanuel Klein testified that "I never use anaesthetics, where it is not necessary for convenience". In addition to the charge that anaesthetics were a smokescreen for cruelty, their use as a technology of care was further complicated by practical limitations to their use in some experiments and by their complicity in the problem of animal death. The purpose of the paper will be show how proponents of anaesthetics as an integral part of humane experimentation dealt with these ideological, practical and ethical challenges in order to fashion a working consensus, and what assumptions and exclusions underwrote this consensus, drawing in particular on Gieryn's concept of "boundary work".

It's a fine line between pleasure and pain: Comparing positive and negative animal welfare

Heather Browning, Australian National University, Australia

Animal welfare is often described as a single state – measurable on a continuum from good to poor – but in fact there are a large variety of subjective mental states that an animal can experience, both negative and positive. How can we then speak of welfare as a single state, if it is actually a combination of all of these different affects? How can we compare these different experiences, or combine them into a single measure? To do so, we must find a "common currency" through which we can determine the relative weightings of different affects in their contribution to overall welfare. In this paper I argue that we can find such a common currency. This will allow us to make meaningful comparisons between positive and negative welfare, so we can understand the impact of pain experience on overall welfare and make more informed decisions on acceptable trade-offs.

How researchers construct ethical narratives for negative animal experiences

Rebecca L. Walker, University of North Carolina at Chapel Hill, USA
Jill A. Fisher, University of North Carolina at Chapel Hill, USA

Promotion of animal welfare and adherence to the 3Rs (reduction, refinement, replacement) is the globally recognized ethical framework guiding animal research practices. Yet animals used in biomedical research frequently experience pain and distress due to protocol interventions as well as limitations in research facility environments. How, then, do researchers construct narratives accounting for these animal experiences? In particular what do they perceive are the ethical dimensions of these aspects of the research enterprise? We conducted 47 semi-structured interviews with animal researchers, asking about welfare, the 3Rs and ethical issues, among other themes. While many researchers relayed that animals did experience some pain and distress as part of their study inclusion, they typically justified such animal use by appealing to its potentiality for human benefit. Researchers sometimes contrasted their own animal use with more invasive practices or the use of species perceived to be more sensitive, such as nonhuman primates. When asked about personal ethical difficulties with animal research, most researchers did not reference animal pain and distress, in some cases appearing not to view negative animal experiences as specifically "ethical" issues. Some researchers addressed ethical struggles over negative animal experiences but indicated these had been personally resolved or reported that any ethical difficulties had been managed by research decisions. This paper bridges philosophical and sociological approaches by engaging directly with animal researcher narratives regarding animal pain and distress and offering insight into how researchers construct – and dissemble – the ethical dimensions of animal experiences occurring as part of the research enterprise.

Research on human embryos and fetuses in the mid-twentieth century

ORGANIZERS
Nick Hopwood, University of Cambridge, UK
Solveig Jülich, Uppsala University, Sweden

With medical authority and biomedicine on the rise in the mid-twentieth century, it looked for several decades as though researchers on human embryos and fetuses had overcome their major obstacle: access to the bodies of pregnant women. The Carnegie Department of Embryology and its associates pursued two complementary strategies that elucidated the earliest stages of human development and contributed to working out the menstrual cycle. They established monkey colonies that allowed far greater control than hunting expeditions, and between the 1930s and the 1950s they collaborated with gynaecologists to extend elements of that control to clinics. The department eventually marginalized this research programme as too descriptive for an age of physiology, biochemistry and molecular biology. From 1960, by contrast, various researchers intensified those studies of the physiology of living (or rather, dying) fetuses after abortion that the US anatomist Davenport Hooker had pioneered some decades before. The Stockholm endocrinologist Egon Diczfalusy took advantage of his country's relatively liberal abortion law to perform "perfusion studies" of the "fetoplacental unit" with a view to developing new techniques of contraception and abortion. In the early 1970s, however, his research – and similar work elsewhere – ended abruptly. Amidst the general rise of bioethics and a new politics of abortion, highly public debates changed attitudes to research using not just human fetuses, but also non-human animals, especially primates. Many experiments of the previous decades – on embryos as well as on fetuses – were now unrepeatable; they struck numerous observers as ethically dubious if not frankly barbaric. The resulting regulatory frameworks, categories and ideals still shape research today. This session will explore the salient features of mid-century research programmes on human embryos and fetuses and seek to explain their rise, fall and significance.

Human embryology between “monkey gynaecology” and “egg hunts”

Nick Hopwood, University of Cambridge, UK

The Carnegie Institution of Washington Department of Embryology at the Johns Hopkins University was founded to research human embryos. Yet its colony of rhesus macaques played a more important role in human embryology even than Elizabeth Hanson, Lynn Morgan and Emily Wilson have suggested. First, the degree of control that George Corner and Carl Hartman achieved as “monkey gynaecologists” inspired not one but two collaborations to obtain human eggs “via a more or less planned route”. Around 1930, the anatomist Edgar Allen persuaded clinicians in St Louis and Detroit to take unfertilized eggs from patients’ fallopian tubes and correlate their presence with menstrual history and the condition of the corpora lutea. Between 1939 and 1953, Arthur T. Hertig and John Rock of Harvard Medical School went further: they removed fertilized eggs and very early embryos after Miriam Menkin encouraged patients to have intercourse on specific days before clinically indicated hysterectomies. Second, Hartman’s account of macaque development served as a template for the still-standard “Carnegie stages” of human embryos. In the early 1940s, when George Streeter began to set these up, he accepted Hartman’s answer to the difficult question, “Who shall tell us the age of human embryos?”: “The monkey shall tell us.” Somewhat controversially, this put human embryos in a subordinate position within the institution established to study them in their own right. In light of these transfers between primates, the talk will reflect on the “species politics” of embryology.

The rise and fall of the fetoplacental empire: Human fetal research in Sweden, 1950–1970

Solveig Jülich, Uppsala University, Sweden

Between 1960 and 1971 the Swedish endocrinologist Egon Diczfalusy and his research team at Karolinska Institutet in Stockholm performed “perfusion studies” on aborted human fetuses. A “fetus chamber" that kept the fetuses "alive" outside the uterus enabled the researchers to examine the hormonal regulation of fetal physiology and development. Diczfalusy coined the term "fetoplacental unit" to describe the close interactions between the fetus, the placenta and the mother. During a period of population "crisis", fetal research at the institute was increasingly oriented towards developing new contraceptives and methods for termination of pregnancy. In the early 1970s, however, the "fetoplacental empire" (Diczfalusy) came to a sudden end and has yet to find its historian. This paper investigates for the first time some of the conditions that were decisive in promoting Diczfalusy's perfusion studies, and discusses why these were eventually stopped. Using medical publications, policy documents and grant applications it will demonstrate the active role played by Swedish and American funding agencies in supporting biomedical uses of fetuses taken from women who underwent legal abortions in Sweden in the decades after World War II. Newspaper reports and television programmes are examined to highlight the role of the media in making fetal research public, how Diczfalusy's studies were framed as controversial, and the consequences for developing national and international ethical guidelines and legislation.

Lives worth living: Swedish debates about fetal and animal research in the 1970s

Helena Tinnerholm Ljungberg, Uppsala University, Sweden
Per-Anders Svärd, Örebro University, Sweden

Responding to postwar demands for ethical regulation of scientific practices as well as demands from new social movements, notably for animal protection, women's and reproductive rights, Sweden saw a number of political debates over the ethics of research in the 1970s. Many of the debates centred on issues including fetal research and animal experiments. At stake were questions of moral permissibility, public transparency and scientific freedom. These debates, however, did not only reveal different moral perspectives on how to conduct scientific research – they also contributed to the construction of ontological boundaries between different life-forms. This paper explores the political debates over research on fetuses and animals that took place in the 1970s and laid the groundwork for current modes of ethical regulation in Sweden, particularly in the form of research ethics committees. Taking a post-structuralist approach to policy analysis, the paper aims to show how both the “human” and the “animal” in human/animal relationships emerged as contingent and context-specific concepts that were shaped by the need to overcome a mounting legitimacy crisis for medical research. By analyzing Swedish government bills, reports, motions and parliamentary debates from the 1970s, we ask how animal and fetal research were constructed as particular kinds of policy problems and linked to a particular set of legitimacy-boosting solutions. A special focus is placed on the extent to which human adults, fetuses and non-human animals were deemed worthy of protection, and how the vulnerability of these categories was negotiated and problematized. By comparing the debates about human, fetal and animal research, we furthermore argue that it is possible to discern the rules of a broader discursive regime that not only defined the borders between humanity and animality, but also produced a particular ideal of the life worth living.

Function and health in ecology, part I

ORGANIZER

S. Andrew Inkpen, Brandon University, Canada

This session will address the concepts of function and health in ecology. The goal will be to provide a sustained, critical discussion that is relevant to both philosophers of science and ecologists. Functional ascription is central to the discourse of modern ecology, both microbial and macrobial, and these ascriptions are made in a variety of contexts. Ecologists assign functions when they specify the causal roles played by organisms as constituents of ecosystems (e.g., designating a group of organisms as “primary producers”): indeed the word "system" often implies collective functionality. Theoreticians and experimentalists classify species into functional groups on the basis of their shared adaptive strategies (e.g., the functional group of "pollinators"), and debate community and ecosystem function (i.e., the capacities these systems manifest, such as nutrient cycling or digestion). Moreover, function is intimately tied to understandings of community and ecosystem health that are popular in clinical and environmental discussions. This diversity provokes three immediate philosophical questions:

1. Can current philosophical accounts of function improve our understanding of these functional ascriptions (in the same way that etiological or "selected effect" theories improved our understanding of teleological and normative language in evolutionary biology)?
2. Is one philosophical account enough or should the diversity of scientific goals motivating these projects force us to adopt within-discipline functional pluralism in ecology?
3. How does ecological function relate to the concept of ecosystem health?

Heeding the rich diversity of problems, contexts, and histories within which function is invoked, this session will provide a philosophical analysis of function in this discipline, aiming to help address these questions.

Ecological functions in ecosystem ecology: A defense of the systemic capacity account

Jay Odenbaugh, Lewis & Clark College, USA

Along with (Maclaurin and Sterelny, 2008), I have argued the best account of ecosystem functions are systemic capacity functions (Cummins, 1975). Two approaches to ecological function in ecosystem ecology have sprung up: the organizational account (Nunes-Neto et al., 2014) and the persistence account (Dussault and Bouchard, 2017). In this talk, I argue both the organizational and persistence accounts go beyond the minimalism of the systemic capacity account. Moreover, an ecosystem's closure of constraints or propensity to persist are not necessary for ecosystem to have functions, and there are ecosystem functions they cannot make sense of. Thus, we should accept the systemic capacity account if we are to make sense of the ecosystem functioning.

Ecological functions as contributions to ecosystem resilience

Antoine Dussault, Centre interuniversitaire de recherche sur la science et la technologie & Collège Lionel-Groulx, Canada

This presentation will build on recent arguments that the selected effect theory of function – often called the "standard line" on functions (Allen and Bekoff 1995) – does not constitute a promising starting point for developing an account of ecological functions that meets the theoretical needs of functional ecology (Dussault 2018, forthcoming). In line with those arguments, I will maintain that ecological functions should be conceived ahistorically, as present or potential contributions to resilient ecosystem functioning. I will first argue that, although the causal role account of ecological functions (Maclaurin and Sterelny 2008; Odenbaugh 2010) adequately captures some central aspects of the practice of functional ecologists, it remains too liberal in light of functional ecologists' interest in studying the relationship between biodiversity and ecosystem resilience. Next, I will argue that, although the alternative organizational account of ecological functions (Nunes-Neto, Moreno, and El-Hani 2014) fixes some of the limitations of the causal role account, it does so only at the price of becoming too restrictive in light of the fact that functional ecologists do not usually consider ecological functions as explanatory of the presence of their bearers. This will lead me to maintain that an account of ecological functions as present or potential contributions to ecosystem resilience strikes a promising balance between the excessive liberality and excessive restrictiveness of the causal role and organizational accounts. Such an account of ecological functions, I will observe, has some commonalities with goal contribution and life chances accounts of function developed for conceptualizing the functions of parts and traits within individual organisms (Boorse 1976, 2002; Walsh 1996; Wouters 2003).

Ecological finalism without panglossism: The organizational account facing the challenge of the broad scope of ecological functions

Victor Lefevre, Pantheon-Sorbonne University, France and INCT IN-TREE, Brazil.
Nei Nunes-Neto, Federal University of Bahia and INC IN-TREE, Brazil.
Charbel Niño El-Hani, Federal University of Bahia and INCT IN-TREE, Brazil

In this paper, we use the concept of closure of constraints elaborated by Montévil and Mossio (2015) to improve the organizational theory of ecosystems which was elaborated by Nunes-Neto, El-Hani, Moreno, and other colleagues, in previous works (see Nunes-Neto, and al., 2016 ; Nunes-Neto and al., 2014 ; Nunes-Neto, and al., 2016). In a nutshell, we consider an ecological function as an ecological constraint being a part of a set of constraints which produce each other. We address the following question: does our theory deal well with the broad scope of functional ascriptions made by ecologists? We defend that our approach allows ecologists to ascribe functions to abiotic parts of ecosystems (for example, fires and beaver dams) without being too liberal like the role causal approach adopted by Odenbaugh (2010). The non-liberality is an important feature for our approach because it considers functional explanations as teleological explanations and it is inclined to realism. Therefore, being too liberal would mean for us falling in panglossism, for example pretending that the rain exists to feed plants. However, one might think our approach is too much restrictive regarding the ecologists practices. We assume to defend a revision of scientific practices: for a given ecosystem, our distinction between ecological constraints inside the closure and outside the closure is a helpful distinction between entities that, on the one hand, participate to the self-determination of the ecosystem and are objects of genuis teleological explanations, and, on the other hand, entities that are merely useful for the ecosystem without being parts of it and having to be explained teleologically.

Function and health in ecology, part II

Ecosystem function, dysfunction, and the concepts of disease

Tamar Schneider, University of California, Davis, USA

Definitions of dysfunctional ecosystems ascribe certain functions the ecosystem ought to have as a “normal’ or within its normative capacities. However, attributing a dysfunction to an ecosystem narrows them to their desired functions. Instead, the notion “Role function” (i.e., function as a causal contribution to systematic capacity) looks at the function as a causal contribution embedded in a system of interactions that is open (to other systems). A dysfunction presupposes definitions of necessary functions, thus, clear boundaries as well as the identity of the entity/organ/ecosystem (i.e., the identity is its function).

However, I argue that there can be more than one function and that functions are dynamic and can be redundant or change. Thus, it is not possible to know all the necessary functions, only of some sufficient functions, therefore we cannot argue for dysfunction in general. We can argue for dysfunction in local and situated cases -- in a specific context with the desired function for a certain purpose that is not obtained.

Defining ecosystem dysfunction is to have a close set of function that the ecosystem ought to have, and by not having it the ecosystem is dysfunctional. Without such definition, we can think of the ecosystem as possessing various functions within a web of interactions such that it reacts to changes and can change accordingly or die. Such openness and interactionist approaches change the perspective of boundaries as well as the terminology of functions. To argue that I will use the holobiont notion as an ecosystem and the notion of holobiont's immunity, i.e., holobiont self, demonstrating an alternative perspective on immune system function as part of the ecosystem of the holobiont. Thus, I argue that we need to change the definition or analogy of disease from dysfunction to the lack of role function. Acknowledging that this is a local claim, also has social and political value. For example, arguing that fertility organs after menopause (or for women who don't desire children) are dysfunctional leads to higher rates of hysterectomy in benign conditions which correlate with increased rates of heart diseases (Parker et al. 2009, 2013).

Dysfunction and health in ecology

S. Andrew Inkpen, Brandon University, Canada

There is a near consensus among philosophers of ecology that functional ascriptions in ecology are not selected effect functions. For one thing, in the areas of ecology that draw most explicitly on functional analyses, ecologists do not in fact draw on backward-looking functions in their analyses. Rather, ecologists tend to adopt a broadly metabolic perspective towards ecosystems according to which functions are effects that contribute to system goals, irrespective of history. Furthermore, regardless of what ecologists do in fact do, there is also a near consensus that ecological systems do not have the right kind of history (that is, a history of selection) to support selected effect functions anyway. This argument usually proceeds by showing that ecosystems are not units of natural selection and thus their parts are not selected for the system-level effects they contribute. With selected effect functions off-the-table, many have accepted that ecological functions are present- or forward-looking functions, the most commonly invoked account being the causal role account (or a modification, like the fitness-enhancing propensity account). But there is a problem with this answer. This is the problem of explaining ecological dysfunction or, in general, functional normativity: how can an entity possess a function that it cannot perform? Although the selected effect account can accommodate dysfunction, forward-looking accounts, by themselves, cannot. But, the question is, if the selected effect account is off-the-table in ecology, can we make sense of dysfunction in ecology? This talk will address this question. And since naturalistic theories of health involve dysfunction, it will also consider a closely related question: is a naturalistic theory of ecological health possible?

Rivers, humans, and microbes: Ruth Patrick's limnological approach to measuring the health of ecological systems, 1940–1960

Lloyd Ackert, Drexel University, USA

In the 1940s Ruth Patrick (1907–2013) developed a novel approach to studying rivers as biological and ecological systems. Applying limnology methods to study the Conestoga river basin Patrick measured the human impact on nature, especially related to water sanitation and industrial pollution. Her multidisciplinary team approach to surveying the chemical make-up, and diversity of organisms ranging from microorganisms, especially diatoms to larger organisms, became known as the Patrick Principle" coined by the conservation biologist Thomas Lovejoy. This "Principle", founded on her doctoral training in botany (University of Virginia) and close collaboration with leading scientists including especially G. Evelyn Hutchinson, would characterize her ecosystems research during her seventy-year career at the Academy of Natural Sciences (now of Drexel University) in Philadelphia (ANS). There she pioneered a unique model of "ecosystem services" that placed ecology at the service of industry and government institutions. Based on Patrick's extensive and newly available archival materials at the ANS, this talk will highlight her Conestoga survey and how she correlated microbial species diversity with the health of an ecological system. This report also will necessarily engage related topics important for understanding how she succeeded in negotiating the spheres of science, government, and industry. These include her biography, experiences as a woman in 20th century biology, and personality.

Contesting entomological practices

ORGANIZER

Dolly Jørgensen, University of Stavanger, Norway

Acceptable scientific practices become defined over time by communities of practitioners in social and technological contexts, as Bruno Latour discussed in his classic *Science in Action* (1988). “Proper” practice, however, can be contested both by those inside the accepted communities and those excluded from them. In this panel, the three presenters focus on contestations within entomology, the scientific study of insects, in order to explore how such conflicts play out during biological collection and description activities. The first paper focuses on Maria Sibylla Merian (1647–1717) who is well-known for her elaborate books containing prints of the metamorphosis of caterpillars into butterflies and moths. Through her images, Merian contested the belief in spontaneous generation And certain enlightenment scientific practices. The second paper turns to a controversy in the mid-1800s over a newly discovered parasitic insect from beavers. A complex scientific argument emerged as different scientists attempted to classify the insect while relying on a very limited number of specimens. The third paper moves into the early 20th century with the entomologist Margaret Elizabeth Fountaine, who used a varied repertoire of practices: collecting, classifying, painting, breeding butterflies, observing larvae and butterfly behaviour, and publishing scientific articles. She pushed back on accepted entomological practice as an obligatory amateur and obligatory collector.

Summerbirds of indescribable beauty: At the margins of Merian’s metamorphosis-pictures

André Krebber, University of Kassel, Germany

In the second half of the 17th century, the artist Maria Sibylla Merian (1647–1717) devoted her life to the study of the metamorphosis of caterpillars into butterflies and moths. Francesco Redi

(1626–1697) is famous for having first disproven the theory of spontaneous generation – the assumption that insects develop spontaneously from inanimate matter rather than from eggs – already in the 1680s, but his undertaking was something quite different from Merian's endeavor.

Redi disproved spontaneous generation by way of sealing meat in a container and observing maggots appearing on its outer cloth-lid, thus suggesting that they were deriving from a parental organism that had deposited eggs on the cloth rather than from the rotting meat itself. Merian, by contrast, provided evidence for the existence of a metamorphosis through a practice of collection and laborious experiments that saw her identify the various radically differently appearing stages that Lepidopteran species transition through during their individual life cycles as one and the same species by way of nursing caterpillars and sometimes eggs to their adult winged form.

She disseminated her studies through elaborate books containing prints collating the different stages of the life cycle of individual species on their feeding plant and written descriptions of the process, thus bringing the metamorphosis from parent to egg to caterpillar to pupa to life for her readers. My paper explores how Merian's images thereby not only provided a powerful argument for contesting the believe into spontaneous generation but move beyond the conditions of an exact science that builds on the complete decoding of its objects of knowledge.

Instead, Merian's images contest their own representation of the insects and their metamorphosis as representatives of a species and a standard universal process by incorporating the individuality of both the objects and the process. By employing artistic modes of studying the world in her entomological research, the representations of her objects of knowledge thus contest not just certain enlightened practices, which in fact enabled Merian just as much as her male colleagues in revealing the process of metamorphosis, but also the universal reach of our scientific categories.

Scale of her objects of knowledge as well as the topic of metamorphosis matter here, by providing a source of change and flux.

By making the change of perspective that the gaze on the insects through the magnifying-glass affords explicit as well as a composition that actively sets the individual elements of her images against one another, her metamorphosis-pictures capture the continues change of the world, for which the metamorphosis with its de- and re-composition of matter stands, as a limit for our knowledge production. Thereby, Merian's entomology finally provides an opportunity to contest an enlightened scientific practice while opening up an alternative scientific enlightenment that promises capable of coming to terms with our current experience of nature by inscribing its indeterminacy into our deciphering of the world.

Entomological entanglements: The controversy over the beaver beetle parasite

Dolly Jørgensen, University of Stavanger, Norway

In 1869 two descriptions were published of a small parasitic insect that had been collected from a beaver in the Rotterdam zoological gardens. The Dutch entomologist Ritsema and the English entomologist Westwood came to different conclusions about the insect in hand: one claiming it was a flea and the other put it into a new insect order. A third entomologist from France, Le Conte, intervened in 1872 and declared both wrong by identifying the insect as a beetle. Even after this "definitive" description, the insect continued to be debated in entomological circles, with even ad hominem attacks on some of the scientists. The insect, which became known as the beaver beetle *Platypsyllus castoris,* was difficult to describe because it was difficult to find samples, a condition caused by the rarity of its host (beavers) in Europe at the time, and because of differing descriptive practices.

By exploring the case of the beaver beetle and the scientific practices around it, this paper will shed light on how entomological controversies can arise and can fail to find a quick resolution. Both parasites and entomologists live in communities and are entangled with the other members of those communities.

Obligatory collector and imperial traveller: The entomological practices of Margaret Elizabeth Fountaine between 1892 and 1940

Leore Joanne Green, University of Cambridge, UK

This paper posits at its centre British lepidopterist Margaret Fountaine's set of entomological practices, and considers how they were shaped by her gender, class, and position in the entomological community. Little attention has been paid to the gendering of practices, and to how women navigated it – while there are a few studies on the subject of women's scientific writing, much less has been written about other scientific methods, such as illustration, collecting, and classifying, in the context of gender. Women often employed different practices from men, or adapted available entomological routines to make them acceptable and suitable to respectable women, while some scientific procedures were simply inaccessible to female practitioners because they required the use of expensive equipment, like high-magnitude microscopes, that was kept in laboratories which did not employ women.

One of Fountaine's main accomplishments was a collection of 22,000 specimens of butterflies. The type of collection Fountaine constructed was only possible for members of the upper classes – it boasted exotic specimens and was constructed as a global compendium, and together with her specialised knowledge of unknown larvae, gave her authority and credence in the entomological community allowing her to surmount the strictures of her gender.

I will show that despite being predominantly known as a collector, Fountaine used a varied repertoire of practices: collecting, classifying, painting, breeding butterflies, observing larvae and butterfly behaviour, and publishing scientific articles. However, I will also argue that as a female entomologist, the options available to her were limited. Like many other women at the time, she was not just an obligatory amateur (per Marilyn Ogilvie's definition), but also an obligatory collector. Despite her conflicted feelings towards killing insects, she had no choice but to continue collecting in order to practice entomology. Although she used other practices, such as classifying and writing scientific articles, were not considered as amateur or feminine, Fountaine limited herself by adapting these practices and never venturing far from what was acceptable for a female practitioner. She was careful to avoid anything that could be deemed as overstepping her bounds, such as contesting taxonomical classifications and the description and naming of new species. She was also limited in how she could write, and in how she could convey her feelings towards her objects of observation and study. In her scientific writing she had to mask her true feelings toward killing butterflies, and portrayed only a part of her persona and emotions, for sympathetic feelings were considered feminine and unscientific, and thus unacceptable. As a result, her sympathies towards insects are recorded only in her diary, while in her publications she strategically appropriated a traditionally male and imperial narrative, that of the hunt. This narrative served two purposes: first, it allowed Fountaine to repress any ambivalence by revelling in the chase, and second, it lent her an aura of authority and credibility.

Philosophy in biology and medicine: Biological individuality and fetal parthood, part I

ORGANIZER

Elselijn Kingma, University of Southampton, UK

Every human, and indeed every placental mammal, is the product of a pregnancy – a protracted period of development inside the maternal organism's body. Philosophers have explored some issues related to pregnancy, most obviously abortion and the value and metaphysics of coming into existence, but have paid relatively little philosophical attention to the actual biological process of pregnancy. That is a remarkable omission because this life-changing process raises fascinating philosophical questions, almost all of which have been under-investigated: what is the relationship between foetus and maternal organism? How do pregnant organisms and/or persons relate to their potential future offspring and to their pre- and post-pregnant selves?

How are both pregnant organisms/persons and foetuses changed by pregnancy? These questions are not just interesting and important in their own right, they may affect adjacent topics that do feature prominently in wider philosophical enquiry. Examples include questions about personhood, personal identity and personal persistence; the boundaries of the self and the relationship between self and body; coming into existence; and a variety of theoretical and practical topics in reproductive ethics, such as the rights over and obligations towards foetuses and/or (future) offspring. These may not just be affected by a better understanding of pregnancy; it may be necessary to understand pregnancy before we can adequately tackle these other topics at all. Pregnancy does not fit the legal, social and philosophical paradigm of humans as discrete independent individuals with firm boundaries. In this unique physiological process, the boundaries between human beings are blurred: physically, biologically, experientially and perhaps even metaphysically. Accommodating pregnancy, as we must, may therefore require racially rethinking key conceptual schemes in several parts of philosophy. In forthcoming work, Kingma begins to tackle the above questions. She investigates the relationship between the fetus and the maternal organism, arguing that that the fetus should be considered part of the maternal organism. She moreover suggests that the physical/physiological intertwinement in pregnancy raises questions for biological individuality. This is interesting; problems of individuality are typically raised in terms of the biology of plants, microbes or other organisms, such as Portuguese man o' war, very distantly related to *Homo sapiens.* By contrast, mammals have been viewed as relatively unproblematic when it comes to the question of counting organisms (notwithstanding contemporary literature on symbiotic gut flora and so-called "holobiont" theory). Close consideration of pregnancy suggests that it is a significant and overlooked source of "problems of individuality" in mammals. This symposium takes up and investigate further the questions raised by Kingma, at the intersection of metaphysics and philosophy of biology. Should the parthood thesis be accepted, or are there further options? What other evidence supports or contravenes the parthood thesis? And what does this imply for biological individuality? It thus aims to develop a biologically informed metaphysics of pregnancy, and introduces a novel research area within the philosophy of biomedicine: one with great potential to interact with wider philosophical research.

Part, process and pregnancy

Paul E. Griffiths, University of Sydney, Australia

Kingma (2018, In Press) has proposed that the fetus is a part of the mother as well as a part of the offspring, raising the more general issue of whether and when organisms share parts. Griffiths and Stotz (2018) proposed a developmental systems account of the organism according to which an organism is a process whose principle of genidentity is a life-history strategy. In this presentation I explore Kingma's proposal from the perspective of this theory of the organism. To allow a more concrete treatment, I ignore all but the genetic elements of the developmental system. The key issue, I suggest, is whether the phenotype that a genetically individuated organism manifests at in some age class is an expression of the life-history strategy of that genetic individual, or the strategy of another genetic individual(s), or some compromise between these. This perspective is implicit in some existing scientific discussions of the identity of the placenta and associated structures. From this perspective it is entirely possible that the very earliest stages of the fetus are part of the mother but not part of the offspring.

Pregnancy, parthood and proper overlap

Alexander Geddes, University of Southampton, UK

Elselijn Kingma (forthcoming) defends what she calls the "parthood view" of pregnancy, according to which "the foster is part of the gravida" (rough translation: the post-implantation embryo or fetus is part of the organism that gestates it.) More specifically, she argues that this view is widely rejected, but for no good reason, and that considerations drawn from biologically-informed accounts of organisms can be shown to support it. In this paper, I identify a number of shortcomings in Kingma's case for this view, and defend an alternative that she fails to consider.

In §1, I introduce some important mereological and temporal possibilities that her discussion elides, and argue that these possibilities must be taken seriously if we are to properly assess the import of the biological evidence. In §2, I raise a general worry for Kingma's argumentative strategy, by pointing out a problematic double standard at work in her argument: she dismisses principles that run counter to the parthood view on certain grounds, and yet relies unquestioningly on accounts of organisms that seem to be criticisable on those very same grounds. And in §3, I raise some more specific worries for her claim that the biological evidence speaks in favour of the parthood view. First, the accounts of organisms on which she draws do not adequately distinguish between questions of organismic individuation or existence and questions of organismic parthood. Second, and most significantly, even if we treat the four criteria Kingma favours as criteria for organismic parthood, they do not clearly or consistently speak in favour of the parthood view of pregnancy. Rather, to the extent that any verdict emerges as the most plausible, it is one of proper overlap throughout pregnancy.

One or two? A process perspective on pregnant individuals

Anne Sophie Meincke, University of Southampton, UK

How many individuals are present where we see a so-called pregnant individual? It seems there are exactly two possible answers to this question: a pregnant individual "is", as it were, either one or two individuals. The standard answer is the latter, championed most prominently by the predominant Containment View of pregnancy, according to which the foetus, or "foster", resides in the gestating organism like in a container (Smith & Brogaard 2003, Oderberg 2008). The first answer has recently found some support in the Parthood View, according to which the foster is a part of the gestating organism (Kingma forthcoming).

In my paper, I propose a third answer: a pregnant individual has to be understood as a bifurcating hypercomplex process and, hence, is neither two individuals nor one individual but something in between one and two. The Process View, by acknowledging the processual nature of organisms (Meincke 2018a, Meincke 2018b, Meincke forthcoming, Nicholson & Dupré 2018, Dupré 2012), overcomes the difficulties the Parthood View encounters when combined with the widely-shared view that organisms are substances.

I proceed in two steps. First, I assess the Parthood View, arguing that it rightly opposes the Containment View by stressing the functional integration of the foster in the gestating organism, but that it

i. operates with a notion of parthood that is either inappropriate or too vague, and
ii. struggles to maintain, in a substance ontological framework, the natural assumption that fosters are entities that continue to exist through and after birth.

Second, I present the Process View. After briefly explicating the general reasons that speak for a process view of organisms, I explain why we should think of a pregnant mammalian organism as a bifurcating hypercomplex process, i.e., a process that incorporates and actively maintains an asymmetric internal relation between organised complexes of lower-level processes through processes of both mutual stabilisation and successive disentanglement. I argue that the Process View is able to reconcile the "parthood claim" that the foster is a part of the gestating organism and the assumption that the foster is numerically identical with the new-born baby.

Philosophy in biology and medicine: Selected effects and dysfunction, part II

ORGANIZER

Peter Takacs, University of Sydney, Australia

Diagnosed medical disorders and pathologies – physiological, morphological, behavioral, or psychological – presume contextual impropriety or systematic dysfunction. Any such disorder accordingly implies an account of proper functioning. For etiological-historical accounts informed by evolutionary considerations (or “selected effects accounts”), dysfunction occurs when a trait fails to perform the function whose effect on fitness was selected for in [N]ormal conditions and, thereby, explains the origin or subsequent retention of the trait (Millikan 1984; Neander 1991; Griffiths 1993; Godfrey-Smith 1994). This session will explore the adequacy of selected effects accounts of biomedical dysfunction and subsequent prescriptions for intervention, clinical and otherwise.

Assessing fitness functions in selected effects accounts of psychological dysfunction

Peter Takacs, University of Sydney, Australia

Selected effects accounts have recently been proposed for mental disorders, such as depression and generalized anxiety disorder. Two distinct approaches and seemingly inconsistent conclusions have subsequently emerged. One approach maintains that common mental disorders are objectively dysfunctional in an evolutionary sense and therefore focuses on elucidating the genetic mechanisms which maintain susceptibility (Nesse 2004, 2019; Keller et al. 2006; Vercken et al. 2012). Others have argued that at least some common mental disorders might be developmental mismatches due to phenotypic plasticity and, although genuine disorders, are not dysfunctional from an evolutionary perspective (Glover 2011; Garson 2018; Griffiths and Matthewson 2018). The cogency of either approach hinges on which component(s) of fitness is(are) maximized. I examine how the two approaches differ and whether the biological interpretations of the distinctive formal fitness functions can be reconciled.

The fundamental problem with evolutionary definitions of disease

Joshua Christie, University of Sydney, Australia

A much-criticised view in the philosophy of medicine defines a pathological phenotype as one that fails to perform the function that it was selected for by evolution. Here we sidestep issues regarding whether this "selected effects" approach is a useful heuristic for characterizing pathological states and instead consider a more fundamental problem. The evolutionary definition presumes that when a phenotypic trait evolves by natural selection, some activity or activities of that phenotype, in interaction with ancestral environments, explains why ancestors with the phenotype proliferated or persisted. In other words, the trait will be an adaptation for one or more specific functions. For the selected effects account to be valid, a trait's evolution must be driven by at least one identifiable function performed by that trait.

But does natural selection always transpire in such a way that we can identify a function's specific contributions to the evolution of a trait, even in idealized theoretical models? When selected effects functions can be theoretically attributed to traits, can we in practice identify the historical signatures of selection (e.g. in DNA sequences)? Here we will use mathematical and computational models to consider the limitations of the selected effects position when applied to biological systems. Specifically, we are concerned with

i. characterizing when selected effects are well-defined in models used by theoretical biologists;
ii. how the choice of modelling framework influences interpretation of selected effects functions; and
iii. whether signatures of selected effects can be identified in real populations.

Why medical dysfunction is (still) not selected effects dysfunction

Elselijn Kingma, University of Southampton, UK

Griffiths & Matthewson (2018) have recently defended the so-called "selected effects account" of dysfunction as the best candidate for a naturalist account of disease. Their paper is a welcome and important contribution to a literature in which, amongst the naturalist position, undue focus has rested on Christopher Boorse's biostatistical account of dysfunction/disease. Griffiths & Matthewson's up-to-date-with-current biology account does much to strengthen and improve a position that so far has suffered from being mainly defended by people insufficiently attuned to the details of (evolutionary) biology.

This paper examines whether Griffiths and Matthewson's improved selected effect accounts can survive the following problem: in those cases where traits and effects have been affected by organisms' development in "new" environments, can the account state whether these traits are functional or dysfunctional, and therefore healthy or disordered? This question builds on a general tenet of developmental biology, which is that traits and their effects do not exist in but are the result of the environment in which an organism develops. Immune systems, for example, develop in and are primed by the environment.

Griffiths and Matthewson's account is meant to accommodate such developmental plasticity. Nonetheless I argue that it lacks the resources to accommodate disorders that in some sense are the result of our developing in non-ancestral environments. And since many disorders are likely to be the result – in one way or the other – of our developing in "new" environments, this spells trouble for the selected effects account of disorder – even in its most sophisticated form. The trouble may be avoided by significant revision of our concept of medical disorder. But that – I argue – takes us too far from the central interests of medicine to serve it appropriately.

Idealizations in computational neuroscience: Facticity, pragmatics and the coding heuristics

ORGANIZER

Daniel Kostic, University Bordeaux Montaigne & University of Paris 1 Panthéon-Sorbonne, France

The ever-growing use of models in scientific practice over the last few decades has elicited a great deal of philosophical interest, particularly regarding the questions such as: how scientific models represent, when they explain and whether idealized models can provide understanding. However, not enough attention so far has been devoted to the following tightly interconnected questions: can idealized models provide understanding via non-causal explanations (facticity), does explanatory power and target explananda change when transferring models from one field to another, e.g. from economics to biology, or from primatology to human computational neuroscience (pragmatics), and finally, is there a heuristic for detecting and eliminating agent-based epistemological and cognitive biases in neurocomputational modeling (coding heuristics). This interdisciplinary session will explore these issues and the ways in which they are interconnected in a systematic way. Namely, the facticity of understanding itself is a relatively well discussed issue in the context of causal explanations, but it is not quite clear whether the same epistemic norms apply to non-causal explanations and understanding. The problem of facticity figures in both pragmatic and heuristic questions. In this sense, the epistemic norms under which the idealized models provide understanding should be preserved in model migration, i.e. we want to know when the model is transferred from one domain to the next that both the representation relation, explanatory power and understanding remain unchanged. Both facticity and pragmatics of idealizations are also very important parts of what it is for the code in a neurocomputational model to be explanatory, especially when the code itself can be used in multiple models, at multiple scales and in multiple domains. We approach these issues from three different perspectives (epistemology of explanatory power and understanding, epistemology and methodology of modeling, and coding in integrative neuroscience) and offer a framework for thinking more systematically about these deeply interconnected issues.

Non-causal understanding via spatially embedded networks in the brain

Daniel Kostic, University Bordeaux Montaigne & University of Paris 1 Panthéon-Sorbonne, France

In the literature on scientific explanation, the interest in facticity of understanding is ever growing. There are two general camps in this debate, factivists and non-factivists. Factivists argue that idealizations can provide understanding only if they are partially (Strevens 2007) or approximately true (Khalifa 2017). On the other hand, non-factivists claim that idealizations can provide understanding independently from the explanation in virtue of being effective or by exemplifying the features of interest (Elgin 2007, 2018; de Regt 2009).

In this talk, I argue that spatial embedding of networks in neuroscience provide explanations that are non-causal and idealized, which prima facie seems to support the idea of understanding without explanation. However, I show that they provide understanding that is both explanatory and factive.

This point is most evident from the cases where structure determines the function. The term "structure" is posited in many different ways, most of which sidestep what would be considered the causal organization of the brain. For example, Bassett and Stiso (2018) represent brains as spatially embedded networks and argue that the wiring rules that differ in healthy brains and in neurodevelopmental disorders such as schizophrenia are driven by wiring cost, which itself is determined by the spatially localized modules and hierarchically nested topology. Topology in this sense refers to the abstract mathematical properties of the network. But how can this abstract mathematical structure constrain the functional wiring drivers in health and disease, if it sidesteps the causal organization in the brain?

Bassett and Stiso's explanation of how topological structure affects and determines cognitive function describes counterfactual dependencies between wiring minimization, spatially localized modules, and physical Rentian scaling. These counterfactual dependencies don't capture the core causal factors, thus the spatially embedded networks are idealizations that provide non-causal, which in effect means that the understanding from them is both explanatory and factive.

I conclude that the distinction between different kinds of facticity (causal and non-causal) perhaps better accommodates the diversity of scientific explanatory practices than the distinction between factivism and non-factivism.

Pragmatic constraints on transferring models in interdisciplinary science: The case of neuroeconomics

Cédric Brun, Université Bordeaux Montaigne & Université de Bordeaux, France

Recent research in philosophy of science has paid a considerable amount of attention to the epistemic and ontological aspects of modeling in science. For example, when building models at different levels of detail we want to know what kind of details are representationally and explanatorily relevant. Indeed, the practices of science entail elaborating models that are simplifications, abstractions or idealizations of very complex systems, in order to produce explanatorily and predictively relevant theories of the phenomena under scrutiny. If one takes seriously the view that models' elaboration is intimately linked to explanatory purposes which are specific to a domain of phenomena, the issue of model's borrowing or model's transferring becomes critical. What are the conditions under which transferring a scientific model from one domain to another can be legitimate against the chances that it might be misused, and, therefore, might provide irrelevant results? This question can be seen as a subproduct of "the problem of scientific representation" (Callender and Cohen 2006). Building our argument on a deflationary representationalist account of models (akin to Suarez 2003), we show that borrowing models from one scientific field to another rests on the recognition of pragmatic norms which need to be precisely defined. As a case study, we will examine how non-human primate models in neuroeconomics are depending on such model transferring, in order to assess the soundness of our argument. In particular, we will be looking into the experimental work on prototypic money exchange models in capuchin monkeys and how it relies on a set of behavioral and neurobiological models of decision making.

The eye of the modeler

Nicolas Rougier, Inria Bordeaux Sud-Ouest & Université de Bordeaux, France.

The three-levels analysis (computational theory, representation, and algorithm, hardware implementation) proposed by D. Marr has profoundly influenced the neuroscience community during the last few decades. At the higher computational level, Marr proposes to investigate what is the goal of the computation, why is it appropriate, and what is the logic of the strategy by which it can be carried out? There is however a hidden difficulty for the modeler since the goal and the logic she may find in a behaving organism is biased by her own cognition. It thus draws consequences on the core design of a model but maybe, more importantly, it draws consequences on the interpretation and the explanation this model may provide. Using a simple model of decision making, we'll show how its interpretation remains ambiguous until it is actually incarnated into a body (i.e. a robot). Yet, if such embodiment helps in the interpretation of the model by giving us access to the observation of its behavior, it still does not guarantee the interpretation is unbiased. We'll illustrate this conundrum on a simple but fully specified formal model whose "behavior" can be naturally interpreted but does not correspond to the underlying hardware implementation.

The statisticalist-causalist debate: New contributions

ORGANIZER

Adam Krashniak, Tel Aviv University, Israel

The last couple of decades have seen a heated debate among philosophers of biology regarding the structure of evolutionary theory and the roles that natural selection and drift play in the theory. On one side, the "causalists" argue that selection and drift are two distinct forces or causal factors that affect evolutionary change, such that selection causes fitter variants to increase in frequency and drift causes divergence from the expected evolutionary outcomes (e.g., Sober 1984; Stephens 2004; Millstein 2006). On the other side, the "statisticalists" argue that selection and drift are not causes of evolutionary change but rather refer to two kinds of population-level outcomes of the many different causes that take place in populations, which are explained and predicted by statistical properties of these populations (e.g., Walsh et al. 2002; Matthen & Ariew 2002). Selection is explained by the fact that some variants are expected to increase in frequency in the long run as a result of the different causal interactions that take place in the population, and drift is explained by the fact that when populations are finite the actual evolutionary outcome will tend to diverge from the expected one. The statisticalist-causalist debate has consequences for other important questions in evolutionary biology, for instance the question regarding units and levels of selection (Walsh 2004), or the question whether and how selection explains adaptation (Walsh 2000; 2003). The papers in this session present new contributions to the debate by presenting new arguments in favor of the causalist and the statisticalist positions. In talk 1, Krashniak will present a new take on the traditional conception of selection as the causal influence of the adaptedness of variants and difference thereof on evolutionary change, which was highly criticized by the statisticalists as incoherent, and show how selection can be coherently depicted as a factor that involves this causal influence. In talk 2, Huneman will discuss different evolutionary questions and the explanatory projects that aim to answer these questions, and will argue that in some explanatory projects selection does play the role of a cause, while in others it does not. In talk 3, Matthen will provide two new arguments in support of statisticalism. The first is a new argument showing that selection and drift are model dependent and thus cannot be objectively distinguished from one another. The second is a new argument showing that evolutionary change results only from causes at the individual level and thus that selection, which takes place at the population level, is not a cause. The session will be chaired by André Ariew.

Selection and adaptedness

Adam Krashniak, Tel Aviv University, Israel

In a series of papers, Matthen and Ariew (2002; 2005; 2009) criticize a common, traditional account of natural selection as a cause of evolutionary change. According to the traditional account selection is distinct from other factors that affect evolutionary change such as inheritance or mutation rate and reflects the degree of adaptedness of different variants in the population. Matthen and Ariew argue that this view is incoherent because there is no way to formally define adaptedness and to measure the evolutionary effect of differences in adaptedness separately from the effects of other factors. The only measure of selection that we have, they argue, is a measure of the growth rates of variants, which is affected by many factors in addition to their adaptedness, such as the mechanisms of inheritance and the mutation rate. This leads Matthen and Ariew to argue that selection is the abstract description of differences in growth rates of variants, which can be the result of many different kinds of causes. Selection is realized in different populations by different causes that lead to differences in growth rates of variants, but it is these realizations of selection that cause evolutionary change and not selection itself, which is merely the abstract description of this change.

In contrast to Matthen and Ariew's arguments, this paper aims to show that selection can be formally construed as a distinct causal factor that consists of the influence of adaptedness of variants and difference thereof on evolutionary change, in line with the traditional account of selection described above. I discuss a set of causal relations between phenotypes and the environment, and argue that when these causal relations hold and lead to differences between variants in reproductive success, these differences in reproductive success are due to differences in adaptedness. This means that if one identifies selection with this set of causal relations, then selection is a distinct causal factor that consists of differences in adaptedness.

Natural selection as a cause and the causes of selection

Philippe Huneman, Université Paris I Sorbonne, France

Several authors (e.g. Glennan 2009; Huneman 2012) have proposed views of natural selection emphasizing a dimension of counterfactual dependence involved in selectionist explanations (hence a dimension concerning the causal relevance of traits to their frequency change), which accounts for the causal status of natural selection. Under this counterfactual view of selection, the critiques of selection as a superimposed cause by statisticalists (e.g. Matthen and Ariew 2009) are widely accepted, but depending upon whether "cause" is understood in terms of production or of difference-making (e.g. Millstein 2006), a dimension of causal relevance can still be present in selectionist explanations (Huneman 2013). The present paper questions the relationship between this causal relevance and selection itself as a cause, emphasizing the fact that such a relation depends upon the explanatory strategy undertaken.

The paper first distinguishes between questions about the fact of selection – as it is investigated for example in tests such as the Kreitmann test, about its dynamics – as it is modeled by population genetics, and about the causes of selection – which are a major target of behavioral ecology, as well as some paleobiological inquiries. Then I will consider from a pragmatic viewpoint the way causes and causal relevance are related in general in science, arguing that there are many ways to construe "the cause of X" on the basis of our knowledge of many relations of the form "a is causally relevant to X". Finally, in relation to the partition of evolutionary questions previously exposed, I will argue that, in several explanatory projects selection can genuinely be considered "a cause of trait X/allele x", whereas in other projects one is not equally entitled to speak of selection as a cause when considering the causal relevance of traits to their frequency change.

In order to present, in each explanatory project, the peculiar intertwining of two crucial epistemic dimensions of evolution by natural selection, namely chance vs. determination (on the one hand), and factual relations of causal relevance in ecological settings vs. mathematically constructed measured of fitness and of the force of selection (on the other hand), my argument will use two analogies relevant to biological fitness and evolution by natural selection: the conceptual space of card games involving more or less chance events (poker, blackjack, battle …), and the practice of ranking of sport competitors based on data about scores of series of particular games and tournaments.

Causation and reduction in natural selection

Mohan Matthen, University of Toronto, Canada

According to the Statistical Interpretation of the Theory of Natural Selection, fitness is a statistical measure of organism types in an environment. It is not a cause of natural selection.

This paper gives two new arguments in support of statisticalism. The first argument considers the interpretation of drift as opposed to natural selection. Drift is the quantity of evolutionary change attributable to chance factors; natural selection is the quantity of change attributable to adaptation. The key point to be considered here is what we consider to be chance. Take an environment in which there is a certain amount of fluctuation of summer rainfall from year to year. Relative to different characterizations of weather patterns, different events will be considered to be attributable to chance. In an exceptionally arid year, type **t1** increases relative to **t2**. Should we consider this to be a chance event, or one that is explained by the adaptation of t1 to weather fluctuations? It depends on the model that we apply to the case. This shows that natural selection and drift are intensional phenomena, much as Fodor and Piatelli-Palmerini allege in their notorious polemic. Because causation is not intensional, these authors conclude that the Theory of Natural Selection is refuted. On the statistical interpretation, this negative conclusion is unwarranted.

The second argument has to do with levels of causation. If the causal interpretation of natural selection is correct, there are causes of evolutionary change at two different levels of analysis – the population level and the individual level. This suggests a redundancy of causation as alleged by Jaegwon Kim with regard to mental causation. But in the case of the mind, the problem is solved by the posit of an organizational structure in the mind, which ensures that material causation will enable and realize mental causation. There is no such organizational structure in the case of evolution. The proposed solution to the problem in this domain is that the population-level phenomenon is not causal, but rather statistically predictive. Two consequences of this proposal are sketched: the substrate neutrality of natural selection and its multiple realizability.

Dehumanization in connection with biological determinism, anthropomorphism, and essentialism

ORGANIZERS
Maria Kronfeldner, Central European University, Hungary
Erika Milam, Princeton University, USA
Rohan Deb Roy, University of Reading, UK

Dehumanization – that some people are regarded, depicted and treated as not human or less human – is a phenomenon well known from the history and philosophy of the life sciences. It connects with racism, sexism, colonialism and other kinds of postulating hierarchies and/or justifying power and subordination – be this between humans, or between humans and other entities, e.g. animals. Dehumanization can exist in many forms that depend on context. It is a phenomenon that helps illuminate how the boundaries between humans and nonhumans are constantly reconstituted. In this interdisciplinary session, we will look at two historical contexts in which a particular form of dehumanization occurred, one context from the "West" (post-WWII North America), one from the "East" (South Asia). The systematic focus is on how dehumanization connects with biological determinism, zoomorphism and anthropomorphism. We then add a systematic reflection on a standardly made assumption, namely that dehumanization presupposes an essentialism of biological kinds.

The dehumanization of humanity and critiques of biological determinism

Erika Milam, Princeton University, USA

After the Second World War, paleoanthropologists crafted a vision of humanity as originating in Africa, united by common history and a shared struggle against the environment. Drawn out over millions of years, they reasoned, the process of humanization required synergistic interactions between nature and culture – a positive feedback system that magnified those traits that came to define *Homo sapiens* and distinguished humans from their hominid kin. By the mid-1960s, rather than seeing human exceptionalism in reasoned cooperation, the read-ing public grabbed ahold of a new idea, that human intelligence might instead have been linked to human's apparently unique capacity to murder members of their own species. This much darker version of human history sat awkwardly against the hopeful message of the immediate postwar era. Critics of this zoomorphic perspective accused its main advocates of dehumanizing humanity as a whole. One grumpy reviewer noted in *The New York Times* that "his only serious objection ... was that it left out almost everything – language, abstract reasoning, art, institutions, etc. – that distinguished man from other primates, rats, ants, worms, asparagus" (Oct. 28, 1969). This paper charts how critics of zoomorphism worked to categorize such thought as one form of biologically essentialist thinking, effectively uniting sexism and racism as conjoined intellectual enterprises that worked according to similar logics. The invention of "biological determinism" acted as an umbrella concept, covering a wide array of dehumanizing thought couched in the language of science. I suggest that the emergence of such critiques against biological determinism coincided with a new emphasis on universal human rights.

The white ant's burden: Anthropomorphism, dehumanization, and British colonialism in South Asia

Rohan Deb Roy, University of Reading, UK

In a series of speeches in 2018, the president of the ruling political party in India described alleged "illegal immigrants" as white ants (termites). This paper situates these statements within a long historical perspective by drawing on examples from the history of white ants in colonial and post-colonial India. White ants were ubiquitous and fundamental to the shaping of British colonial power. British rule in India was persistently vulnerable to these insects be-cause they consumed paper and wood, the key material foundations of nineteenth-century colonial bureaucracy and infrastructure. In retaliation, the sphere of strict governmental intervention was extended to include both animate and inanimate nonhumans, making the colonial state more resilient and intrusive. More significantly, white ants reveal how British colonialism in India thrived on the simultaneous operation of the twin processes of anthropomorphism and dehumanization. English texts in the British imperial age allegorically imagined that white ants constituted a parallel, if subterranean, world of "sovereignty" and "dominion". White ants' nests were frequently described as a "colony" consisting of innumerable workers and soldiers, who blindly served the reproductive royal couple with the "respect ... attendance and honours, due to sovereigns". At the same time, British columnists, naturalists and bureaucrats invoked white ants as sinister symbols to characterize colonized landscapes, peoples and cultures. Recalcitrant frontier tribes and ostensibly stagnated races were compared with white ants. Some authors implied that the problem of white ants in India and Africa could be mitigated by the introduction of colonial rule; one columnist even recommended slavery. Over time, colonized and post-colonial South Asians, too, used white ants to articulate their

own distinct political agendas. South Asian commentators featured white ants variously as metaphors for Islamic decadence, British colonial exploitation, communism, democratic socialism, political opponents, and more recently, alleged illegal immigrants. This paper argues that the intersecting histories of anthropomorphism and dehumanization were shaped by the political contexts of power, subordination and resistance. These contexts determined the ways in which the boundaries between humans and nonhumans were drawn, blurred and redefined.

Essentialism and dehumanization

Maria Kronfeldner, Central European University, Hungary

Essentialism is often taken to be a core aspect of dehumanization. If essentialism is taken to be a metaphysical or scientific claim applied to humans, then it entails that there are – in the mind-independent world – essential properties of being human, i.e., something that

1. allows establishing sharp boundaries between kinds of beings (e.g., between humans and other animals), that
2. allows classifying an individual as either human or not, and that
3. allows to explain why those classified as humans are the way they are. Since
4. essences often provide normalcy assumptions, which point to an ideal (the norm), those who are "abnormal", non-ideal are often degraded as less human.

This paper will review the knowledge that has been accumulated on how exactly essentialism connects with dehumanization, how it relates to entitativity, generalization and generic language usage. The aim is to show that even though essentialism can function as a catalyzer for dehumanization (and might even be sufficient for it, if every essentialist claim involves dehumanization), essentialist thinking is nonetheless not necessary for dehumanization, since dehumanization can and does happen with-out essentialist thinking. The problem of dehumanization is deeper than the problem of prejudicial attitudes arising from essentialist thinking.

Rethinking foundational assumptions about the “local”, “global”, “postcolonial”, and “transnational” in science: Connected, shared, and entangled histories of biology and the life sciences, part I

ORGANIZERS
William Leeming, OCAD University, Canada
Ana Barahona, Universidad Nacional Autónoma de México, Mexico

The aim of the session is to provide a forum for historical investigation that moves beyond diffusionist models of the history of science which represent innovations as originating in a single centre and diffusing in a one-way relationship with centres outside of the centre. Postcolonial critiques of diffusionist “centre-periphery” models inherited from the Cold War era have been highly influential in this regard for their exposure of the deeply embedded Eurocentrism of prevailing narratives in which social, cultural, and political formations are depicted as one-way relationships of “sending” colonisers and “receiving” colonial subjects. These critiques have generated other lines of inquiry which feature what have variously been called “connected,” “shared,” and “entangled” approaches to history that stress networked relations and processes of mutual influencing in establishing innovation relationships. These lines of inquiry permit a foretaste of what can be achieved by untangling and reconnecting local histories of science in ways that do not strictly rely on asymmetrical centre-periphery narratives. The four papers presented in this session attempt to transcend the deeply rooted territorial approaches of the past by exploring various movements and relationships across borders.

“These primitives, for whom life counts so little”: Early social science racial categories, French military doctrine, and the introduction of West Africa combat troops into Europe during the First World War

Joe Lunn, University of Michigan-Dearborn, USA

During the First World War, more than 150,000 West Africans were forcibly recruited into the French Army and served as combatants on the Western Front. This first mass contact by Africans with Europe has never been surpassed in scale during a comparable period, while the unintended effects of this unprecedented cross-cultural encounter ranged far beyond the outcome on the battlefields.

This paper examines one critical aspect of this novel French wartime policy: the interplay between the racial categorizations of Africans proposed by the emerging social sciences at the beginning of the twentieth century, and the appropriation of these ideas by the French military in order to sanction the implementation of an African recruitment program to augment French strength in the event of a European war. In so doing, it affords an opportunity to examine the racial preconceptions underpinning the creation of la force noire and the enduring and often negative consequences these ideas had for the individual African soldiers affected.

This analysis, which synthesizes aspects of my earlier published work, addresses three principle themes:

1. pre-war racial categorizations of Africans drawn from a series of social science disciplines, including especially biology, but also sociology, anthropology and psychology, and emphasizing the works of particularly influential individuals such as Herbert Spencer and Gustave LeBon, as well as institutions, including the Sociètè d’anthropologie de Paris;
2. the appropriation of many of these ideas by military proponents, and particularly Colonial Army officers associated with Charles Mangin, for undertaking expanded French recruitment in West

Africa, which laid the foundation for the subsequent deployment of these soldiers in Europe; and
3. the consequences for African troops of the application of race theory to them as shock troops in combat, while being segregated behind French lines, and while being massacred or taken prisoner by Germans--during two World Wars.

In so doing, I hope to shed new light not only on French military views of Africans at the beginning of the twentieth century, but also to exemplify the very real human consequences of the interplay between theory and practice, which continues to resonate in patterns of Afro-European interaction, especially among sub-Saharan migrants, to this day.

Collaborative networks and transnational knowledge in the study of the life sciences in Mexico during the Cold War. Mexico 1968

Ana Barahona, Universidad Nacional Autónoma de México, Mexico

In December 1962 the then regent of Mexico City, Ernesto P. Uruchurto, presented the candidacy of Mexico to compete against Detroit, Lyon and Buenos Aires. At the IOC assembly in October 16, 1963 in Germany, the Mexican candidacy was approved due mainly to three factors: economic and political stability, sports infrastructure, and Mexican non-aggression foreign policy. The candidacy won amidst the climate of intrinsic tension of the Cold War, to which the IOC was no stranger. Mexico won the headquarters of the Olympic Games in 1963 by 30 votes, against 14 from Detroit, 12 from Lyon, and 2 from Buenos Aires.

The games in Mexico were mosaic and mirror. They reflected global and general conflicts, tensions and hopes. The Olympics of Mexico 68, had a strong technological component not seen before, a national and international political climate that caused great uncertainty, and the demonstration that the Olympic movement was not immune to the pressures of the Cold War. World problems such as the Vietnam War, the French May, the Soviet invasion of

Czechoslovakia, the assassination of Martin Luther King and Robert Keneddy, and the guerrilla insurrection in Latin America, placed the 1968 games in a scenario of uncertainty, multiplied by the Tlateloco massacre ten days before the opening of the games. It is not possible to disconnect the impact of the Mexican student movement on the Mexican politics of the time.

Favored by innovative materials such as the synthetic track of the Olympic stadium, the touchpad in the Olympic pool, fiberglass poles, foam mattresses for the landing of athletes in jumps, electronic timing and the system of photosprint in athletics competitions, and the first games not to be carried out at sea level but at 2,240 meters of height. They were the first Olympics broadcast via satellite live and in full color, using 67 television channels to be seen by 600 million people through a station in Tulalcingo de Bravo in Hidalgo, and the ATS3 satellite for retransmission to Europe and the USA, giving Mexican television industry a huge boost. The television industry was consolidated as the preferred means of entertainment and a key factor in modeling the sport in terms of audiences, ratings, and commercial purposes.The games were inaugurated on October 12, 1968, an it was the first time that the Olympic flame was lit by a women.

Also, the Olympic Games included innovative practices and technological knowledge on human biology: The first time that cytogenetic techniques were applied to athletes was in the 1966 European Championship in Budapest, and for the first time to Olympic athletes in the 1968 Olympic Games in Mexico City. For this purpose, in 1966 the Genetics and Human Biology Program was created in close collaboration with the Local Olympic Organizing Committee. Although Mexican geneticist Alfonso León de Garay led the project, the head of the Program was Mexican geneticist Rodolfo Félix Estrada. The main objective of the Program was to study the genetic and anthropological components which determine an Olympic athlete's abilities. This investigation included 1,265 games participants and covered family studies, cytological investigations, research on single genes, and analysis of finger and palm prints. The studies were carried out by independent teams, working in close collaboration with each other: the karyotyping technique used was that of Barbara

Honyman Heath and Lindsay Carter, both of whom carried out most of the work along with Johanna Faulhaber and Mexican geneticists Olga Olvera and Rosario Rodríguez. Another team headed by physician Alejo Romero studied the distribution of blood groups. Other personnel participated with Ursula Mittwoch of the Galton Laboratory in the sex determination of the athletes using sexual chromatin and buccal smear tests. In terms of influence beyond Mexico, this project was very important as a site of transnational collaboration.

Disentangling postcolonial and indigenous ways of knowing and controlling biological systems

Christian H. Ross, Arizona State University, USA

In New Zealand, indigenous communities have deeply entangled and at times tense relationships with former colonial of scientific and political institutions, particularly around the governance of native biodiversity and natural resources. Proposals to control invasive species on the nation's islands through genetic engineering technologies have raised significant questions about the controllability and governance of such technologies. Aware of the significant ethical, cultural, and governance concerns, Kevin Esvelt, a genetic scientist from the Massachusetts Institute of Technology (MIT), has spearheaded extensive public engagement initiatives with Maori communities and local policymakers to discuss the potential risks and benefits. However, I argue that even in attempts to promote more shared and connected governance of biological control, embedded in scientific understandings are western, mechanistic ways of knowing and notions of what it means to control biological systems that implicitly subjugate indigenous cultural values and ways of knowing but also provide opportunities to move beyond territorial and often paternalistic patterns of the past.

Bound up within gene drive technologies are accounts of biology in which control is closely tied to explanations in terms of cause and effect of biological components. However, such mechanistic ways of knowing carry different distinctions between living and non-living worlds than some more holistic or vitalist Maori ways of knowing the natural world and humankind's place within it. Additionally, Maori principles like *kaitiakitanga* (guardianship) suggests control of biological systems as more about responsibility and the wise management of natural resources and biodiversity than mechanistic cause-effect explanations. These disjunctures highlight key ontological differences of living and non-living systems, which underpin notions of the purposes and forms of biological control. By untangling the interwoven relations of colonial powers and indigenous communities and their heterogeneous ontologies, we can more clearly recognize the sites of mutual influence and interconnection which prompt innovative, shared re-imaginations of control of biological systems.

Rethinking foundational assumptions about the "local," "global," "postcolonial," and "transnational" in science: (Re) articulating the modern biology paradigm beyond the "West", part II

ORGANIZERS

Hallam Stevens, Nanyang Technological University, India
Abhinav Tyagi, Indian Institute of Technology, India

This session will examine the process of knowledge production in modern biology from a non-western perspective. Recent events in biotechnology and biomedicine seem to indicate parity between north and south, developed and developing, west and east and so on. The process of knowledge production has moved beyond the adaptationist or diffusionist model of a western-centric narrative of biotechnology to a networked and collaborative model of research practice. In the context of biological knowledge production, the level of engagement outside the "west" has increased in all the major biotechnological initiatives. Although, the nature of their participation remained limited mainly to become the biological subjects for trials and testing of novel biotech initiatives such as GM crops, insects and machines. The non-western world has become a site for introducing novel representations of biological entities, new kinds of institutions, new biological metaphors, and introducing new technologies to manipulate the biological objects. Reflection on these can provide a deeper understanding the contemporary global networked model of knowledge production. Japanese contributions in bringing in the systems perspective to biotechnology, contemporary Chinese boom of biotechnology and its linkages with the traditional medicinal system are a few instances of departure from the past. These initiatives have shifted the balance of knowledge production between south-north, east-west and so on. The panel is interested in calling for the narratives outside the western world (especially from latin america, asia, africa and oceania) that can provide reflections about their role in the contemporary biotechnological movements since mid of the twentieth century. The session is open for the papers that can provide an assessment from the historical, sociological and bio-political perspective about the location of the non-western world in the process of biological knowledge production.

The emergence of biotechnology in India: Collaboration, contestation and a non-western perspective

Abhinav Tyagi, Indian Institute of Technology, India

In the modern biological and biotechnological paradigm, “west” has been the source and site for the knowledge production. This paper attempts to engage with the development of biotechnological initiatives in India. During its inception days, the thrust for the development of biotechnology as a stream of biological science came from different sources such as genetics, biochemistry, etc. In the Indian context, biological sciences coming together with chemical engineering formulated a new branch of biochemical engineering which later becomes biotechnology. Biochemical engineering research centre (BERC henceforth) at IIT Delhi, India came into existence with Swiss and British collaboration. Within few years of its inception, BERC emerged as a formidable force in the area of biofuels and non-conventional energy. From the late 1970s till mid-80s BERC has chaired and led various committees and conferences worldwide having focused on biofuels and non-conventional energy sources. Paper engages with different forms of archival material such as research reports from leading scientific institutes, records of their international collaborations, keynotes addresses of a major international conference, communication exchange between scientists and government institutions and records of an emerging form of governance structure for "Biotechnology". The journey of BERC, IIT Delhi was one of the miles stone in establishing biotechnology in India and has significant impressions on the research pedagogies of the biotechnology in the country. BERC is an interesting case study to understand the compulsions and characteristic of collaborative research between "western" and the "eastern" institutions. From the perspective of history of science, the changes taking place at the micro-level intractions such as usage of raw material, the social-cultural context of research and technologies shaped the research trajectory of the disciple as a whole. The paper would further like to complicate the dichotomous nature of so-called "eastern" and "western" science.

Mechanization by insect: Multi-species ecologies in the transnational plantationocene

Aaron van Neste, Harvard University, USA

This paper explores the human-assisted transoceanic migration and resettlement of the African Palm Weevil in Malaysia and S.E. Asia, and the consequent environmental and social transformation that emerged from the intersection of biological symbiosis, neocolonial labor policies, accelerating economic change, and biodiversity heritage. In the 1960s and 70s, as Malaysia was transitioning away from rubber plantations and towards palm oil, British planters conjectured that yields were lower in SE Asia than in the palm's native West Africa due to the absence of a native pollinator. Funded by Unilever and the Commonwealth Institute of Biological Control, a Pakistani entomologist, R.A. Syed, traveled to Cameroon and received permission from the Malaysian government to import African Palm Weevils, which he had discovered to be obligate pollinators and symbiotes of oil palm. Within a few years of the insects' release, Malaysian palm oil production became both more efficient and economically dominant, and deforestation and biodiversity loss accelerated. The predominantly female human labor force who had been hand-pollinating the palms before found their jobs replaced by an insect, in what can be alternately viewed as a form of biotechnological automation or an alteration or even restoration of the palm plantation holobiome. By engaging with symbiosis, this story complicates traditional narratives of ecological invasion and control. It also troubles notions of post-colonial science and contact zones, by asking how south-south knowledge exchanges actually operate and are mediated, and by showing the hybrid nature of nations and scientific organization. This paper "thinks with" Donna Haraway's holobiomes, Juno Salazar Parreñas' de-colonial multi-species ethnography, Susan Leigh Star and James Griesemer's boundary objects, and Anna Tsing's musings on the underdetermination of "globalization".

Collecting blood, flies, and ideas: David and Mary Bruce, the game-nagana link, and the role of "Zulu knowledge", c. 1890–1920s

Jules Skotnes-Brown, University of Cambridge, UK

In the 1890s, the British sought to open the Colony of Zululand to European settlement. The country, characterised by abundant green pastures, was a paradise for cattle, but had been plagued by a livestock disease that the Zulu called *uNakane* (Anglicised as *nagana*). Its cause, Zulu farmers argued, was the presence of legally-protected big-game, yet settlers in the region insisted that it was the "tsetse fly disease". David Bruce, a Scottish surgeon-major who worked closely with his wife, Mary Bruce, was commissioned to investigate. From 1893–1902, the couple collected local theories within the Mkuzi Game Reserve and tested these in their field-laboratory atop the Lebombo Mountain Range. Their influential series of reports would provide the bacteriological foundations for studying nagana and stimulate a thirty-year controversy into the "game-nagana link" – whether big-game were the source of the disease, and whether exterminating them would eradicate nagana. In 1920, this culminated in a field-experiment dubbed "The Great Game Drive", in which two-thousand settlers and six-hundred Zulu attempted to exterminate all wildlife south of the White Umfolozi River. This "experiment" and its reception shaped nagana science in Zululand and entangled the fate of the fauna in a web of class and race conflicts.

The fieldwork and reception of David and Mary Bruce, as well as their unnamed Zulu informants, provides a valuable case study in showing the African origins of nagana research, and how such origins were subsequently obscured and forgotten. Although the Bruces were candid in acknowledging a "native theory", in the game-nagana debates, animal-conservationists constructed "Zulu knowledge" as a form of "African primitivity", and the antithesis of science.

Rethinking foundational assumptions about the "local," "global," "postcolonial," and "transnational" in science: Coming together and "mutual influencing" in local histories of biology and the life sciences, part III

ORGANIZERS

William Leeming, OCAD University
Ana Barahona, Universidad Nacional Autónoma de México, Mexico

The two papers presented in this session show how local histories of biology and the life sciences in various countries have unfolded against strikingly different backgrounds. More specifically, they show instances in which the growth and development of practical undertakings in biology and the life sciences have taken different paths. A central argument follows that there are exchanges of novel ideas that go on across national borders which demonstrate different types of "mutual influencing" going on between local groups and organizations with different interests.

Fauna in Serra do Japi and Mocóca, São Paulo, Brazil: From 19th century naturalists to 20th century scientific chronicles

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European colonization of Brazil's São Paulo State began in the 16th century, and over the years, settlers increasingly explored the state's interior by waterways and trails in search of mineral riches. By the mid-18th century, as mining declined, São Paulo grew into a vast agricultural enterprise producing cane sugar for export. Only in the 19th century, however, with the Portuguese crown relocating to Brazil and rising multinational immigration, did scientific exploration take hold. Our study focuses on the period's historical documentation of the faunas of two particular localities over different time frames: Serra do Japi near the capital city of São Paulo, and Mococa, a remote region bordering Minas Gerais State. The Serra do Japi was accessible from two important roads, one to the west through the village of Santana do Parnaíba (est. 1580) and one to the east through Jundiahy (est. 1665). Mococa land grants (1820–1822) were spurred by the growing international demand for coffee. Situated on the Rio Pardo, Mococa soon became a major coffee producing region in São Paulo Province. To reconstruct historical inventories of the faunas of these two regions, we surveyed diaries, published reports and museum collections made by visiting naturalists (1815–1835), as well as registers of venomous animals received by the Instituto Butantan (1906–1940) and listings of specimens in the Revista do Museu Paulista (1892–1930). We compiled data for the main travel route by Rio Tietê and roads to Goyazes to each side of Serra do Japi. The Goyazes route also passed near Mococa. Burchell, on his way to Goyazes in 1827, collected 13 *Lepidoptera* species at Mococa. Scrottky and Brethes during short trips to Japi in 1900 obtained 92 species of wasps and bees (Ihering). Pelzeln and Ihering listed 29 bird species in Mococa (none in Japi), including a harpy eagle sighting. In each region, local collectors provided the Butantan Institute with similar counts for snake (28 from Japi vs 26 from Mococa) and spider species (7 vs 6). Material from Mococa also includes scorpions, toads and frogs. Fishes have been surveyed more recently in the vicinity of Serra do Japi and the middle of Rio Pardo, with 24 and 42 species, respectively. A variety of *Crustacea* inhabit both Rio Tiete and Rio Grande (where the Rio Pardo discharges), but additional verifications of collection localities will be required to make accurate lists. Although Japi was accessible to collectors much earlier than Mococa, this had little influence on biological information obtained prior to 1900. Collectors like Burchell and Natterer passed by Japi only to collect specimens in Mococa. Faunal information concerning the São Paulo region grew markedly during the 19th century as agriculture expanded. After 1900 Japi became increasingly sampled by investigators intent on building biological collections at the Museu Paulista (est. 1898) and Instituto Agronômico de Campinas (est. 1887).

Starting-up biology: BGI and the making of life in Shenzhen

Hallam Stevens, NTU Institute of Science & Technology for Humanity, Singapore

BGI, based in Shenzhen, is one of the world's largest and most successful genomics companies. Most commentaries on BGI have focused, quite narrowly, on the organization's ambitions for scaling-up biology into a high-throughput production line. My approach, drawing on ethnography, performance studies, and urban studies, aims to situate BGI's laboratories and work within the local economic, social, political, and urban contexts within which it exists. Rather than seeing BGI as a "factory," I suggest that the appropriate description is a unique kind of "start-up." BGI draws deeply on the local culture and "spirit" of Shenzhen, but blends this with the ethos of Silicon Valley entrepreneurialism. The result is that BGI's laboratories comprise a model polity, enacting a youthful, modern, productive, innovative, cosmopolitan, meritocratic society for China. Describing BGI in these modes suggests new possibilities for understanding the growth of biotechnology and biomedicine in China on its own terms.

Organism naming practices in and out of biology, part I

ORGANIZER

Sabina Leonelli, University of Exeter, UK

Biological names provide a currency for communicating information about units of diversity at different scales of life. Within biology, for example, scientists have developed different standards for naming transposable elements, genes, microbial species, and clades. These formalized rules for valid naming, however, have come under strain recently as genome sequencing has accelerated the discovery rate of biodiversity and bioinformatics has automated data integration at a global scale. Furthermore, informal nomenclature is common in many areas of biology such as ecology, where taxonomic expertise is often missing, or microbiology, where institutional mechanisms for approving valid names are unable to keep up with metagenomic sequencing. Moreover, valuable data about biodiversity loss or organismal phenotype are often only linked to common species names that have uncertain or noisy relationships to official taxonomic names. Other traditions of naming from data science and computer ontology design are also playing an increasing role in mediating data-centric biology, but they often resist the tradition of "taxonomic freedom" cultivated by systematists for classifying biodiversity. This session brings together historical, sociological and philosophical work on different traditions of naming practices for organisms. We are particularly interested in intersections between these communities and labelling practices, such as when breeders use bio-ontologies to inform their work or when taxonomists use nomenclatural rules to regulate the ability of outsiders to coin new species names. Considered holistically, these intersections articulate sites for the exertion and accumulation of power that pose important and still underanalyzed challenges for biodiversity data stewardship and governance.

Naming, ontology and translation: A case study from the Laplandic highlands

Staffan Müller-Wille, University of Exeter, UK

During his journey through Lapland in 1732, the Swedish naturalist Linnaeus noted down observations on several occasions about warble flies, whose larvae develop under the skin of rodents, including reindeer. In order to access such observations for later publication projects, Linnaeus numbered the observations in his travel diary, and worked out an elaborate index, which also included an entry for the reindeer warble fly (*Hypoderma tarandi* [L.]). Two things are remarkable about this particular entry: First, that Linnaeus used the Sámi name *curbma* to refer to this insect species; and second, that this name appears in two places in the index, once under the heading "reindeer diseases" (*morbi Rhangiferorum*), and once under the heading "insects" (*insecta*). I will present a close reading of the original observations in Linnaeus travel journal and their later publication history, that reveals that the ambiguous meaning of curbma reflects how the Sámi had a holist understanding of the life history of the reindeer warble fly that Linnaeus later translated into his own, published accounts of this fly species. While he analytically separated the taxonomic name for the species in *Systema naturae* (1758) from the disease it caused in reindeer, the connection was retained in elaborate accounts of the parasitic fly's vital contribution to reindeer economy, which inverted the usual perspective on "pests" and emphasized the inherent value and usefulness of parasitic life forms. Tracing such translations from the original diary notes to various manuscripts and publications through time reveals how Linnaeus's Sámi informants not only provided him with a provisional, vernacular name for a species that he replaced with the binominal name *Oestrus tarandi* in *Systema naturae* (1758). They also shared with him anatomical, veterinary, ecological, and economic knowledge associated with that species, which Linnaeus deployed throughout his career for a variety of literary and rhetorical purposes.

Informal and formal lichen naming practices

Catherine Kendig, Michigan State University, USA

Lichens were long relied upon as a source of food (*Cetraria islandica*), medicine (*Usnea* spp.), and textile dyes (*Parmelia saxatilis* and *Parmelia omphalodes*) by rural communities such as the Sámi (Llano 1948), Limbu and Sherpa (Devkota et al. 2017). In lichenometry they are employed as a means to date gravestones (Pringle 2017). They were identified by Linnaeus (1753) and characterized as symbionts (Schwendener 1868). Defined as a symbiotic system, a lichen includes a fungus (mycobiont) and a photosynthetic partner (photobiont), such as algae or cyanobacteria. The standard view has been that lichens are systems that have one fungus – typically an *Ascomycete* or *Basidiomycete* (Nash 2010). Accordingly, the criterion for lichen stability is the presence of the same mycobiont in the lichen system and underpins classificatory practices that rely on the fungus to name lichens. The lichen symbiont, as an organic whole, is treated as a "non-Linnaean kind" (Minelli 2017), a grouping of biological objects to which Linnaean nomenclature does not legitimately apply. Rather than a grouping with its own uniquely identifying classificatory rules, lichens are named as if they were fungi, as "lichenizing fungi" (Nash 2010). This means that formal naming practices of the lichen symbiont rely on knowing its photobiont-mycobiont metaphysics, but also on privileging the role of certain mycobiont-symbiont partners over others justifying their use (over the algal or other fungal partners) in naming practices. In this talk, I explore how lichens are named and classified using informal and formal naming practices, for what purpose these practices are used, how they are employed, what ontological commitments they rely upon to do so, and what grounds we have for relying on these different ontologies. Because lichens have been and continue to be classified outside the Linnaean system by both lichenologists and indigenous communities, the use of “grey names” is frequent and persistent, where “grey names” are understood to be names that are either intentionally or accidentally non-Code compliant (Minelli 2017). As such, there is strong motivation for exploring ways that retain these informal naming practices and the information encoded by them from different communities. I conclude with a discussion of the stakes that must be considered for any attempt to preserve and retain these grey names in a way that preserves their source-specific informational content and connects them to the Linnaean system.

From golden bum fly to scaptia beyonceae: New species and naming practices down under

Rachel A. Ankeny, University of Adelaide, Australia

Recent estimates indicate that as many as 400,000 as-yet unknown animals, plants, fungi, microbes, and other organisms exist in Australia, which is equivalent to about 70% of all species across the continent. The approximately 2,500 species which are found and classified each year also require names. This paper explores naming practices in recent Australian biology, particularly within the context of the new initiative being promoted by the Australian Academy of Science (and New Zealand’s Royal Society Te Apārangi) to register hundreds of thousands of previously unknown species. Using published academic and popular literature as well as fieldwork with Australian scientists, I explore the trade-offs inherent in naming practices. Considerations include compliance with explicit standards and codes as well as accuracy, creativity, ability to muster resources and gain public attention, and likely longevity.

Using a series of recent Australian examples, I consider how these trade-offs are navigated in this unique biological and sociocultural space to reinforce and create various relations within scientific communities and with the general public, and reflect on the implications for taxonomical practices more generally.

Organism naming practices in and out of biology, part II

ORGANIZER

Beckett Sterner, Arizona State University, USA

What's in a name? The globalisation of plant descriptors and its relevance to biological research

Sabina Leonelli, University of Exeter, UK

A key task for data science is to develop classification systems through which diverse types of data can be aligned to provide common ground for data mining and discovery. These systems determine how data are mined and incorporated into machine learning algorithms; which claims – and about what – data are taken as evidence for; whose knowledge is legitimized or excluded by data infrastructures and related algorithms; and whose perspective is incorporated within data-driven knowledge systems. Within biology, traditional taxonomic practices appear to provide a perfect starting point for the global classification of data about organisms – and particularly phenotypic data. In this paper, I discuss some aspects of the recent history of naming species and traits in plant phenomics (especially that performed "in the field") and its relation to attempts to share phenomic data about crops across different locations, focusing particularly on the Crop Ontology and its efforts to document and link the diversity of tools, terminologies and variables used to describe widely diverse species in different parts of the world. I argue that such practices do not relate in straightforward ways to traditional taxonomic practices, and in fact defy existing understandings of systematization in biology and beyond. The study of plant phenomics in the field involves enormously complex efforts of data collection and analysis. There are countless parameters of potential relevance ranging from the information about the soil, relevant microbiomes, plants at different stages of development, changing climatic conditions and so forth; and significant differences in expectations, goals and working conditions among researchers, breeders and technicians involved in data collection and reuse. Here is a case where reliance on a universal approach to identifying and labelling traits has repeatedly proved problematic for two main reasons:

1. agreement on widely applicable standards unavoidably involves loss of system-specific information that may be of crucial importance to data interpretation; and
2. the variety of stakeholders, data sources and locations at play inevitably results in a proliferation of classification systems and increasing tensions among different interest groups around what system to adopt and impose on others.

Considering the intersections between standard taxonomic systems and emerging modes of data classification is a step towards developing effective data linkage systems at the global level, as well as situated ways of knowing geared towards specific uses.

Taxonomic freedom and nomenclatural governance in the data age

Joeri Witteveen, Utrecht University, Netherlands & University of Copenhagen, Denmark

Taxonomic names serve vital epistemic and communicative roles as identifiers for taxonomic groups. Yet most taxonomic names are poor vehicles for communicating taxonomic content – names don’t wear their meaning on their sleeves. For names to have meaning, they must be associated with fallible and subjective judgments about the proper circumscription of the taxonomic groups they refer to. So while the practices of naming and taxonomizing are principally distinct, they closely depend on each other. With a twist on Kant's famous dictum, one could say that "nomenclature without taxonomy is empty; taxonomy without nomenclature is blind."

This clear distinction – yet intimate connection – between nomenclature and taxonomy is enshrined in the major codes of taxonomic nomenclature as the principle of taxonomic freedom: the codes only govern the application of names, they don't lay down principles for taxonomic practice. What counts as a "good" taxonomic judgment is not codified but is left to taxonomic science and the individual taxonomist. In recent years, the principle of taxonomic freedom has come under attack from various side in scientific journals, on taxonomic mailing lists, and in the popular press. It has been argued that in contemporary (networked, data-intensive) taxonomic practice, taxonomic freedom all too often results in taxonomic free-for-all. Names based on poor-quality taxonomic hypotheses make their way into databases and end up misleading taxonomists and non-taxonomic end users, including policy makers on conservation efforts. This raises the question whether taxonomic freedom should continue to be a central principle, or whether it should be restricted to allow for additional quality assurance mechanisms on taxonomic judgment. Or would this be fundamentally unscientific and do more harm than good to taxonomy?

In this talk, I will provide a closer look at recent arguments for and against the principle of taxonomic freedom. I will suggest that we should distinguish between different versions of the principle and argue for a pluralist proposal to respecting and reforming taxonomic freedom in different areas of biological taxonomy.

Biodiversity data stewardship and the future of biological naming

Beckett Sterner, Arizona State University, USA

We are likely entering a period of experimentation and upheaval in naming practices across biology, with major implications for core data science values such as reproducibility, reuse, accessibility, and provenance. Without identifiers that describe where to look, we have no way of finding data on a computer. What works best for reliable and efficient computation, however, is often unintelligible for human users. Naming practices for human audiences, however, also span a wide range of formalization from official taxonomic codes of nomenclature to common names in everyday language. Efforts to bring big data to biodiversity are introducing multiple disruptions to the ecosystem of organizations that coin official biological names and sustain their human utility over time. Metagenomic sequencing, for example, has uncovered enormous new biodiversity in the microbial world, but the nomenclatural groups responsible for coining official taxonomic names for microbial life are not necessarily well-positioned to adapt. Similarly, biologists are publishing a growing number of phylogenetic trees, but they often lack the training or desire to translate these into official taxonomic classifications. As a result, informal names outside the traditional codes will probably become more common as communities try out new approaches to fill the gap. The dominant priority for biodiversity data stewardship, though, has been the provisioning of unique identifiers suitable for computational data discovery and integration. The human value of these identifiers, however, will depend on how well we use them to augment biological names, especially at the leading edge between formal and informal naming practices.

The cultivation of the future: Dystopia, utopia, and plants as technologies

ORGANIZER

John Lidwell-Durnin, University of Oxford, UK

Many of our greatest fears for the future are entangled with our anxieties over food production. The failure of cultivated varieties and crops has been a constant, global threat throughout history. At the same time, the promise of better varieties, stronger crops and better yields have motivated numerous utopian visions of the future. This session will seek to draw together research from a broad array of time periods and sites of activity focused on how the material history of plants has informed, shaped, or threatened projections of the future. Technology plays a familiar role in the construction of both our ideal and our most-feared future outcomes for society. How have plants informed societies' expectations of the near or distant future? What role has been played by disease and unexpected variations in shaping these expectations? What kinds of cultivating practices and knowledge have strengthened conviction that nature can be controlled? There are also significant ways in which plants have shown potential for (and subsequently frustrated) the vision of a world without disease. The papers in this session highlight the role played by the cultivation and breeding of plants in informing scientific visions of utopia and also of disaster, either in the near or distant future.

A high mountain utopia: History of ecology at the Finse research station in Norway

Peder Anker, New York University, USA

The chief place Norwegian ecologists would meet, train their students and explore the environment was The High Mountain Ecology Research Station, established at Finse in 1965 and located at one of the most beautiful mountain regions of Norway. When finished in 1972 it was, perhaps, the largest and most expensive ecological research station in Europe. It could house large courses, which were usually given in August, and the way ecologists came to understand the environment would reflect their experience of nature as a place of recreation. The formative years of ecological research in Norway took place at Finse and were supported by ecologists such as Arne Semb-Johansson, Eilif Dahl, Rolf Vik, and Eivind Østbye. They were involved in the Norwegian division of the International Biological Program, which was active between 1964 and 1974. Their chief concern was problems related to food production and management of natural resources in light of a rapidly increasing human population and widespread malnutrition in the world. The picturesque Research Station at Finse was idyllic in comparison to the ecological destruction described in a growing body of environmental literature. To the ecologists it was a matter of continuing human existence to research the ecology of the mountains as future production and recreation areas for Norwegians. The world may face starvation, so production of food in the mountains was of key importance to the process of making the country self-sufficient. These worries first surfaced with the publication of Rachel Carson's famous warning against pesticides in *The Silent Spring* (1962). The ecologists at Finse became powerful lobbyists in favor of large-scale national parks in the nation's periphery. They would frequently argue that being in proximity of untouched nature was necessary for the nation's health. They sought an "eco-politics" founded on science, as our common future depended on the development of a "steady state" social economy that would mirror the steady-state balance of the zero-growth economy of nature at Finse.

Plants as solutions to our projected problems: Rising carbon dioxide levels, nutrient deficiencies, food security

Yilmaz Özlem, Istanbul Technical University, Turkey

In the Synthesis Report (2014) of IPCC there are "Representative Concentration Pathways (RCPs)" describing different 21st century pathways of greenhouse gases emissions and atmospheric concentrations, air pollutant emissions and land use. According to those RCPs, towards the end of this century, expected CO_2 concentrations in the atmosphere are between 430 ppm (best-case scenario in which we make all the good political decisions and do the mitigation strategies) to more than 1000 ppm (worst-case scenario). When we look at the possible future scenarios, our first reaction is usually an effort to find ways to force policy actions for reaching the optimistic scenarios; but also, we find ourselves thinking on what we will do, if we end-up with a bad scenario. And the crop plants are one of the biggest concerns. We think: even today we have the food-security problem, so what shall we do when we have much more population to feed, along with very different growth conditions for plants. This whole situation creates a challenge for plant scientists too: to better understand plant responses to possible increase in CO_2 concentration in the atmosphere and to other environmental changes. While at first glance, elevated CO_2 seems to cause an increase in photosynthesis rate and sugar production, but it also interacts with other environmental parameters and in certain contexts it may become detrimental for the plants. And climate research tells us, in the different regions of the world, plants will face different combinations of stressors. Because of that, plant scientists work on plant responses to elevated carbon dioxide levels in combination with other stressors: drought, nutrient deficiencies, high and low temperature etc. In this paper, last two decades of plant science papers on elevated CO_2 in combination with nutrient deficiencies will be examined through their descriptions, warnings and recommendations about the subject problems. Plants are very complex entities that are constituted by the network of many processes interacting with each other and with the environment actively and very dynamically. When a plant gives responses to a change in its environment, all the factors in this encounter may have a role in the response production. For example: "What are the other environmental parameters?", "has the plant (or its parents or its older ancestors) encountered this kind of or a similar kind of change in the environment before?" And the understanding of plant responses is not the only challenge for plant scientists, they also work on how to produce more nutritious plants. A plant coping well with the changing environment is not enough, we also want it to have a good-combination and an adequate quantity of nutrients. Growing more, stronger and more nutritious crop plants seems to be one of the solutions for our projected problems related to climate change and food security that includes hidden hunger (nutrient deficiency related disorders).

Debates over plant physiology, population, and potatoes as a staple crop before the Great Famine in Ireland

John Lidwell-Durnin, University of Oxford, UK

In the decades prior to the Great Famine in Ireland, numerous horticulturalists and botanists expressed alarm at the widespread cultivation of the potato. For followers of Alexander von Humboldt's ideas about plants and geography, knowing the latitude, longitude and conditions from which the potato plant originated could help in understanding how to improve it. But confusion over the exact geographical origin of the plant furthered suspicion and reservation about its suitability to the northern European climate, despite its popularity with farmers and the apparent ease with which several varieties were improved. While blight would lead to devastating famine in the 1840s, horticultural science had long anticipated and even predicted such a danger, most notably from Thomas Andrew Knight, the president of the Royal Horticultural Society. This paper seeks to examine the experiments and observations made on the potato in the early nineteenth century with the express aim of understanding these experiments as parts of a wider (unsuccessful) effort to avert a crisis. By focusing on the intersection between horticultural practices and larger debates over physiology and heredity, this paper shows that a diverse and contested field of authority on plant breeding sought to improve this staple food source while firmly convinced that a future disaster was very likely.

The many faces of epistemic tools, part I

ORGANIZER
Chia-Hua Lin, University of South Carolina, USA

Instruments, analysis techniques, models, theories, and concepts: what these various types of objects share is their role in furthering our knowledge and shifting the normative, epistemic, and metaphysical landscapes of scientific practice. They are each examples of what we call epistemic tools. In these symposia we advocate for the foregrounding of tool-use and tool-development in the philosophy of science and philosophy of engineering. Tool-use and tool-development are not foreign to contemporary philosophers. From the perspectives of experimentation, instrumentation, and measurement, philosophers tend to discuss how tools fulfill our existing epistemic and practical concerns. That is, they examine the extent to which existing tools give us reliable knowledge, and the extent to which they allow scientists to achieve their goals. In contrast, our symposiums approach tool-use and tool-development from combined metaphysical and epistemic perspectives. Metaphysically, we interrogate what tools are and what commitments tend to be factored into the development and use of tools. One common intuition might be that tools are concrete material objects, most likely with complex designs. But researchers often use models, concepts, and data transformations as tools. In this regard, Mieke Boon will open the symposiums with an account of how models function as epistemic tools by giving an analysis of the interplay between the development of technological instruments, experiments and models in experimental research practices. Jessy Wright, our second speaker, argues that the utility of an epistemic tool depends on the users understanding of the tool by contrasting the epistemic and metaphysical standing of those who develop techniques for interpreting neuroimaging data and the scientists who use those techniques. To close the first of our double symposiums, Rick Shang will present a case showing how researchers' metaphysical commitment to the existence "unobservables" impacts scientific practice. We consider the epistemic value of tools both narrowly and broadly. In the most immediate context of developing and using tools, we almost never observe a smooth ride: researchers come up with a design, materialize the design, and realize their pre-set goals. Instead, tool development is commonly riddled with changing goals, considerations, and uses. To this effect, Natalia Carrillo-Escalera and Tarja Knuuttila open the second symposium with a case demonstrating that the analogical models can serve to "recruit" tools and skills from other domains and across disciplines. Eden Smith will discuss the connection between the literature of scientific concepts and material instruments, and suggest how the converging accounts from these each contributes to our understandings of the uses of tools in scientific research. Finally, our last speaker Chia-Hua Lin will report a case of the cross-disciplinary development of mathematical constructs and discuss how such practice, which she calls “tool migration”, inspires the innovative use of tools. In summary, our symposiums are a call for action. Tools can influence and sometimes dictate knowledge production and evaluation, exhibited in distinct patterns of practical development and normative evaluation. Given both the significance and distinctiveness of tools, we advocate for foregrounding tool-use and tool-development in philosophy.

Models as epistemic tools in the engineering sciences

Mieke Boon, University of Twente, Netherlands

Models and modeling practices are ubiquitous in the engineering sciences. In this context, Tarja Knuuttila and I (2009, 2011) have defended the notion of models as epistemic tools. The idea is that models are constructed entities that can be used by (skilled) epistemic agents for specific epistemic tasks, and in that very sense, models can be called a tool. Scientific models, for instance, guide and enable different kinds of inferential reasoning, such as in deductive, inductive, quantitative, qualitative, explanatory, predictive, investigative, creative, or hypothetical reasoning about the target system.

The rough idea of scientific models as epistemic tools is that models are hubs in which relevant knowledge and information of all sorts are brought together and fused by the researchers into a coherent whole that allows for inferential reasoning. We have proposed that a scientific model usually can be systematically analyzed in terms of several ingredients that refer to choices made in the construction of the model (Boon 2019). These aspects are mutually related and must be made coherent, and can be summarized as:

i. the technological problem context;
ii. the target-system or phenomenon (P) for which the model is built (where P is relevant to the broader problem context);
iii. the intended epistemic function of the model (e.g., in view of solving the problem);

iv. the model type (in view of the epistemic purpose);
v. the (physical) circumstances and properties relevant to the phenomenon or target system (in view of the previous aspects);
vi. the measurable (physical) variables (which also explains how the model is connected to the real-world);
vii. idealizations, simplifications and abstractions (in view of epistemic criteria and pragmatic constraints);
viii. knowledge and background principles relevant to P;
ix. hypotheses (e.g., new concepts or explanations); and
x. the testing of the model.

Conversely, in the philosophy of science, scientific models are typically understood as representations of a specific target system, and philosophers have aimed at accounts of this representational relationship. Well-known is Giere's (2002) similarity account of representation. Getting away from this kind of representational view of models appears to be hard. Answers to the question "in virtue of what a scientific model can function as an epistemic tool in scientific reasoning processes?" usually refer to the "correct" representational relationship between model and target.

In this paper,

1. philosophical arguments against the similarity view of models will be summarized, and
2. an account of why models can function as epistemic tools for reasoning about their target system will be presented by in-depth analysis of the interplay between the development of technological instruments, experiments and (scientific) models in experimental research practices.

It is claimed that this epistemological process is guided by apparent ontological and epistemological presuppositions. Crucial to this account is the idea that ontological and epistemological principles must be understood as regulative principles that guide and enable research practices, not constitutive principles about reality. Examples from the engineering sciences are interesting because the modeled target system often does not exist in advance.

Data analysis methods: Tools or techniques?

Jessey Wright, Stanford University, USA

Human neuroimaging research consists in the search for neural explanations of human cognitive capacities. Neural and cognitive phenomena cannot be directly measured in humans. The reliance on indirect measures, such as behavior and changes in blood oxygenation levels, combined with the causal complexity of cognitive and biological systems presents a persistent epistemic challenge that is overcome through data analysis. The development and use of tools for transforming data are central to discovery and confirmation in cognitive neuroscience. For instance, the uptake of multi-voxel pattern analysis methods made it possible to decode information from the brain (e.g., Davis and Poldrack 2013), and the recent proliferation of network-based accounts of human cognitive function driven by the refinement of techniques for conducting network analyses of neuroimaging data (e.g., Medaglia et al 2015). In these cases analytic methods were developed to facilitate the advancement of a specific theory, and then they took on a life of their own as they become encoded into software packages. These data analysis tools are used to isolate data patterns that are interpretable in terms of the cognitive and neural processes underlying imaging data (Wright 2018). In this essay I examine what makes a pattern in data interpretable, and articulate factors that influence the meaning ascribed to data patterns. To do so I contrast the epistemic relationships between data analysis methods, developers, and users.

I argue that tool developers treat analysis methods as techniques. While they are tuned to isolate patterns of a particular kind, they can be adapted to fulfill other purposes. Developers recognize that analysis tools provide limited epistemic access to phenomena, and that those limitations are constantly being discovered and negotiated. Their conceptualization of the target phenomena, and intended use of the tool, directs decisions made during the encoding of an analytic method or procedure into a software package. Tool users, on the other hand, tend to treat analysis methods as templates. They are used to isolate patterns with prescribed meanings. The template-like use of analysis tools transfers epistemic authority from the users to the analysis tools. I conclude by considering the positive epistemic aspects of analysis tools, including the distribution and transfer of understanding and expertise amongst members of a community, and the negative epistemic aspects of these tools, including the impact of tool uptake on methodological diversity within the community (e.g., Lewontin 1991). In doing so I propose that epistemically productive tools have two central properties:

1. they are flexible, inspiring and allowing for multiple applications, and
2. they are not easy-to-use.

A transcendental argument for realism: The metaphysics of tool development

Rick Shang, Washington University of St. Louis, USA

Positron Emission Tomography (PET) is a general detection technology to detect radioactive intensity from the outside to produce non-invasive, three-dimensional images of the internals of objects, often of organs inside the human body. The value of PET resides in the fact that researchers can use regional radioactive intensity as a proxy for information of interest to them. For cognitive and medical research, researchers often use regional radioactive intensity as a proxy for intensity of biological processes such as cognitive processes. Thanks to PET, researchers can produce non-invasive, three-dimensional images of cancer development or the neural activities during human cognition.

One interesting feature of PET is that researchers' lack of direct observation. Researchers could not observe the biological processes (the target) they chose in the early years of PET or radiation (the means of detection) in any direct way. But they managed to put those unobservables together and create a commercially and scientifically successful detection technology.

The success of PET and other detection technologies demand philosophers to explain researchers' aims, commitments, and

practices in tool development. In other words, I combine the methodologies of van Fraassen and Hacking. van Fraassen's method for his empirical constructivism is to explore and explain researchers' commitments and aims in their theories, models, and explanations (van Fraassen, 1980). I intend to borrow his method to explore and explain researchers' commitments and practices in their experimentation and instrumentation practices, following Hacking's and many other philosophers' interests in scientific practices.

By combining van Fraassen and Hacking, I propose a Transcendental Argument for Realism as the best explanation of researchers' commitments and practices in their design of instruments and performance of experiments. The argument goes as follows:

Premise 1: If researchers do not believe in the existence of the entities under their investigation, their designs and experiments will be incoherent.

Premise 2: Researchers' designs and experiments are coherent.

Conclusion: Researchers do believe in the existence of the entities under their investigation.

By existence, I mean that researchers believe:

1. the entities of concern are in the natural stock of the physical world;
2. the entities have basic physical features;
3. the entities are causally efficacious.

The Transcendental Argument is a version of Hacking' Entity Realism. Hacking's well-known Entity Realism suggests that experiments provide evidence for scientific realism because, through experiments, we can manipulate unobservable entities and use them causally for our purposes (Hacking, 1982). Here, I argue (and in agreement with some of Hacking's gestures), that researchers bother to manipulate unobservables, design experiments, and construct instruments accordingly precisely because they already believe in their existence.

Transcendental Realism, in its own sentence version, is: "Researchers do not always need to commit to the existence of entities in their models and theories, but they often have to commit to the existence of entities involved in their experiments for their experiments to be possible and coherent."

The many faces of epistemic tools, part II

Analogies and tool recruitment in nerve signal research

Tarja Knuuttila, University of Vienna, Austria
Natalia Carrillo-Escalera, Universidad Nacional Autónoma de México, Mexico

Analogies and models are intimately related; many models are based on analogies, and in philosophical discussion the idea of models as analogs of real-world targets, and analogies between two domains of inquiry often coalesce. We suggest caution with respect to such leaps between models and (several) real-world targets, and suggest instead that analogies could be approached as particular kinds of epistemic artefacts recruiting conceptual, representational and formal tools from other areas of study. We study this process of recruitment through the nerve signal research.

We focus on two analogies that have been very important in the development of the current electrical view of the nerve impulse. The first is an analogy between nervous transmission and physicochemical dynamics as observed in the galvanic cell. The second is the analogy between the nerve cell membrane's physicochemical dynamics and an electric circuit. We call these "analogical models" and are interested in the kind of epistemic work that they have done for nerve signal research. We argue that the case shows that the analogical models of the galvanic cell and the electrical circuit played very important roles in neurophysiology in recruiting tools and skills from physical chemistry, on the one hand, and electronics on the other. The analogy with the galvanic cell recruits the tools for qualitative analysis developed for these preparations (galvanic cells) in the context of physical chemistry, based on Nernst's equation. The analogy with the electric circuit allows, in turn, for

the utilization of laws from electronics to develop a mathematical expression that simulates experiments in squid axons, in particular Kirchhoff's laws, Faraday's law and Ohm's law. The integration of both analogical models resulted in a Nobel Prize-winning mathematical model that can simulate the recordings on real nerves (Hodgkin and Huxley 1952).

Our study of the research on nerve signal shows that the role of analogies cannot adequately be accounted for in terms of model-world relationships. In contrast to the conventional representational perspective, we focus on how modelers recruit skills and tools from other scientific fields by way of analogical reasoning. We suggest that understanding these analogical models under the artifactual framework developed in (Knuuttila 2011) is a more suitable strategy to account for their non-representational contributions to nerve signal research.

Using scientific concepts as investigative tools: Beyond representation and materiality

Eden T. Smith, University of Melbourne, Australia

Scientific concepts can function as tools that contribute to investigative practices (Feest 2010). Building on this notion, I seek to strengthen the bridge between accounts of scientific concepts and material instruments, as each are used in practice. The need for this bridge stems, in part, from the separate contexts for studying scientific concepts and material instruments respectively. Questions about tools have long highlighted the material contributions to experiments, while scientific concepts are typically viewed as mental or linguistic representations that aid theoretical development. However, recent scholarship offers new avenues for investigation. In addition to experiments, questions of materiality now extend to investigative practices more broadly – including accounts of paper tools (Klein 2001) and the use of models as tools (Boon and Knuttilla 2009). Likewise, interest has returned to studying scientific concepts beyond, and sometimes independently of, their roles in theories (Arabatzis and Nersessian

2015). Indeed, far from being limited to referential components, concepts can function usefully regardless of whether they reliably pick out natural kinds (Bloch 2012). Furthermore, uses of scientific concepts can also evolve unpredictably within dynamic socio-cultural-material interactions that develop over generations of community practices (Pickering 2006). Taken together, these areas of scholarship suggest that scientific concepts should be investigated as one of the many elements relevant to broader aspects of scientific practice, such as calibration practices (Soler et al. 2013) and the use of epistemic tools more generally (Boon 2015). I propose that drawing these converging accounts of scientific concepts and material instruments together can contribute to our understandings of the uses of tools in investigative practices.

From foes to friends: Competing research approaches integrated through tool migration

Chia-Hua Lin, University of South Carolina, USA

Mathematical constructs that are formulated for inquiry in one discipline are sometimes used in another, a phenomenon that I analyze as “tool migration”. Philosophers of science have discussed this phenomenon in terms of “templates” (Humphreys 2002, 2004; Knuuttila and Loettgers 2014, 2016) or “epistemic tools” (Boon and Knuuttila 2009). Building on these approaches, the term “tool migration” aims to capture both the “situatedness” of a mathematical construct that was established in its home discipline and the effort it takes to “re-situate” it in a foreign discipline. Thus, tool migration can be seen as the cross-disciplinary development and application of mathematical constructs in science. More importantly, by tracing the trajectory of a given mathematical construct, a philosophical study of tool migration seeks to reveal its impacts, one of which is the integration of different research approaches.

This paper argues that the migration of formal language theory – from linguistics through computer science to biology – has brought together two competing scientific traditions into one research field in cognitive biology. Formal language theory, including its components such as automata theory and the Chomsky hierarchy, is the study of mathematically defined languages. Cognitive biology is the study of cognition as a biological function, one strand of which aims to understand both the evolution of and neural substrate for human linguistic capacity. It does so by experimentally applying formal language theory to unravel the abilities of nonhuman animals to learn artificial grammars. Between its initial formulation by Chomsky to study natural languages in linguistics and its recent, novel applications in cognitive biology, formal language theory received intervening development in computer science for improving the design of programming languages and their corresponding recognizers, called "automata".

Bringing animal model organisms in contact with formal models of languages to investigate human linguistic capacity presents an intriguing case of tool migration. On the one hand, using animal model organisms for the inquiry of human psychology has been a trademark of the behaviorist program, whose decline is often credited to Chomsky (1959a). On the other hand, the return of songbirds and nonhuman primates to the quest of understanding the faculty of human language is based on the classification scheme – the skeleton of which was single-handedly constructed by Chomsky (1956, 1959b). One may ask: How do scientists marry the behaviorist and the cognitivist approaches by bringing animals as model organisms back to the study of the linguistic capacity of humans?

I argue that the key to this integrating branch of cognitive biology lies in an innovative insight from the migrating trajectory of formal language theory. In particular, the cognitive biologists "enables" the Chomsky hierarchy – specifically, the scheme that computer scientists use to classify automata – to classify different systems of animal cognition, humans included. This innovation thus integrates animal model organisms with formal models of languages into one scientific enterprise. However, tool migration is not without risks. I close the paper by discussing both the appeals and perils of this renewed study of human linguistic capacity.

Exploring biological ontologies through the interdisciplinary lens of ethnobiology

ORGANIZER

David Ludwig, Wageningen University, Netherlands

Ontological issues feature prominently in current debates about biological practice from the philosophy of natural kinds to the history of biological nomenclature to the sociology of racial categories in the life sciences. The aim of this session is to explore biological ontologies through the lens of ethnobiological research. Ethnobiology has grown into a dynamic field at the intersection of biological and social sciences that investigates the biological knowledge and practices of Indigenous and other local communities. By developing both empirical and theoretical research on the ontological dimensions of ethnobiological knowledge systems, this session provides novel perspectives on wider philosophical debates and on the applied functions of ontologies as biocultural heritage. First, we want to show how ethnobiological research can contribute to philosophical and theoretical debates such as the role of epistemic and social values in biological classifications. Partly based on our own fieldwork from fishing villages in Brazil to museum collections in Mexico, we explore local configurations of ontologies and their significance for wider debates from "ontological pluralism" and "natural kinds" in philosophy to the "ontological turn" and "radical alterity" in anthropology. Rather than advocating simple forms of ontological universalism or relativism, our research demonstrates that ethnobiology can contribute to a better understanding of the complex relations among epistemic communities both in producing cross-culturally shared ontological ground and in developing diverging ontological traditions. Second, we also aim to show how theoretically informed debates about biological ontologies can contribute to empirical research in ethnobiology and applied negotiations of biological knowledge in cross-cultural settings. Resources from philosophy, history, and social studies of biology can provide new angles for foundational issues in cross-cultural comparison from ethnotaxonomic questions about species categories to anthropological encounters with “radical alterity” of metaphysical assumptions. Furthermore, we also show how ontological issues reach beyond pure theory and become materialized in socially relevant practices such as intercultural negotiations of science education, co-creation of conservation practices, and the organization of museum collections. By locating these issues in our own interdisciplinary research, we show how the emerging field of “philosophy of ethnobiology” can contribute to the development of novel intellectual tools such as “inter-ontological dialogue” that provide reflective methods of interaction between heterogeneous stakeholders.

Inter-ontological dialogue in conservation and intercultural education

Charbel N. El-Hani, Federal University of Bahia, Brazil

In recent years, it has become increasingly common to find in the literature advocacy for integrating scientific knowledge and traditional knowledge in conservation and sustainable management. The importance of traditional knowledge for understanding and managing local environments has been emphasized, contributing to debates about “co-creation”, “co-management”, “participation”, “transdisciplinarity”. Moreover, it has been shown that, besides context-relevant knowledge, traditional communities also build causal explanations that can generalize. From a philosophical point of view, to integrate different knowledge systems, which embed different ways of knowing and validating knowledge, as well as different ontologies and value systems, is no free lunch. A number of philosophical issues emerge and need examination. In a different but related vein, a trend towards integrating traditional knowledge into schools has also been advocated as a necessity in multicultural societies. Thus, intercultural dialogue has been increasingly advocated as an important educational goal in the last years. Again, we have no free lunch here, and a plethora of relevant philosophical issues come to the fore. Philosophy of ethnobiology is one of the fields for tackling these issues.

In this paper, we consider success and failure as possible outcomes of integrating efforts, addressing the fundamental methodological questions raised by them and proposing theoretical models to deal with these questions. We intend to both extend a set of models initially proposed by Ludwig to tackle knowledge integration in conservation for educational cases, and to develop the models themselves by examining empirical data gathered in our field studies in fishermen communities in the north shore of Bahia, Brazil. We discuss thus possibilities and limits of inter-ontological dialogue in knowledge co-production and integration. We first consider why this dialogue, albeit complex, is inevitable when building discourses and practices affecting a whole socio-ecological system, as in conservation and education. We discuss then the necessity of theorizing about inter-ontological dialogue and knowledge integration in terms that recognize both prospects and limitations, and work out a methodology for dealing with inter-ontological dialogue in terms of partially overlapping ontologies. We apply this methodology to original data on ethnobiological knowledge of traditional fishermen communities and discuss intercultural education proposals based on such application. Finally, we theorize on how to position ourselves when inter-ontological dialogue fails, combining three theoretical tools in an approach to the limits to knowledge integration: standpoint theory, from feminist philosophy of science; ontological self-determination, from anthropological studies; and meaning-productive relational empathy, from intercultural communication.

Comparative ontology: Exploring the limitations of cross-cultural pluralism

David Ludwig, Wageningen University, Netherlands

The aim of this talk is to explore the limitations of ontological pluralism through the metaphysical assumptions of traditional communities and academically trained scientists. While pluralist frameworks are helpful for understanding cross-cultural variation of biological taxonomies (Ludwig 2017, 2018), it remains unclear whether they can be extended to more general metaphysical issues in traditional and western accounts of biological world. This article starts with a framework of “reflective pluralism” that is developed through ethnotaxonomic studies. In a second step, this framework is brought into anthropological discussions about the “ontological turn” that tend to focus on deep metaphysical differences regarding Indigenous assumptions about issues such as shamanic transformations (Viveiros de Castro 2014) or thinking forests (Kohn 2013).

Ethnotaxonomic studies of local classificatory systems provide an important methodological tool for exploring ontological plurality across cultures. On the one hand, local classifications often depart from scientific taxonomies and illustrate how ontologies are shaped by culturally variable epistemic and social concerns. Ethnotaxa do not depart from scientific taxa because they misunderstand biological structures but rather because they typically involve recognition of (e.g. ecological, economic, medicinal, or morphological) patterns that are of unique importance for local communities. On the other hand, it has also become increasingly clear that this pluralist picture needs to be qualified through robust evidence of cross-cultural convergence in the recognition of species and other biological phenomena that are salient for heterogeneous epistemic communities across different cultures.

Philosophical reflection on this rich tradition of ethnotaxonomic studies leads to a picture of reflective pluralism that involves what Ludwig (2016) has called “partially overlapping ontologies”. However, it is far from clear whether such a reflective pluralism can be extended from taxonomy towards a more general debates about the relations between Indigenous and Western metaphysics. While it is easy to find ontological similarities and differences under the microscope of ethnotaxonomy, anthropologists often address Indigenous metaphysics with a focus on wider differences that are assumed to involve radically incommensurable worlds. In contrast to such assumptions about radical incommensurability, this talk explores the prospects of a reflective pluralism in addressing deep metaphysical issues such as Indigenous accounts of animism (Descola 2013) and especially Kohn's (2013) seminal *How Forests Think.* Based on current controversies about the boundaries of cognition in externalist cognitive science and plant cognition, it is argued that reflective pluralism is actually a viable option in wider debates about cross-cultural relations between metaphysical assumptions about the biological world.

The garden, the museum, and the "ontological turn": Ethnobiology's concepts in the mirror of anthropological critique

Francisco Vergara-Silva, Universidad Nacional Autónoma de México, Mexico

Historically, the primary concern of ethnobiology –as practiced in metropolitan academic centers, as well as (their) peripheries– has been the variety of contexts and ways in which non-Western human groups build knowledge systems of/about "the natural world". Recently, in line with its increasing interdisciplinarity, efforts to (further) develop theory in/for ethnobiology have forced relevant authors to come to terms with certain recent debates in sociocultural anthropology. These debates derive from mutually independent –but nevertheless ideologically related– strands of anthropological research and writing, all linked together by similar criticisms of the underpinnings of Western modernity's "nature-culture (N-C) dualism" and associated "essentialist" conceptions. Among these academic productions, the retrospectively called "ontological turn" (OT) – commonly associated in the first phase of its rise with the works of Philippe Descola, Bruno Latour and Eduardo Viveiros de Castro – has been also deemed highly contentious by its detractors. Interestingly for philosophy of science-oriented publics, the OT involves assumptions and issues easily identifiable as epistemological – namely, the claim that the diverse (and largely non-Euro-American) cognitive/linguistic/social configurations of relationships between "the human and the non-human" entail a corresponding diversity of conceptions on "what there is", which are discontinuous with standard Western dichotomies involving "nature" and "culture".

Informed by emerging aspects of the present stage of discussion around the OT – e. g. an avoidance of metaphysical considerations (i.e. "ontology" in the standard philosophical sense of the word) and a focus on ethnographic description (sensu Martin Holbraad & Morten Pedersen)– but respecting heterogeneity of stances among authors, here I describe the design and framework of a "philosophy of ethnobiology" (PEB) study on the influence of OT-related works on ethnobiological research practiced in botanical gardens and natural history museums. This prototype for a wider, "meta-ethnobiological" research initiative is supported by preliminary analyses of data collected in two Mexican institutions (Jardín Botánico del Instituto de Biología, UNAM, and Museo Nacional de Antropología, INAH), centered on the use of the notions of "species" and "indigenous knowledge" by ethnobiologists (both in research as well as in public understanding of science-related activities). For interpretation of the latter data sets, special attention is paid to scholar, critical observations on the OT by Roy Ellen and other ethnobiologists interested in the potential contribution of OT-related debates to theory-oriented conversations in their own academic community. Echoing OT's skeptical, forward-looking leanings –identified as "speculative futurism" by critics Lucas Bessire & David Bond– but eschewing partisanism, I finally comment on how ethnographic studies of ethnobiology –an "anthropology of science" long-term project, by all means– might constitute a useful contribution to the development of PEB as a philosophy of biology specialty in its own right.

Cell theory, evolutionary theory, and the concept of individuality

ORGANIZER

Sherrie L. Lyons, Union College, USA

The cell theory claims that the cell is the smallest independent unit of life. Nevertheless, such a claim posed certain problems in trying to elucidate how a single cell eventually gives rise to a multi-celled organism. If a cell has an independent existence, then what is its relationship to the whole organism? In other words, how does one define an individual? This session explores the difficulties in defining biological individuality and the implications for both cell theory and evolutionary theory. Lyons discusses Thomas Huxley's 1853 address "On Animal Individuality" in which he adopted William Carpenter's definition of a biological individual, which was not based on its independence. Instead Huxley wrote "the individual animal is the sum of the phenomena presented by a single life: it is all those animal forms which proceed from a single egg taken together." Huxley's emphasis was on the whole organism. It didn't matter that cells were capable of an independent existence, because that is not how they functioned in a multi-celled organism. Thinking of them as independent as the cell theory implied, was counterproductive to understanding development. Gilbert discusses the work of John Bonner who adopts Huxley's concept of the individual, applying it to evolution and argues that the life cycle is the unit of selection. Bonner expands it by pointing out that development extends beyond the body and into interactions with other organisms which he refers to as the holobiont life cycle. Gilbert uses this concept of the holobiont life cycle to argue that many important evolutionary transitions can be accomplished by various forms of symbiosis. These include the origin of the eukaryotic cell, meiosis and multicellularity, the original function of the nervous system, and the multiple origins of herbivory in the animal kingdom. These findings bring in to question the primacy of the cell and highlight the importance of development and the holobiont in analyses of evolution. Baluška argues that only archaeal and bacterial organisms can truly be considered individuals with the unitary self. All eukaryotic organisms are complex supracellular entities, resulting from the merging of several individuals with distinct genomes. The unitary self of multicellular organisms must be negotiated via synaptic cell-cell communication. He proposes a neo-energide model of eukaryotic cell evolution in which two different ancient archaea species generated both the cytoplasm enclosed with the plasma membrane and the nucleus associated with centriole/centrosome-based microtubular cytoskeleton. This latter part of the cell he calls Neo-Energide or Cell Body in memory of Julius von Sachs and Daniel Mazia. The modern eukaryotic cell has a composite individuality. Baluška's work implies that the cell body, rather than the cell should be considered the smallest independent unit of life and along with Gilbert also gives a much more prominent role to symbiosis in the evolution of diverse life forms.

Thomas Huxley's "upon animal individuality" and his critique of the cell theory

Sherrie L. Lyons, Union College, USA

An individual is typically defined as a "single thing of the same kind." Huxley claimed that such a definition quickly led to absurdities when applied to the biological world and that how to define a biological individual was a profound and difficult question. He addressed these problems in his 1852 address "On Animal Individuality". This essay provides insight into his critique of the cell theory which appeared in an extensive review in 1853. Both essays reflected his interest as a morphologist trying to understand the nature of form. Huxley adopted William Carpenter's definition of a biological individual, which was not based on its independence, but rather consisted of the entire product of a single fertilized ovum. He argued that biological individuality was defined by a law of succession, or a definite cycle. For most higher organisms, these stages were not separated, but passed imperceptibly from one to another. But many other exhibited an alternation of generations, particularly plants, where two or more different forms existed. Various invertebrates also had two distinct forms. One such example that Huxley studied was the salp, which had two different forms: Salpa democratica and Salpha mucronate. For Huxley individuals existed in many different modes and it might be useful to distinguish them for purposes of classification. But he concluded "The individual animal is the sum of the phenomena presented by a single life: it is all those animal forms which proceed from a single egg taken together." By bypassing the common criteria of independence as the defining characteristic, and instead defining an individual by its entire developmental history, Huxley's emphasis was on the whole organism. It didn't matter that cells were capable of an independent existence, because that is not how they functioned in a multi-celled organism. Huxley maintained that thinking of them as independent as the cell theory implied, was counterproductive to understanding development. His views provide a window into the controversies surrounding morphogenesis, as scientists pondered what would be the best strategy in unraveling this difficult problem of development. Many problematic aspects the cell theory are finally being addressed today, but Huxley had raised them over 150 years ago.

John T. Bonner and the holobiont life cycle

Scott Gilbert, Swarthmore College, USA

There are numerous “evolutionary transitions” where life appears to have risen to new levels or organization. These transitions include the origins of the eukaryotic cell, the origins of meiosis, the origins of multicellularity, and the origins of the nervous system. This talk analyses the mechanisms for those transitions in light of two of Dr. John T. Bonner’s hypotheses, made in the 1950s and 1960s. First, Bonner has adopted Thomas Huxley’s view (from “On Animal Individuality”) that the life cycle is the unit of evolutionary selection. However, Bonner expands this view by noting that development extends beyond the body and into interactions with other organisms. Bonner thus prepares us for the notion of the holobiont life cycle, where development includes both the zygote-derived cells and the symbiotic microbes acquired during various stages of development. Using this notion of the holobiont life cycle, this talk attempts to show that these evolutionary transitions can be accomplished through various means of symbiosis. The eukaryotic cell is thought to have been formed by endosymbiosis of a bacterium by an Archaean; meiosis and multicellularity can be induced in choanoflagellates by different species of bacteria; and the original function of the nervous system may have been the regulation of symbiont location within the body axis. The multiple origins of herbivory throughout the animal kingdom can also be explained as a holobiont function.

These findings highlight the importance of development and the holobiont in analyses of evolution.

Neo-energide model of eukaryotic cell: Integration of composite individuality

František Baluška, University of Bonn, Germany

In the strict sense, only archaeal and bacterial organisms are individuals with the unitary self (Margulis 2001, Baluška and Reber 2019) having single senome/genome (Baluška and Miller 2018). All eukaryotic organisms, both unicellular and multicellular, are complex supracellular entities based on several individuals having their self-specific senomes and genomes (Baluška et al. 2004a,b, 2006; Baluška and Lyons 2018, Baluška and Miller 2018, Miller et al. 2019). This means that the unitary self of multicellular organisms must be negotiated via synaptic cell-cell communication (Baluška and Mancuso 2014). On both the cellular and supracellular levels, active behavior of organisms is based on consciousness and cognition (agency) which is solving organismal problems (defence of self), navigating via their evolution (Miller et al. 2019, Baluška and Reber 2019). In the Neo-Energide based model of eukaryotic cell evolution and organization (Baluška et al. 2006, Baluška and Lyons 2018), the first symbiotic merging of two proto-eukaryotic cell resulted in formation of the nucleated cell. Available evidences suggest that two different ancient archaea species generated both the cytoplasm enclosed with the plasma membrane and the nucleus associated with centriole/centrosome-based microtubular cytoskeleton (Baluška et al. 2004a,b, 2006; Baluška and Lyons 2018). The latter part of the eukaryotic cell is termed Neo-Energide or Cell Body in memory of Julius von Sachs and Daniel Mazia (Baluška and Lyons 2018). Subsequently, nucleated cells internalized bacteria which transformed into mitochondria and plastids enjoying their own senomes and genomes. In conclusion, the modern eukaryotic cell is having composite individuality which generates its unitary self de novo at the higher level of coplexity via synaptic and senomic principles.

Tracing regeneration

ORGANIZER

Kate MacCord, Marine Biological Laboratory, USA

This symposium explores regeneration, how it works and what we can learn from studying regeneration in various contexts. Regeneration, or the process of renewal or restoration in the face of events that cause disturbances or damage to a system, is traditionally thought of as a phenomenon occurring within organisms. However, recent research shows that the phenomenon extends from microbial communities, to the genomic and cellular content of organisms, to ecosystems. In this session, we use the study of regeneration and steady state to question some dogmas, through historical, biological/experimental, and philosophical approaches. In the first talk, MacCord and Özpolat will question the germ/soma barrier, i.e. the idea that germ cells and somatic cells are two separate cell lineages, through an examination of ongoing experimental data and historical precedents. The second talk, by Perié, will discuss the traditional view of hematopoiesis and question the idea that blood cells are produced by a very small fraction of distinct cells called hematopoietic stem cells. It will provide both the most recent technologies and ambiguities around the current interpretation of the data, as well as personal experimental data. The last talk, by Laplane, will wrap up by comparing germline stem cells and hematopoietic stem cells and question both the unity of the "stem cell" category and the stability of the stemness property in homeostasis, regeneration, and cancer contexts. This symposium is a shared symposium between the "regeneration" symposiums, supported by the McDonnell Initiative at the Marine Biological Laboratory, and "Philosophy in Biology and Medicine" symposiums. It is supported by the James S. McDonnell Foundation and an ERC-starting grant.

Germ line regeneration in metazoans

Kate MacCord, Marine Biological Laboratory, USA
B. Duygu Özpolat, Marine Biological Laboratory, USA

For nearly 150 years, the distinction between germ cells (the reproductive cells and their progenitors) and somatic cells (the rest of the cells in the body) has been considered inviolable, leading to a dogma along the following lines: germ and soma are discrete cell types and somatic cells cannot differentiate into germ cells. This thinking is, in part, due to the long-held notion that there must be a continuity of the germ line (i.e. information passed from one generation to the next cannot be broken), and has led to the understanding that germ cells, once lost, cannot be replaced. The inability to replace germ cells has been tested and shown continually over the past century by looking at traditional model organisms, such as the fruit fly, nematodes, frog, chicken, and mouse, which cannot replace their germ cells once lost or removed. Despite their inability to regenerate germ cells, research continues on a large scale in traditional model systems, in part because of the immense biomedical relevance of regaining lost reproductive functions.

An increasing amount of recent research in non-traditional model organisms shows that the barrier between germ cells and soma is far more permeable than previously envisioned. Several studies show that a phylogenetically broad range of animals, such as flatworms, fish, Hydra, salamanders, segmented worms, echinoderms, and tunicates not only are capable of regenerating lost germ cells, but sometimes do so by breaking the germ/soma barrier. Regeneration of germ cells can take place at different stages of the life cycle: ablation or removal of germ cell progenitors in the embryo nevertheless result in fertile adults in segmented worms, and sea urchins, while fertile adults can be regenerated from pieces of body lacking any reproductive organs or cells in sea stars, flatworms and segmented worms. The cellular origins and mechanisms for germ cell regeneration also vary across metazoans. While some organisms (e.g. tunicates) use somatic lineages to replace the lost germ cell lineage, others (e.g. flatworms and *Hydra*) appear to use pluripotent stem cells that can replace both somatic and germ cells, in many other species the cellular mechanisms are still unknown.

Investigations of non-traditional model organisms, drawn from broad swaths of the metazoan clade, are beginning to reveal that the barrier between germ and soma, as well as the regenerative capacity of germ cells, is far from as limited as we have previously understood. These findings lead to many intriguing questions, such as to what extent inheritance of acquired characteristics contributes to evolution where germ cells can be regenerated from soma, and whether new technologies can capitalize on this identity-flexibility to modify generations. Even more pertinent is the question of how some species are capable of these processes while traditional model species (and humans) are not. As we learn more about this phenomenon, we may have to reconsider the dichotomous germ-soma view of the body; one of the most fundamental assumptions in animal biology.

Comparing regeneration and steady state dynamics of hematopoietic stem cells: What is the data telling us?

Leïla Perié, Sorbonne Universités, France

Stem cells have the ability to continuously produce cells during adulthood. After damage, they also regenerate tissues. Hematopoietic stem cells that produce blood cells, have long since served as a reference model for stem cell biology and will be the focus of this talk. Most of the knowledge on hematopoietic stem cells comes from experiments where the cells are transplanted into an irradiated animal. Because irradiation induces damage to the hematopoietic cells and the micro-environment, transplantation experiments should mimic more a regeneration situation. However, until recently, technologies to study stem cells into steady state were lacking.

Thanks to the emergence of new single cell technologies, comparison of hematopoietic stem cells activity in steady state or after damage starts to be addressed. These new technologies emerged in two waves. The first wave allowed to trace differentiation and division of stem cells individually after transplantation by introducing a tag in each stem cell. These single cell tracing technologies have revealed that each stem cells behave differently and cannot therefore be analyzed at the population level. The second wave allowed to single cell trace stem cells without transplantation by generating a tag in each stem cell without taking the cells out of the animal thanks to a transgenic model. Studies using these technologies have concluded that hematopoietic stem cells are not contributing extensively to steady state production of cells, which would change our conceptual understanding of stem cell biology. However, I will develop in the presentation that these results are controversial. I will also show some of our data comparing transplantation after irradiation and steady state and summarize where the field stands.

Stemness in homeostasis, regeneration, and cancer

Lucie Laplane, IHPST, CNRS & Université Paris 1 Panthéon-Sorbonne, France

Stem cells are characterized by the ability to self-renew, that is to maintain a pool of stem cells throughout the life of the organism, and the ability to differentiate, that is to produce the cell types that constitute the tissues of the organism. With these two properties, stem cells can ensure tissue renewal as well as tissue repair and, to some extent, regeneration. However, there are some marked differences between stem cells of different tissues. This talk will bound under the two previous talks and argue that:

1. Stemness, the property that defines stem cells is not the same type of property in the germline stem cells (GSCs) and in the hematopoietic stem cells (HSCs). In the first case, non-stem cells can dedifferentiate into stem cells. In mice it was shown that in the absence of GSCs, differentiating cells migrate back to the stem cell niche where they reacquire stemness. In sharp contrast, transplantation assays of hematopoietic cells suggest that hematopoietic non-stem cells are unable to regenerate a pool of HSCs.
2. Stemness is not the same in homeostasis and regeneration. In GSCs, while stemness can be acquired by non-stem cells in regeneration or repair in order to compensate for the loss of the initial stem cell population, such plasticity apparently does not

occur in homeostasis. In the hematopoietic system, the comparison of regeneration and homeostasis raised the question of whether it is the same cells that act as stem cells in these two contexts.

3. Cancer is often compared to regeneration, as "a wound that never heals." However, at least in the hematopoietic system, some data suggest that stemness can work still another way. Most notably, while the niche plays a determinant role in stemness in both normal and regenerative hematopoiesis, some mutations of the Mpl-Jack-Stat pathway can render malignant HSCs independent from the niche.

These differences can be summarized with a very simple framework in which stemness can exist under the guise of four types of property (a categorical property, a dispositional property, a relational property, or a systemic property). I will end by exploring the consequences of this framework for oncology and phylogeny.

The machine metaphor in nanobiology: Molecular motors

ORGANIZER

Guglielmo Militello, University of the Basque Country, Spain

The neo-mechanistic accounts have closely examined both the operations of biological mechanisms and the explanatory power of mechanistic explanations in life sciences. Yet, a significant aspect, not yet explored, is the fact that some biological mechanisms are able to perform work, in the sense of generating motion by degrading free energy. In particular, some proteins (e.g. myosin, kinesin, dynein, ATPases) can transform the free energy, stored in ion or proton gradients or molecules such as ATP, into motion. Accordingly, this subset of biological macromolecules has been labelled "molecular motors" by analogy with macroscopic (mechanical) machines. Nevertheless, it has been recently argued that the machine-like analogy does not adequately apply to the microscopic biological devices because of different physicochemical forces operating at the macroscopic and microscopic level. Furthermore, it has been maintained that a designer is required to produce the specific design of a machine; therefore only artefacts, and not biological macromolecules, can be considered machines or motors. In view of the above, the purpose of this session is twofold: first, to characterize the mechanisms underlying some biological macromolecules usually regarded as machines; second, to discuss two opposing arguments for and against the machine-like analogy, respectively. The session will be divided into three parts. The first talk, entitled "Studying Biological Mechanisms that Transform Energy into Work: Dynein Motors as Exemplars", is designed to analyze the operations of dynein motors so as to illuminate the dynamics of the biological mechanisms that transform energy into work. The second talk, entitled "Structural and organizational conditions for being a machine", is aimed at providing some criteria for the definition of machines and assessing whether the machine-like analogy is appropriate for describing the behaviour of some synthetic and biological microscopic devices. The third talk, entitled "On why, after all, it might be better not to conceive biological parts as machines", focuses on the differences between the teleological dimension of artefacts, on the one hand, and of parts of biological organisms, on the other hand.

Studying biological mechanisms that transform energy into work: Dynein motors as exemplars

William Bechtel, University of California, USA

A feature of biological mechanisms that has been little discussed is that they perform work. Work requires degrading free energy to generate motion. Until recently little was known about how energy, stored in ion or proton gradients or molecules such as ATP, is transformed directly into motion without being changed into intermediate forms of energy such as heat. Research on different motor proteins, starting with myosins and kinesins and expanding to dyneins, is providing insight into the mechanisms by which energy is converted to motion. Dyneins were first discovered as the ATPase in the cilia of *Tetrahymena pyriformis* but soon thereafter identified in neurons in which they transport cargo (including endosomes, autophagosomes, lysosomes, peroxisomes, mitochondria, and vesicles from the endoplasmic reticulum (ER) destined for the Golgi apparatus) along microtubules towards the minus end of microtubules, typically near the nucleus. They also exert forces on microtubules, affecting their location.

This talk will focus on the investigations in recent years that are revealing how the dynein motor operates. As with motors humans design, what is particular important is the physical movement of parts of the of the machinery with respect to each other. Through various electron microscopy, fluorescent imaging, and related techniques, the kinetics of the motor's operation are largely understood. Dyneins are members of the AAA+ superfamily (ATPases associated with diverse activities). The motor domain consists of a ring of six AAA+ modules, a tail that binds to cargo that is associated through a linker domain, and a stalk that contains a microtubule binding domain (MTBD) at its tip. The operation of the motor begins with the binding of ATP in at least the first AAA module (AAA1), which is followed by the dissociation of the MTBD from the microtubule, a bending of the linker domain at a hinge, and the movement of the MTBD along the microtubule. ATP is then hydrolyzed to ADP and inorganic phosphate (Pi) and initiates a new binding to the microtubule. With the expulsion of the Pi, the linker domain straightens and as it does so, it pulls the cargo along.

The above account is an example of many mechanistic explanations in biology, describing characteristic operations but it does not supply the dynamics. To understand the dynamics, researchers have had to work at a yet more detailed level of spatial structure at which they can determine the forces operative between molecules. This has led to the hypothesis that when the linker is bent, it stores mechanical energy. The expulsion of the Pi allows the MTBD to bind again to the microtubule and this generates physical gaps between AAA1 and AAA2 and between AAA4 and AAA5. The mechanical energy stored in linker causes it to straighten and move the motor and pull its cargo along the microtubule. By pursuing detailed determination of molecular forces, researchers are developing mechanistic explanations as to how work is accomplished by biological mechanisms.

Structural and organizational conditions for being a machine

Guglielmo Militello, University of the Basque Country, Spain

The notion of “machine-like system” plays a pivotal role in the conceptual framework of neo-mechanistic accounts, inasmuch as many biological mechanisms have been regarded as the functional components of a system which behaves like a machine (Bechtel and Richardson 1993 (2010); Glennan 1996). Furthermore, the analogy between machines and certain biological macromolecular structures has been drawn in nanotechnology, as some kinds of macromolecules are artificially reproduced by considering them machine-like systems. Yet, it has been recently argued (Moore 2012; Skillings 2015) that molecular devices (biological and synthetic as well) are not machines since they are subject to physicochemical forces that are different from those of macroscopic machines. Nicholson (2013) has stressed that, since the concept of “machine” implies that of designer, biological macromolecules cannot be considered machines.

Despite this, the structural and physicochemical conditions that allow both macroscopic machines and microscopic devices to work and perform new functions, through a combination of elemental functional parts, have not yet been examined. In order to fill this void, this talk has a threefold aim: first, to clarify the structural and organisational conditions of macroscopic machines and microscopic devices; second, to determine whether the machine-like analogy fits nanoscale devices; and third, to assess whether the machine-like analogy is appropriate for describing the behaviour of some biological macromolecules.

In order to address these issues, the presentation will be divided into three parts. Firstly, the criticisms (Moore 2012; Nicholson 2013; Skillings 2015) levelled at the machine-likeness of molecular devices will be discussed. Particular attention will be devoted to the question of whether or not the different structures and the different physicochemical behaviour of macroscopic and molecular machines prevent us from employing the term “machine” at the molecular level. Secondly, the structural and physicochemical conditions underlying both macroscopic (e.g. mechanical machines) and microscopic (biological as well as synthetic) devices will be examined. Finally, a comparative analysis of synthetic (e.g. artificial DNA architectures) and biological (e.g. myosin, dynein, and F0F1ATPase) machines will be carried out so as to appreciate their differences and the distinctive character of biological molecular devices.

In line with Militello and Moreno (2018), this talk suggests that, even though macroscopic and molecular machines exhibit different component parts, a distinct design, and different physical laws (Newtonian mechanics underlying macroscopic machines and quantum mechanics governing microscopic ones), both kinds of devices share a common organisation which is the ontological basis for being a machine: they are sets of functional components that harness a flow of energy so as to do work and perform function(s). This essential characteristic stresses that, contrary to what have been claimed by Moore (2012), Nicholson (2013), Skillings (2015), a number of microscopic devices can rightly be regarded as machines.

It will be argued that the status of “machine” of some biological macromolecules opened up a domain of functional diversification during evolution, as new forms of mechanistically-complex functions could be achieved through different combinations of parts.

On why, after all, it might be better not to conceive biological parts as machines

Matteo Mossio, Université Paris 1 Panthéon-Sorbonne, France

The analogy between machines and biological organisms has a long history. In this talk, I will argue that, even though very recent philosophical contributions have framed the analogy in an original and more sophisticated way, we should resist from conceiving biological organisms, as well as their parts, as machines. My argument will be twofold.

First, I will argue that the classical comparison between machines and organisms (understood as whole systems) is profoundly misleading. To do so, I will appeal to the organisational perspective in biology and, in particular, to the conceptual connection between organisation and purposiveness (as developed by Mossio & Bich, 2017). As self-maintaining systems, biological organisms realise intrinsic purposiveness, which means that the circular relation between their existence and their activity takes place within the boundaries of their constitutive organisation. Functional parts of organisms, in turn, possess extrinsic purposiveness. The effects of their activity also contribute to explain their existence although, in this case, the connection between "being" and "doing" cannot be assessed by considering the part in isolation, but requires taking into account the organised system to which the part belongs. With that distinction in hand, I will claim that the analogy between machines and organisms is misleading because it compares entities endowed with extrinsic purposiveness (machines) to entities endowed with intrinsic purposiveness (organisms). As a result, it should not be surprising that, in spite of a long philosophical debate, machines and organisms exhibit profound qualitative differences. Recently, Militello and Moreno (2018) have framed the issue by asking whether specific parts of organisms can be legitimately understood as machines. From the organisational perspective, this comparison is undoubtedly much more relevant, insofar as it relates entities that both realise extrinsic purposiveness.

Second, I will discuss why I remain sceptical on the idea that, in spite of Militello and Moreno's challenging claim, some parts of biological organisms can be pertinently and fruitfully conceived as machines. I will focus on two aspects. On the one hand, the conditions of existence of any particular biological functional part depend on its activity in a sense that does not apply to particular machines in general. While the existence of machines as kinds does depend on their effects within organisations to which they belong, particular machines are statically stable, which means that their persistence does not require that they perform their function. This makes an important qualitative difference. On the other hand, machines are artefacts. As such, their conditions of production seem to be different from those of biological parts, which have emerged by mutual differentiation during development or cell division. Machines, in turn, are produced through dedicated processes governed by already formed organised systems. Both aspects are, I submit, implications of the fact that machines play their functional role at temporal, spatial and organisational scales, which are different from those of biological parts. Describing biological parts as machines might imply overlooking some of these differences, without a substantial explanatory gain.

Where are we after 160 years of communication between evolutionary biology and economic and social sciences? Perspectives from history, philosophy and social sciences

ORGANIZER

Naïd Mubalegh, University of Lisbon, Portugal & University Paris 1 Panthéon Sorbonne, France

Economics have been a prominent source of inspiration for evolutionary biology and ecology since their very beginning. The heuristic and explanatory value of various models and concepts borrowed from economics such as, for example, game theory, has now been established, and neoclassical economics in particular play a prominent role in the framework of mainstream evolutionary ecology and biology. In particular, devoting a lot of attention to natural selection as a main factor of evolution, which made game theory particularly relevant for studies in evolutionary biology, was also one element that moved the discipline towards unification. Parallel to this, in the last decades, social sciences in general and economics in particular have undergone a process of naturalization. Results and elements from neurosciences, cognitive sciences, evolutionary biology, etc., have been integrated into these fields. Knowledge of mankind as a biological species, whose behaviours and features are informed by long evolutionary processes, is being used in various research fields of the social sciences. And studies of cultural evolution also build upon knowledge produced by the field of evolutionary biology (in analogical or reductionistic perspectives). By crossing perspectives from history of science, history of economic thought and philosophy (Barbara Stiegler, Université Bordeaux Montaigne), social sciences and evolutionary biology (Nina Witoszek, University of Oslo) and history and philosophy of biology (Naïd Mubalegh, University of Lisbon, University Paris I Sorbonne), we hope that this session will bring elements of answer to the following questions: How does interdisciplinarity actually operate between the fields of evolutionary biology and social sciences (with a focus on economics), and which new modes of interactions can be proposed? How can contemporary issues related to the use of biological theories in social sciences be linked to questions that were raised one century ago, in the meeting of economics and evolutionary biology? What is the relevance of criticisms pointing at the inherent impossibility for economics or biology to be purely objective, and underlining the ontological and ethical consequences of using concepts and models from economics to model ecological and biological phenomena? How to rethink the question of the evolutionary narrative in the light of an updated view of perspectives within economics?

The evolutionist sources of neoliberalism: A critique of neoclassical economics

Barbara Stiegler, Université Bordeaux Montaigne, France

Where does the diffuse and increasingly shared feeling of a generalized backwardness of human species come from, a feeling that is reinforced by the constant injunction to adapt to the rhythm of mutations in a complex world? How to explain the progressive colonization of the economic, social and political fields by the lexicon of evolutionary biology?

Following the genealogy of this imperative leads us back to the 1930s, to the sources of a powerful and structured political thought, that proposes an articulated narrative about the backwardness of human species with respect to its environment and its future. It received the name of “neoliberalism”. Neoliberalism is often spontaneously associated with neoclassical economics. But the historical genealogy of new liberalism, which emerges in the 1930s under the joint influence of Friedrich Hayek and Ludwig von Mises on the one hand and of Walter Lippmann on the other hand shows that it consists, to the contrary, in a critique of the principal postulate of neoclassical thought, namely that of *Homo oeconomicus* being a rational subject.

My presentation will focus on the Lippmannian criticism of this postulate. Building upon Darwinism and evolutionist psychology, Lippmann imposes the idea of the human species being misfit to their environment, which announces the current topics of behavioral economics (cognitive biases, irrationality of behaviors, weight of emotions in decisions). Thus, focusing on some aspects of the Lippmannian thought, I will aim at presenting a genealogy of the colonization of various fields of human sciences by concepts from evolutionary biology. I will show how this genealogy leads us until today and can help us understand the historical roots of the naturalization of human sciences, and build a critique of current neoliberalism.

Competitive advantage of collaboration: Cultural-evolutionary perspectives on the Nordic model

Nina Witoszek, University of Oslo, Norway

For a long time, the Nordic countries have been the icons of fair societies with high economic productivity and quality of life. Interestingly, though by no means following the same socio-economic formula, they are all cases of societies with long traditions of prosociality and social cooperation. In this sense they are almost “ideal types” of societies which illustrate some of the tenets of the “third wave of evolutionary biology” which focuses on the role of social collaboration and altruism in promoting social resilience and adaptation to new challenges.

In this presentation I will combine evolutionary and socio-cultural perspectives to illuminate the mainsprings of what I and my colleagues from the Evolution Institute have called the "wellbeing society" (Witoszek, Midttun and Wilson 2019). The main thesis is that the socially sustainable Nordic modernity can be explained through a multilevel selection analysis: its relative success is due to a complex interplay of cooperative and competitive strategies at various levels, and across normative-cultural, socio-political and redistributive domains.

The Nordic combination of competitive market economy and inclusive cooperation rests thus on ambidexterity implemented through an interplay between cooperation and collaboration at various levels. I will show how this ambidextrous model may be contrasted with a neoliberal model, which features simple alignment of competition all the way through, from the micro through the meso to the macro level, and how it also differs from planned economy model which assumes planned co-ordination at all levels and between them. I will also show how the resilience that characterizes Nordic collaborative-competitive ambidexterity rests on socio-culturally and historically determined features of Nordic societies and institutional structures.

Do biologists "minimize influences that are external" to biology and historians of ideas "go to the other extreme"?

Naïd Mubalegh, University of Lisbon, Portugal & University Paris I Sorbonne, France

Claims that (neo-)Darwinism is not as politically neutral as it ought to be appeared as soon as *The Origin of Species* got broadcasted. In Russia, anarchist Piotr Kropotkin (1902) and fellow men of science meant to have identified, in the scientific theory exposed by Charles Darwin, the influence of the political economy that was prevailing in the UK by that time, and with which they disagreed.

Darwin himself (1887) explicitly acknowledged the inspiration he had received from his reading of Thomas Malthus. Historian of ideas

Daniel P. Todes identified two elements in the early Russian criticism of Darwinism: one "anti-Malthusian" element, that had to do with an aversion for what was identified as a British acknowledgement of competition as a major component of interhuman relationships, and whose antithesis was the model of the peasant commune, which allowed "everyone without exception to take his place at the table". Todes also identified a "non-Malthusian" element, or "the failure of Malthusian perceptions to resonate with Russian experience with nature" (1987).

One century later, Ernst Mayr observed that "Biologists, on the whole, tend to minimize external influences [from outside biology], while non-biologists, historians of ideas, and social historians tend to go to the other extreme [invoking arguments from outside biology]". According to him "all the serious Darwin students who have thoroughly analyzed the sources of Darwin's theory [...] agree that Malthus's influence on Darwin was very limited [...] and highly specific", indeed purely mathematical: "What Darwin and Wallace had taken from Malthus was the 'populational arithmetic', but not his political economy. The Marxist claims 'that Darwin and Wallace were extending the laissez-faire capitalist ethos from society to all nature to make a Weltanschauung out of the new captains' of industry's utopia of progress through unfettered struggle' is not supported by any evidence whatsoever" (1982).

In this presentation, I want to question the relevance for today of the distinction drawn by Ernst Mayr between the way biologists relate to "external influences" (external to "pure biology", if such a thing exists), and the way historians of ideas and social historians invoke elements that seemingly stem from outside. Indeed, some scholars do claim nowadays that the Malthusian, non-neutral heritage and posterior inputs from economics

a. are present in the current theorization of biology and
b. raise nontrivial issues from the point of view of social sciences.

Social interactions: Contemporary issues

ORGANIZER

Lucia Carvalho Neco, La Trobe University, Australia

The aim of this session is to explore new perspectives in the biologically-based study of social interactions between individuals. Social interactions are the building blocks of social behavior: there is no social behavior without individuals interacting with each other. Moreover, individuals and their characteristics are central to the study of the evolution, development, and structure of social behavior. Recent studies are increasingly using individuals' interactions as a tool to analyse and compare social systems. The point of this session is to present some of these new developments, coming from different evolutionary perspectives, but with several overlapping themes. In the first talk, Lucia Neco will present an integrative view of social complexity based on individuals' interactions as a metric of sociality and discuss some of the developments on using this approach to compare different social systems. Here she builds on a model introduced in a recent paper, "From classificatory to quantitative concepts in the study of sociality in animals: an epistemological view", published in *Biological Theory.* In the second talk, Jorge Mendonça Júnior is particularly interested in the selection of altruism and argues that once group selection selects the altruistic behavior, it cannot be called altruistic anymore since it does not result in fitness loss. His focus here is the influential work of Elliott Sober and David Sloan Wilson in *Unto Others* (1998). Finally, Rob Wilson explores the so-called "Westermack effect", a proposed developmental mechanism present in humans and other primates that facilitates incest avoidance first proposed by Edvard Westermarck in 1891. He focuses on care-based attachment in the primate lineage to reconcile different existing dimensions in the biological and social sciences and to raise questions about explanation in cultural anthropology.

How different are societies? Developing a descriptive model of social complexity

Lucia Carvalho Neco, La Trobe University, Australia

Sociality encompasses a wide range of social phenotypes and kinds of complexity. Considering that social interactions are a unifying characteristic shared by all social systems and that many additional characteristics are based upon these interactions, I have advocated an integrative view of social complexity based on individuals' interactions as a useful metric of sociality. This model was presented in a recent paper published by Biological Theory (Neco et al., 2018) and describes social complexity using three dimensions: the number of interacting individuals that compose the social system, the differentiation among those individuals, and how they are organized in the social system according to the nature and diversity of their interactions. Although this descriptive model of social complexity still needs further elaboration, it is useful in developing questions about the mechanisms and agents that are involved in this phenomenon in a comparable way. Accordingly, I will discuss a few examples of those developments. The first example is the claim that personality could be an important key to understanding and studying the evolution and complexity of social behavior in animals. I will discuss the relationship between consistent behavioral differences between individuals, cast in terms of personalities, and each of the three dimensions presented. In all of the dimensions, social complexity seems to require consistent behavioral variation among individuals. The argument here is that there is no complexity without differentiation and this descriptive model helps us recognize that. The second example applies this structure of social complexity to types of biological individuals other than organisms and explores the possible role of sociality in their evolution. A broad definition of sociality that allows integrative comparisons among different types of individuals should help us identify similar cooperative interactions among them and build bridges in understanding their similarities and differences.

When altruism is no longer altruistic

Jorge Piaia Mendonça Júnior, La Trobe University, Australia

In their book *Unto Others* (1998), Elliott Sober and David Sloan Wilson argue for a multi-level selection theory, claiming that it could explain the selection of biological altruism. The authors argue that natural selection, in addition to selecting organisms and genes, also occurs in the group level, selecting groups. With the pluralistic idea that natural selection acts on distinct levels, the selection of altruistic behaviors is not only compatible with natural selection but mathematically demonstrable. However, in this presentation, I'll argue that if the model proposed by Sober and Wilson is right, and group selection, alone, without the influence of Kin Selection, can select certain altruistic behaviors, then to keep calling these behaviors "altruistic" is a conceptual mistake. In the model presented by Sober and Wilson, altruism is selected only when being an altruist is correlated with living among other altruists. Such an amalgamation of altruists needs to be done in a very specific way, through a biased mechanism of group formation, which groups altruists together and exclude selfish organisms. The consequence of this mechanism of group formation is that the within-group fitness loss that follows from acting altruistically is overweighed by the between-group advantage of being surrounded by other altruists. Thus, being an altruist ends up increasing these organisms' fitness, and group selection is just a way of improving indirectly one's own fitness, just as Kin Selection, cooperation, reciprocal altruism, etc., are. Since biological altruism is a behavior that decreases the performer's fitness and increases the receiver's fitness, it is a mistake calling a behavior altruistic if it no longer results in a fitness loss. Once the previously altruistic behavior is selected, it is no longer altruistic, since altruism is defined on the basis of the lifetime direct fitness consequences, and, in this case, there isn't a fitness loss anymore. The argument presented here is part of a broader critique of the usage of the concept of altruism in biology, which I'm starting to develop. By the end of my talk, I'll try to draw out some of the ideas underlying this more general critique.

Revisiting the Westermarck Effect

Rob Wilson, La Trobe University, Australia

Over 120 years ago, the anthropologist and philosopher Edvard Westermarck defended the idea that there was a developmental mechanism present in humans that facilitated incest avoidance. In virtue of this mechanism, those who grow up together come to experience sexual aversion or inhibition when they are adults. The claim was lampooned by cultural anthropologists for most of the twentieth-century before being revived (and the term "Westermarck Effect" named) by Robin Fox in the 1960s and explored more systematically by the Stanford anthropologists Arthur Wolf and William Durham in the 1990s. In this talk I articulate and defend a version of the Westermarck Effect, integrating existing clinical, phylogenetic, and philosophical dimensions to the literature in the biological and social sciences on incest avoidance and raising some broader questions about explanation in cultural anthropology. By focusing on care-based attachment in the primate lineage, my formulation of the Effect suggests the power of a phylogenetic argument that is already widely accepted by primatologists but not by cultural anthropologists. For those who know something of the literature here, in effect this talk will draw together the insights of the psychiatrist Mark Erickson with the explorations of "deep structure" of kinship that the primatologist Bernard Chapais has engaged with over the past ten years, starting with his *Primeval Kinship: How Pair Bonding Gave Birth to Human Society* (2008). Identifying post-adoption incest as a phenomenon with under-explored evidential value here, the talk sketches an explanatory strategy for pursuing the project of reconciling the Westermarck Effect with the clinical reality of incest, concluding with an explicit argument summarizing the case it makes against culture-first or conventionalist accounts of incest avoidance prevalent in anthropology until recently.

New considerations on inheritance, heredity and transmission

ORGANIZER

Antonine Nicoglou, Université de Tours & IHPST, France

Our Symposium aims at clarifying some conceptual and theoretical implications of extending biological inheritance to non-genetic mechanisms of biological transmission. The clarifications we want to make concern three different fields in which the issue of non-genetic transmission could have major impacts, namely evolutionary biology, genetics, and biomedicine. It is now widely accepted that there is more than just (nuclear) DNA inheritance. This calls for a reassessment of how and when various forms of transmission between organisms takes place, of their impact on phenotypic variation, and of the evolutionary origin of its different tempos and modes (Merlin & Riboli-Sasco's talk). The precise analysis of the context of emergence of the notion of heritability within the history of genetics and heredity can be newly enlighten by looking at the ways genes-environment relationships have been tackled in this history. This could help to clarify the sometimes-ambiguous distinction between "heritable characters" and "inherited characters" (Nicoglou's talk). Finally, the integration of an extended concept of heredity in biomedicine could have significant theoretical impacts: it could notably modify the notion of hereditary diseases and thereby have an important effect on medical classification (Pontarotti's talk).

More precisely, in this symposium, the following issues will be discussed and reassessed: biological transmission and its associated mechanisms; inheritance/heredity/heritability and their application to transmitted factors and characters in general, and to diseases in particular. From a theoretical point of view, we will focus our analyses on: the role of genes and environment relationships to clarify and define concepts (Nicoglou); the description of transmission mechanisms as evolved and evolving systems (Merlin and Riboli-Sasco); the way in which theoretical studies about non-genetic modes of transmission may modify current medical categories (Pontarotti).

Inheritance as a set of evolved and evolving physiological processes

Francesca Merlin, CNRS & University of Paris 1 Panthéon-Sorbonne, France
Livio Riboli-Sasco, Université Paris 1 Panthéon-Sorbonne, France

The current debate over the need to extend the classical concept of inheritance, which is merely genetic, in the light of forms of non-genetic transmission has seen, since the 1990s, many new definitions of this concept (Griffiths and Gray 1994, Sterelny et al 1996, Merlin 2017) and different ways to categorize various forms of transmission as systems or as channels of inheritance (Jablonka and Lamb 2005, Heläntera and Uller 2010, Danchin et al 2011). A few authors, like us, has left aside the issue of defining what should be considered as inheritance, and has rather focused on how to make sense of the many different transmission mechanisms from an evolutionary point of view. This shall provide meaningful insight into historical contingencies that determine the currently observed modes of transmissions in simple and complex organisms. The available modes of transmission may subsequently influence the available forms of evolution for specific organisms. This will hopefully provide us with a better understanding of stability and variation within evolving populations.

First of all, by introducing a certain number of empirical distinctions, we build an evolutionary conceptual framework that could be useful for tracing different forms of biological transmission, and making sense of their respective tempos and modes from the evolutionary point of view (Merlin and Riboli Sasco 2017). More precisely, we distinguish two channels of transmission (channel 1 and channel 2), two measurements of the temporal dynamics of transmission, across and within generations (durability and residency), and two types of transmitted factors according to their relevance from an evolutionary point of view (selectively relevant and neutral stable factors). Note that by "transmitted factors" we mean "various sorts of physical entities and processes that are passed on between organisms (i.e., the content of transmission such as stretches of DNA sequences, biochemical marks, ecological niches, cultural items). On the basis of these three distinctions, we then argue for a vision of biological transmission as a set of evolved and evolving physiological processes, not restricted to transmission mechanisms stricto sensu. We also argue for an epistemological primacy of the study of these mechanisms in the perspective of improving our understanding of the evolution of biological transmission, i.e., what is passed on across generations, how and why.

Genes and environment relationships in the understandings of inheritance

Antonine Nicoglou, Université de Tours & IHPST, France

In this presentation, I intend to examine how genes and environment relationships have been analyzed in the understanding of heredity from the beginnings of genetics (rediscovery of Mendel Laws) to the early days of molecular biology (1970s). I will particularly focus on Johannsen 1911 seminal's paper in which he introduced the genotype-phenotype distinction and proposed some conceptual clarifications of heredity, inheritance and transmission. While, several studies have looked at this history (e.g, Sapp 1987, Sarkar 1999, Burian 2000) none, to our knowledge, has looked at it also as a potential context for the emergence of the notion of heritability (notion developed in population genetics and primarily in behavioral genetics). First, I argue that Johannsen's paper offered a scientific and conceptual framework for population genetics to develop (Nicoglou 2017). I then suggest that looking at the way genes and external conditions relationships have been depicted in this historical episode enlightens our understanding of heredity both in intragenerational and intergenerational studies. More precisely I will try to show in this presentation what kinds of understandings of inheritance focus more on intragenerational studies and those that focus more on intergenerational studies. Finally, my hypothesis is that the analysis of genes and environment relationships in the understandings of inheritance allows explaining the sometimes-difficult distinction in contemporary biology between "inherited character" and "heritable character". I will try to propose some reasons for this confusion. And I will argue that solutions to the problem of extended inheritance (Helanterä & Uller 2010, Danchin et al 2011) might also appear throughout the clarification of all these concepts.

Extended heredity and disease transmission

Gaëlle Pontarotti, Université Paris-Diderot & IHPST, France

The field of biological heredity has been remarkably widened during the last few years. Many empirical and theoretical studies have indeed suggested that the gene-centered theory, which is prevailing in this domain, should be extended so as to include epigenetic marks, social behaviors, microorganisms and parts of the environment in biological legacies (Jablonka & Lamb, 2005; Griffiths & Stotz, 2013). While many authors have discussed the potential effects of this extension in evolutionary biology (Bonduriansky & Day, 2009; Danchin et al., 2011), very few studies have so far questioned the impact of a widened theory of heredity in biomedicine. In this context, my talk aims at providing an overview of the theoretical perspectives linked to the integration of an extended concept of heredity in this area. I will first question how an extended theory of heredity could modify the notion of hereditary disease. While hereditary diseases were for a long time metaphorically conceptualized on the model of « goods » transmitted from parents to offspring, and while the genetic theory of heredity conceived of them as recurrent pathologies caused by transmitted genetic variants, what these pathologies are in the context of extended heredity still has to be clarified. This clarification requires a meticulous conceptual work that could rest on studies previously developed in philosophy of biology (Griesemer, 2000; Jablonka, 2002; Griffiths & Gray, 2004; Pontarotti, 2015; Merlin, 2017); it should result in the shaping of an operational notion associated with relevant explanations and efficient medical strategies. I will then describe the kind of causality to which hereditary diseases would be related within an extended framework (mechanistic, organicist, etc.). Finally, I will propose some considerations on the new meaning that could be attributed, in this context, to the old notion of « terrain » which traditionally refers to a hereditary susceptibility to a specific disease. To conclude, I will state that a renewed concept of heredity and a connected renewed description of hereditary disease may have a significant impact on medical classification but also on medical – preventive and therapeutic – strategies.

Conceptual integration in biology

ORGANIZER

Aaron Novick, Dalhousie University, Canada

Classic models of theory change in science emphasize competition between theories, paradigms, and research programs – competition that leads, ultimately, to the replacement of the old theory with a new one. Over the past two decades, however, philosophers of biology have noted the central importance of the integration of different approaches in biological research, as an alternative to competition and replacement. This symposium focuses on the role of concepts in both facilitating and hindering such integration. Each paper focuses on how concepts transfer between different disciplines and areas of study, engaging in both first-order clarification of particular concepts and second-order reflection on how concepts participate in and promote integration. The first paper in the session, by Jeremy Wideman (presenting) and Aaron Novick, considers the role of conceptual convergence in facilitating the integration of disciplines. They show that evolutionary cell biology and evolutionary developmental biology have converged on similar types of questions and similar forms of answers, and argue that this allows us to reconceive evo-devo as a special case of evolutionary cell biology. The second paper in the session, by Eve Roberts, investigates the critical relationship between phenomics and the concept of the "phenotype". Using diverse methods, phenomics attempts to describe the phenotype of a given entity inclusively in detail. She argues that the "phenotype" concept is highly complex. Clarification of phenomic methods requires developing this complexity as a strength of the methods. The final paper in the session, by Aaron Novick (presenting) and Ford Doolittle, shows how the patchwork structure of the "species" concept facilitates the transfer of related concepts, investigative methods, and patterns of reasoning between the study of macrobes and microbes. They argue that overly reference-focused views of scientific concepts have led philosophers to overlook the way in which "species" plays this integrative role in biological science.

The return of the cell: What's so special about evo-devo?

Jeremy Wideman, Dalhousie University, Canada
Aaron Novick, Dalhousie University, Canada

Since its emergence in the latter half of the 20th century, evolutionary developmental biology (evo-devo) has been treated by philosophers and historians as somehow special. The central questions of evo-devo include the origin of development, homology, genotype-phenotype relations, evolvability/constraint, epigenetics, and, perhaps most importantly, the origin of novelties (Laublichler 2007). Within the framework of evo-devo, these questions have largely been applied only to multicellular organisms. However, these questions are not specific to multicellular organisms: they can be asked more widely. Recent advances in DNA sequencing and phylogenomics has resulted in the establishment of a relatively stable consensus tree of eukaryotes, which are mostly unicellular protists. This has resulted in an explosion of evolutionary cell biological research, leading to major theoretical that parallel those seen in evo-devo (Lynch et al. 2014). Thus, the major questions and concepts of evo-devo reappear in evolutionary cell biology. For example, the origin of development reappears as the origin of lifecycles; developmental constraints reappear as cellular constraints; and developmental epigenetics reappears as cellular epigenetics. Furthermore, we argue that evolutionary cell biology brings with it philosophically interesting phenomena that are not central to evo-devo. These include phenomena related to biological individuality (e.g., symbiosis, endosymbiosis, and holobiontism), major evolutionary transitions (e.g., the evolution of eukaryotic cells), and saltationism (e.g., horizontal gene transfer and whole genome duplications), all of which are already major subjects of interest in the philosophy of biology. We conclude that since most lineages of eukaryotes are unicellular, multicellular organisms can be viewed as a special class of eukaryotes; in the same vein, evo-devo can be seen as a special case of evolutionary cell biology.

Is phenomics the epistemic superstar of biological/biomedical research?

Eve A. Roberts, University of King’s College, Canada

Increasingly, biological/biomedical researchers are employing experimental designs which feature high-throughput methodology and generate formidable amounts of data – so-called “Big Data”

– which require complex bioinformatics for adequate analysis. Such methodology is not hypothesis-driven. Elsewhere I have argued that this experimental design is system-driven. This methodology is the best available for investigating a system in its entirety and proceeds without the prejudice of a hypothesis as such: it may reveal novel or unexpected results critical to understanding that system and otherwise elusive to investigators. Research classified as "omics" is typically system-driven. Genomics addresses the complete genome(s) of an organism. In mammals, for example, these genomes comprise the nuclear coding and non-coding DNA and mitochondrial genome. There is little flexibility for defining the system under consideration. Proteomics attempts to identify all the proteins in a given system of interest: here the nature of the system and conditions under which it is interrogated can (and must) be specified in detail. Numerous other omics disciplines exist, such as transcriptomics and metabolomics, as well as subdisciplines of some, such as metalloproteomics and phosphoproteomics. Phenomics is a relative newcomer within the firmament of omics. The objective of phenomics is to capture/identify/annotate the phenotype of a given entity inclusively in detail. The justification for this effort is that in the end phenotypes are what really interest us. Phenotypes can be truly informative, whereas genomics and other omics produce an incomplete and/or impractical assessment. Phenomics may hold the analytical key to solving the relationship between genotype and phenotype. Clearly, phenomics is not hypothesis-driven. What is driving it? What is it investigating? The answers to these questions depend less on "phenome" than on "phenotype". The "phenotype" concept has received little attention compare to "gene" and "genotype". The standard definition – observable traits of an organism – includes morphological and behavioral features. Phenotype reflects gene expression, taken broadly, and environment. I argue here that phenomics is system-driven but displays nuances depending on the entity under investigation. For some entities, mainly at the cellular or subcellular level, a phenotype can be defined as the feature(s) of interest, similar to the system in proteomics. At the macroscopic level, with a view toward clinical or practical applications (for example, based on a huge collection of human data including genetic, physiological, and pathophysiological findings), the notion of phenotype is not flexible. It is predetermined by current usage, much like the situation with genomics. In either case, "phenotype" often carries a sense of being dynamic: the phenotype changes over time. If the philosophical issues relating to the conceptual complexity of "phenotype" are ignored, phenomics risks ending up a hit-or-miss unregulated experimental design. Such an outcome would be unfortunate, because in fact phenotypes do matter a lot.

"Species" without species: A patchwork approach to thinking about microbial species

Aaron Novick, Dalhousie University, Canada
W. Ford Doolittle, Dalhousie University, Canada

Biological science makes use of a diversity of "species" concepts. We argue that order can be brought to this diversity if we recognize two of its key features. First, drawing on the work of Mark Wilson, we argue that any given "species" concept is likely to have a patchwork structure, generated by extensions of the concept into new domains. We illustrate this by showing how two "species" concepts (biological and ecological) have been modified from their initial macrobial applications to apply to microbes, and how a third (based on pangemonics) is in the process of extending from microbial into macrobial domains. Second, within any given patch, distinct "species" concepts may interact and hybridize. Putting these together, we defend a semantic picture of the "species" concept as a collection of interacting patchwork structures. This furnishes an argument against the eliminative materialist, who argues that since different "species" concepts pick out different kinds of units, the diversity of uses is reflectively merely of polysemy, and thus that any overarching "species" concept is "theoretically empty." We show that this view misses the unity of the concept by looking in the wrong place. Unity comes from local connections between patches (involving the transfer of methods, reasoning patterns, inferences, and related concepts between uses) and interactions and hybridizations between different patchwork structures. In addition, we push back against the notion that the primary purpose of a “species” concept is to pick out natural units. That is one function of the concept, but there are others. In particular, in the study of microbes, the concept is used to manage inquiry into processes of speciation, even when these processes do not produce clearly delimited species. We show this by analyzing the call, on the part of some microbiologists, to study “speciation without species.”

Unpacking molecular metaphors: Information, programs and codes

ORGANIZER

Gry Oftedal, University of Oslo, Norway

In the life sciences, genes and developmental processes are explicated and understood via concepts of language, communication, and computer science. DNA contains, carries and transmits “information”. The letters of DNA are “codes” transferring “messages” via the processes of “transcription” and “translation”. DNA is “software”, and cells can be “programmed” to perform certain tasks. The content and role of such concepts are still controversial. Are they “just metaphoric” or indicative of something more substantial? On the one hand, the terminology may merely be a matter of using colorful language for communicative purposes. On the other hand, these concepts might play significant theoretical and heuristic roles within molecular biology and may even, as some argue, capture genuinely semantic phenomena. Metaphors allow transfer of concepts and ideas from one area of thought to another and are ubiquitous in science and science communication, as well as in everyday discourse. Researchers disagree whether we should understand the use of concepts such as genetic information, programs and codes in life sciences as metaphorical. We will start from the idea that a metaphorical use need not exclude that these concepts can play genuine theoretical and explanatory roles. In this session we will address the roles of information, program, and code metaphors in genetics and epigenetics and suggest how these metaphors may play significant theoretical roles both from the viewpoint of the history of molecular biology and from the perspective of more current life science approaches. We argue, in particular, that they can support the articulation of hypotheses, emphasize deep similarities between biological phenomena and technological artefacts, and offer heuristic tools for generating new hypotheses.

Genetic information in the 1950s

Ulrich Stegmann, University of Aberdeen, UK

The merit or otherwise of genetic information is often assessed in terms of pre-existing notions of information. On this approach, the extent to which genetic information is a legitimate idea mainly hinges on the extent to which it matches pre-existing notions. Although the approach is illuminating insofar as it reveals potential overlaps with technical or philosophical accounts of information, it also comes with problematic limitations, or so I argue. It risks both underestimating the potential value of idiosyncratic uses of "genetic information" (due to their lack of overlap) and overlooking such uses in the first place (due to selective attention). If the goal is to understand the possible roles of "genetic information" in scientific practice, then explicit attention needs to be paid to how scientists actually employed this expression. This can be achieved by selecting a historical episode in which it was used extensively and for which there are historical sources rich enough to enable an informative reconstruction of actual usage. The findings can then be used to address two philosophical questions:

a. What was the content of "genetic information"?
b. What roles or functions did this concept play in scientific practice, if any?

This paper presents results of an investigation into the use of "genetic information" between 1953 and 1958. It can be shown that the term "genetic information" denoted at least two distinct features,

1. a disposition to cause heritable phenotypic effects (then regarded as one of the two characteristics of the genetic material) and
2. the monomer sequences of nucleic acids and proteins.

Although “genetic information” was ambiguous and represented an idiosyncratic use of information, it also featured well-delineated referents. Furthermore, “genetic information” played several roles at the time, descriptive, explanatory, and heuristic. Here I focus on its descriptive role, i.e. its use in articulating empirical results and various hypotheses. For instance, by the mid-1950s, the expression was commonly used (in the capacity sense) to describe the empirical finding that DNA/RNA is the genetic material. It also helped articulating claims that the genetic capacity was “transmitted” down the generations and “transferred” from one molecule to another. The sequence-sense was rarely employed, although it became decisive for Francis Crick’s articulation of the Central Dogma. It can also be shown that the Central Dogma was merely a set of claims about template-directed synthesis, at least for Crick.

Making sense of “genetic programs”

Mihnea Capraru, Nazabayev University, Kasakhstan

Biologists frequently use the metaphor of a “genetic program” in order to understand the mechanisms by which genetic networks self-regulate their activity. Not only does this metaphor need explanation, however, but it is open to challenge on the grounds that genetic regulatory networks (GRNs) do not have a predetermined schedule of execution, and that therefore they are unlike computer programs. The no-schedule challenge is refuted in this article. GRNs do, indeed, lack a predetermined execution schedule. Such a schedule, however, is not necessary in order to make something a computer program, despite a widespread (and understandable) popular prejudice. The prejudice is explained by the prevalence of predetermined-schedule, von-Neumann–style programming in schools and in the industry. There are, however, other computational architectures, and the one that best mirrors GRNs is that of Post-Newell production systems. Programs of this type contain a memory store populated with expressions that are constantly pattern-checked by a set of IF–THEN conditional instructions. Crucially, the order in which these instructions are written does not matter. Instead – and simplifying a little – all instructions check for their “IF” patterns in parallel, and execute the “THEN” parts whenever the patterns are matched. The most productive way to make sense of the genetic-program metaphor is to see that cell as implementing such a production system. The memory store is implemented by the chemical landscape of transcription factors; the IF–THEN instructions are implemented by promoters (IF) and by the coding regions they regulate (THEN); and the programs’ inputs and outputs are implemented by intercellular signals, as well as by transducers sensitive to the physiological and/or extraorganismal environment.

The role of the histone code in epigenetics

Gry Oftedal, University of Oslo, Norway

The concept of a genetic code has proven useful in molecular biology in depicting the combinatorial relations between DNA bases, RNA bases and amino acids in protein synthesis. The code metaphor has also been shown to have played a significant role as an outset from which to suggest various hypotheses and mechanism sketches of the DNA-RNA-protein relation in the early days of molecular biology. The “histone code” of epigenetics is a more recent use of the code metaphor. Histones are proteins in the cell nucleus around which DNA coils and form nucleosomes. Histones have important roles in the regulation of gene expression, and a range of factors bind to histones and make areas of DNA available or unavailable for gene expression. The “histone code” involves various chemical marks, such as methylation, acetylation, or phosphorylation, that bind to the tails of histone proteins and that may act as “readable” codes and landing sites for proteins that influence chromatin architecture and gene expression.

I show how the code metaphor has played a similar role in research on the “histone code” as in research on the “genetic code": as an outset for suggesting and testing causal hypotheses. The success of the code metaphor in recent epigenetics has, however, turned out much more limited compared to early molecular biology. I suggest that problems with the "histone code" metaphor partly arises because hypotheses suggested with the outset in "code"-thinking turn out too simplistic to account for the highly contextual effects of histone modifications. A problem of transferring the code metaphor to epigenetics is also that the understanding of biological "code" has become very much influenced by our understanding of the DNA-RNA-protein relation, an understanding that is not effortlessly transferred to the context of epigenetics. I suggest that even if the histone code may not be the best metaphor in conveying understanding of mechanisms of histone modifications, it has still played a useful role in hypothesis generation in epigenetics research.

Networks and the ontology of the theory of evolution by means of natural selection, part I

ORGANIZER

François Papale, Université de Montréal, Sorbonne Université, CNRS & Museum National d'Histoire Naturelle, France

Network-based models are at the forefront of contemporary research in evolutionary biology. Whether pictured in a diachronic or synchronic perspective, networks of interactions fashion biodiversity at all levels of organization. This has the potential of transforming our traditional understanding of the theory of evolution by means of natural selection. Given the rising interest in and the proliferation of network-based models, it is urgent for biology and the various disciplines studying it to evaluate the scientific changes this turn promises. This session aims at evaluating the consequences of this network-oriented tendency on the ontology of evolutionary biology. Since the advent of Modern Synthesis, evolutionary biology has been defined by its use of tree-based models of inheritance and phylogeny in the representation of evolutionary pattern. Traditionally, the use of tree-based models was justified by their success in ordering relationships among paradigmatic biological entities, namely genes and organisms, while the same tree-based models corroborated the relevance of those entities. From this justificatory structure followed constraints relative to the objects of inquiry: the processes that sustain branching patterns of divergence one side, the genealogical entities that populate these processes on the other. Conversely, a multitude of objects of inquiry have been under studied: among the neglected processes, we find hybridization, endosymbiosis, lateral gene transfer, regulation of gene expression, various developmental processes, symbiosis, convergent evolution, co-dependent and contingent evolution, etc.; among the neglected entities, we find communities of organisms, mobile genetic elements including transposable elements, ecosystems, memes or cultural units, multilevel systems, biochemical interaction systems involving genes and proteins, functional patterns (songs), etc. These objects have attracted more and more attention in the past decades, despite their friction with tree-based models. Network thinking provides a significantly different and more inclusive view of evolution and the relevant objects worth studying. Proponents of network-based approaches argue that: diachronically, representations of evolution are more accurate when they mobilize complex networks; synchronically, any time slice is best represented as a complex system of interactions; ontologically, biological entities are best conceived as nexuses generated by the coming together of various vectors of influence. If this approach prevails, the core principles of the theory of evolution by natural selection would have to be reinterpreted in a way that expands our understanding of the complexity of evolutionary phenomena. With network thinking, the variation that is the first matter upon which natural selection acts is to be seen as the result of complex interactions. The differential fitness between individuals is to be anchored in an ecological understanding of persistence and reproduction, while the patterns of inheritance are shown to go beyond mere vertical transmission. Given the importance of this potential transition from tree thinking to network-based approaches in evolutionary biology, there is a pressing need to start assessing its philosophical and scientific imports. This session focuses on one of the many aspects of the transition: how network analysis reshapes the ontology of evolutionary biology and what this entails for the theory of evolution by means of natural selection.

Microbiomes to memes and back: François Papale, ITSNTS theory and a deeper Darwinism

W. Ford Doolittle, Dalhousie University, Canada

ITSNTS ("It's The Song, Not The Singer") theory was first formulated as an alternative to a popular view of "holobionts", namely that collectives comprising microbial communities and their macrobial hosts form "units of selection" (Darwinian individuals in Godfrey-Smith's sense). They generally do not, but one way to save the interest in such recurring interactions and account for the common observation that community (metabolic) "function" is more conserved than is community (taxonomic) composition is to see the interactions themselves as such a unit (1,2). Evolution by Natural Selection (ENS) is most often considered to entail the differential reproduction or replication of selected entities, criteria that holobionts do not often meet. But as Bouchard has argued (3), differential persistence can also underwrite it. ITSNTS theory offers a particular formulation of persistence selection in which processes (for example "holobiont" function, developmental interaction patterns, regulatory networks, biogeochemical cycles, community-level metabolism, ecosystem "functions" or cultural practices, all considered as "songs") recruit (encourage the differential reproduction of) things (genes, taxa, cultural practitioners) that re-produce (produce again) or implement ("sing") them. Songs persist, even though no parent-offspring lineages (essential in the accounting of differential reproduction) can be traced between their successive "singings". Songs and singers make up interacting evolutionary domains, not nested levels in a hierarchy, and what looks like co-operation or inter- species altruism can be seen as selfish in both domains.

A practical guide for universal Darwinism

Stefan Linquist, University of Guelph, Canada

When "Darwinian" thinking is extended to some novel domain – whether it is to transposons, cancer cells, or culture – the default tendency is to apply the principle of natural selection. This involves regarding the relevant entities as a phenotypically variable population, and searching for particular ecological factors that exert selection pressure on those variants. However, selectionist hypotheses are already difficult to test in conventional cases, i.e. using populations of familiar organisms in well understood ecological settings. This is why documented examples of natural selection are so rare. It is therefore impractical to begin with a selectionist framework when applying Darwinian thinking to novel domains, where the relevant entities or environments are often poorly understood. Alternatively, it makes more sense to begin with either a "purely ecological" or a "purely evolutionary" framework. The former ignores (for simplicity) phenotypic variation; the latter ignores particular features of the environment. One can then estimate the explanatory significance of each factor in isolation, before deciding whether it is practical to combine them. In this paper, I operationalize the "ecology versus evolution" distinction, and show how it is possible to estimate the influence of each type of factor in two unconventional cases: transposable elements and cultural replicators.

This approach has at least one thing in common with network thinking. Ontological questions about the structure of the theory of natural selection, or about the necessary requirements for being "unit" of selection are intentionally downplayed. This is quite different from the approach taken, for example, by Dawkins in his discussion of memes. He began by asking, what does it take to be a unit of evolution? He then configured the idea of a meme around those requirements. Instead, I recommend beginning with some pattern in nature that calls for explanation, then building up to the question of whether natural selection can explain such patterns.

Beyond genealogy: How networks enable a modelling of the extended present

Nathalie Gontier, University of Lisbon, Portugal

How we understand and depict information on the living and non-living world changes over time in association with varying cosmologies (1). Cosmologies are worldviews that provide theories on the nature of matter, space, and time, and these theories become depicted by cosmographies (2). Western cosmographies have transitioned from cyclic or circular wheels of time over static scales of nature to linear timelines that in turn have transformed into multilinear, bifurcating trees (3, 4, 6). Today, and throughout the sciences, tree models are being replaced by network diagrams. We will analyze how each of these iconic diagrams differentially depict hierarchical aspects of matter, space and time as well as how they are causally explained by different epistemologies. We will then hone in on network models that, in the evolutionary biological sciences in particular, have been introduced to portray aspects of reticulate evolution (5), but also gene-protein-cell interactions, and ecological relationships. Analyzing the power of networks, we will investigate how they enable a modelling of evolution in what can be called an extended present. Such goes beyond attempts to "merely" depict genealogical and historical relationships typical of phylogenetic and paleontological sciences (7), and we will examine how such calls out for ontological pluralism and a different conceptualization of both space and time.

Networks and the ontology of the theory of evolution by means of natural selection, part II

Turning evolutionary biology into a network science

Éric Bapteste, Sorbonne Université, CNRS, Museum National d'Histoire Naturelle, EPHE & Université des Antilles, France

Recent decades have seen the scientific understanding of biological complexity at various levels of organization (molecular, cellular and organismal) make a leap forward. Molecular interaction networks, lateral gene transfer, symbioses and endosymbioses are amongst the many drivers of biological evolution that, for billions of years, have led to the creation of multi-lineages and multi-level collectives. The ubiquity of such collective organizations, usually represented by networks, is now widely recognized and accepted. Ipso facto, evolutionary biology, originally focused on tree-like relationships, appears to be fundamentally turning into a science of dynamic networks. This state of affairs offers an original framework to unify, reconstruct and expend the theory of evolution. On the one hand, network-based analyses allow for a better specification of Lewontin's three conditions of evolution by means of natural selection. On the other hand, this restructuration encourages a new multidisciplinary strategy to investigate evolution, that I call phylosystemics, which unites the short timescale of interactions studies from systems biologists and ecologists with the longer timescale of studies familiar to evolutionary biologists, by taking advantage of methods from network sciences.

Redefining units of selections as networks of interactions: An ontological inquiry

François Papale, Université de Montréal, Sorbonne Université, CNRS & Museum National d'Histoire Naturelle, France

The use of network-based models in evolutionary biology becomes more pervasive by the day. This methodological transition has important consequences, among which the need to review our ontological understanding of evolutionary individuals. In this presentation, I argue that individuals, in the context of Darwinian explanations, should be conceived as integrated networks of interactions to be described by their degree of integration. This view will be contrasted with Godfrey-Smith's Darwinian individual framework (Godfrey-Smith 2009).

Godfrey-Smith defines Darwinian individuals, the building blocks of Darwinian populations, as genealogical entities that can be isolated more or less straightforwardly. This means that a great diversity of entities and processes can be viewed as reproducers and reproduction, respectively: "That is fine, as long as we know who came from whom, and roughly where one begins and another ends." (Godfrey-Smith 2009, 86). In order to provide finer grained descriptions of reproducers, Godfrey-Smith organizes them into three types: scaffolded, simple and collective. The distinction between single and collective reproducers on one side and scaffolded reproducers on the other is that the formers have "the machinery of reproduction internal to [them]" (Godfrey-Smtih 2009, 88). The distinction between single reproducers and collective ones is that the latters are composed of lineages with evolutionary fates potentially independent from that of the whole.

Network analyses of evolutionary dynamics provide a different picture of biological entities: those that do reproduce are phylogenetic mosaics composed of parts that have distinct evolutionary fates; moreover, their reproduction is made possible by complex networks of interactions involving entities at various levels of organization (Bapteste et Huneman 2018). At best, then, all reproducers could be described as scaffolded collectivities. However, even this readjustment is problematic. In the presentation, a network-based analysis of cases that are considered paradigmatic reproducers (genes, organisms like us, prokaryotic cells) will show that two out of the three criteria (bottleneck, germ line, integration) provided by Godfrey-Smith for describing collective reproducers are maladapted to a Darwinian perspective.

Given these limitations, I argue for an alternative framework inspired by the work of various authors (Bouchard 2010; Brandon 1988; Dupré and O'Malley 2009; Millstein 2009): biological entities should be conceived as interactive networks whose degree of functional integration determines whether they can be considered units of selection or not. This degree can be assessed through rate of interactions within the studied biological object, whose boundaries can be drawn where the said rate drops significantly. This definition emphasizes that biological objects are collectivities and provides a more accurate reading of the part they play in evolutionary dynamics.

Astrobiology: Plausibility and astrobiology, part I

ORGANIZER

Emily Parke, University of Auckland, New Zealand

The emerging field of astrobiology explores the origin, evolution, extent, and distribution of life in the universe. In recent years, philosophers have begun to engage with astrobiology primarily through the lens of the debate about the nature of life. This session focuses on a different set of conceptual issues in astrobiology. All three papers explore, from various angles, the plausibility of theories and models in astrobiology, from the perspective of primarily the philosophy, but also sociology of science. Malaterre discusses competing hypotheses about the origin of life on Earth, and proposes that – in light of the strong underdetermination and complexity inherent in the field's subject matter – these hypotheses are evaluated more loosely than many other scientific hypotheses: in terms of their plausibility. Parke discusses the role of plausibility in adjudicating amongst rival models that guide the search for life on other planets, and explores how geophysical systems on Earth serve at the same time as analogue systems for the (Earth's) deep past, and as guides for contemporary searches for analogous habitable systems on other planets. Mariscal focuses on inferences regarding the astrobiological investigation of life in the universe. Astrobiologists draw on a range of methodologies from a range of scientific fields, to construct plausibility arguments about these aspects of life. These approaches coexist, but have an extremely broad range of epistemic features that differ greatly from those in "core", and less interdisciplinary, sciences. Our aim in this session is to develop the discussion about conceptual issues in astrobiology in new and fruitful directions.

Scientific plausibility: Case studies from origins of life research

Christophe Malaterre, L'Université du Québec à Montréal, Canada

Origins of life research has the characteristics that its object of study not only occurred in the deep past (some 4 billion years ago) but also has barely left any trace in the fossil record (due to high and generalized metamorphism of the terrestrial crust in the early ages of our planet). Different elements of possible scenarios for the origin of life have been proposed in the past fifty years (RNA-world, small-molecule-world or metabolism-first), but the puzzle is highly complex, as an explanation requires a multi-stage approach for bridging nonliving matter (as characterized by simple organic compounds in solution) to a unicellular form of living matter (as inferred from reconstructions of possible Last Universal Common Ancestor unicellular organisms). Due to such state of severe historical underdetermination and high complexity, we argue that origins of life hypotheses are not evaluated through a regular process of refutation/corroboration but are judged according to a much looser criteria of "scientific plausibility". Based on case studies, we propose to understand this plausibility as factoring in empirical adequacy terms (quantity, variability, precision etc. of empirical evidence) as well as epistemic terms (in particular "loose" coherence) and sociological terms (e.g. prestige/power of teams/individuals/institutions/publications, "hot topics" within scientific disciplines). Anchored to an analysis of the scientific practice, the notion of scientific plausibility helps make sense of the gradual ways in with which scientists give credence to different hypotheses and theories. We suggest that such plausibility also plays a significant role in many areas of science characterized by severe underdetermination and high complexity.

Warm little ponds and other analogues in astrobiology

Emily Parke, University of Auckland, New Zealand

In November 2018 NASA chose a landing site for its 2020 Mars Rover missions (Jezero Crater, the site of an ancient river delta). The preceding debates focused on which sorts of geological sites would be the most promising places to look for life or evidence of life (for example, some astrobiologists argued that the site of an ancient hot spring would have been more promising). These debates about the most plausible settings to find traces of life in the universe, like related debates about the origin of life itself, rest on a mix of theoretical plausibility arguments and analogue reasoning. Much of this analogue reasoning starts with geophysical systems or phenomena that scientists can examine on Earth today – for example, hot springs, deep-sea hydrothermal vents, or patterns in very old rocks – as a basis for explaining observations or predicting what might be found on other planets.

There has been some discussion in philosophy of science of physical analogue models, such as laboratory black hole analogues (Sterrett 2015) and model organisms (Ankeny and Leonelli 2011). Analogue models in astrobiology play different roles from other analogue models in part due to their dual function: at the same time, they can serve a "traditional" modelling function of guiding explanations or predictions about targets that are inaccessible but assumed to be relevantly similar, as well as serving as analogue systems to guide active exploration in the universe.

The target(s) of astrobiology models are not always clear and uncontroversial. Many aim to help us understand the complex series of transitions from chemistry to biology that occurred on Earth approximately 4 billion years ago, but the transitions themselves, their order, and their endpoint are debated; some are "how possibly" models of the origin of life anywhere, abstracting away from assumptions about how it happened on Earth; and there is no consensus on what counts as minimal life in the first place. In any case, a key explanatory target, the origin of life on Earth, occurred so long ago that there are no clear traces of it. Of course, the latter is not a unique issue; all historical sciences deal with targets that are inaccessible in this way, to varying degrees. But a further issue is the dual role that analogue models in astrobiology play: they are studied not only as analogue systems for understanding some target(s) in the deep past, but also analogues guiding what astrobiologists should look for on other planets, today, to detect life, or at least biosignatures (evidence of life or of past life). I discuss these issues of reasoning with analogues in the context of examples from astrobiology, including the case mentioned above of the “hot spring” model of the origin of life and its influence in decisions about the 2020 Mars landing site.

Assessing the research program(s) of astrobiology

Carlos Mariscal, University of Nevada Reno, USA

Astrobiology is a loosely integrated multidisciplinary science consisting of the study of topics as diverse as origins of life, extremophiles, life detection, exoplanet, and habitability. Conclusions in one of these topics are often used in hypotheses of the others. In this talk, I assess the epistemic character of the idiosyncratic research program(s) of astrobiology. I then survey the extent to which individual branches of astrobiology are justified in accepting the conclusions of other branches.

Some of the projects in astrobiology, such as origins-of-life and extremophile research, include both manipulative and non-manipulative modes. “Manipulative” here is used in the sense of modifying the object of study, meaning synthetic biology and controlled evolution are manipulative, but simple observation or discovery are not. The targets of non-manipulative approaches are often about how life on Earth actually evolved. In these cases, scientists aim to say little about whether such processes are necessary or whether they would be common in similar conditions elsewhere in the Universe. Conversely, manipulative approaches often speak to the possibility of the processes and features of life in the Universe, while saying less about whether biology ever took such paths naturally. Simulations and models, which fit poorly into the manipulative/non-manipulative dichotomy, can be used to address both how-actually and how-possibly explanations.

For practical reasons, other projects, including exoplanet and life detection, have much stronger non-manipulative modes, with manipulation only occurring in models, at least in the foreseeable future. These projects are most often used for the detection of actual exoplanets and organics, save for the occasional hypothesis article or speculative book.

(*Substituting the paper "Warm little ponds and other analogues in astrobiology" by Emily Parke.*)

Soviet astrobotany: Early experiments in earthly analogues for Martian life

Luis Campos, University of New Mexico, USA

While many accounts of the history of astrobiology begin in recent decades, and often focus on the West, the emergence of the Soviet field of "astrobotany" in the 1940s offers a competing history for the emergence of early ideas of earthly analogues for Martian environments. In an effort to study the probable vegetation of Mars, astrobotanist G. A. Tikhov sought to study "the optical properties of terrestrial plants in connection with problems of the limits of physical conditions under which plant life can exist," by spectroscopically studying high-altitude and high-latitude plants in the mountains of Kazakhstan. Tikhov concluded that such efforts would make it "feasible to make more definite conclusions about the vegetation on Mars and even, perhaps, to say to which families of terrestrial plants the Martian plants come closest." Firmly rooted in the insights and principles of dialectical materialism, Tikhov argued for a tight interconnection between the study of life on earth and on other planets, and claimed astrobotany as a fundamentally practical science that avoided mere speculation while also offering clear paths forward for terrestrial agronomy. It was out of such work and the prospect for "studying microorganic life on the giant planets" that astrobotany first began to be called "astrobiology."

Lastly, there are some phenomena that seem to be beyond the bounds of direct observation or manipulation. These include inferring the likelihood of major features of biology, such as biological hierarchy, symmetry, or intelligence. Outside of clever experimental approaches, evidence for these features is most often achieved by abstract analysis or modeling. Astrobiologists have been reluctant to investigate such traits in biology, although they may be particularly appealing to outsiders interested in the field.

Although conflation of these approaches is not common, it does occur and can have fairly costly consequences when it does. Therefore, a careful attention to the different, but overlapping research programs in astrobiology is essential to success in the field. It can also be fruitful for biologists interested in research into the limits of biology.

Astrobiology: Life, ethics and policy, part II

ORGANIZER

Kelly C. Smith, Clemson University, USA

Astrobiology is the newest and most highly interdisciplinary science, and its progress has been nothing short of amazing – in just the past 25 years, we have learned that

1. the building blocks of life are found literally everywhere in our universe,
2. getting these building blocks to engage in the kinds of complex chemistry we associate with life is far easier than we thought and
3. planets where life can occur are extremely common – we have cataloged about 4,000 “exoplanets” in 3,000 different star systems since the first was discovered in 1988!

Given all this, it’s should not be surprising to hear NASA’s chief scientist say, “I think we’re going to have strong indications of life beyond Earth within a decade, and I think we’re going to have definitive evidence within 20 to 30 years.” In short, the search for life beyond Earth is no longer the stuff of science fiction. The discovery of extraterrestrial life would surely rank as one of the most important scientific discoveries of all time, and it clearly raises questions science alone is ill-equipped to answer: “What exactly is life?” “What are our ethical obligations toward alien life?” “What policies should we put in place to guide astrobiological activity?” Given this, it’s strange that so few outside the traditional space science community have stepped up to help address the many philosophical, ethical, and policy issues. A large part of the reason for this is probably a basic unfamiliarity with this new field. This session is thus designed to provide those in the ISHPSSB community an overview of some of the emerging debates in hopes of attracting a more diverse pool of scholars (a new interdisciplinary organization, the Society for Social and Conceptual Issues in Astrobiology or SSoCIA – has recently been formed and will hold its third meeting in March of 2020). To this end, we have chosen papers that introduce three of the major debates: one on life concepts, one on ethics, and one on policy.

Ethical obligations towards extraterrestrial life

Gonzalo Munévar, Lawrence Technological University, USA

Were we to encounter alien life in Mars or Europa, or thousands of years from now in some exoplanet, we would face the question of what ethical obligations we may have towards such life. Indeed, the question already has urgency, since the exploration of Mars is at most decades away, as is the exploration of Europa for the very purpose of looking for alien life. A proper answer should take into account the different varieties of alien life we might encounter: microbial, complex multicellular, animal, and intelligent life. Nevertheless, any sort of alien life would be of extraordinary scientific importance. Studying alien life can teach us a great deal about terrestrial life, for it would allow us to make important comparison that would tell us to what extent our chemistry – based on proteins built from twenty amino acids, a reproductive code (DNA) that makes use of only four bases, and a preference for right-handed sugars and left-handed amino acids – is the result of accidents of organic evolution or based on fundamental biological reasons. A very likely consequence would be a revolution in our understanding of our own biology. Even microbial life would thus have at the very least extraordinary instrumental value for humanity, and thus we would have a very strong obligation to preserve it, unless we discover that it poses a great threat to human survival (although even then we might just wish to stay out of its way until we find a safe way to approach it). As the complexity of alien life rises to, say, plant or animal life (or close-enough equivalents) its scientific value becomes far higher, and so does the strength of our obligation to preserve it. The instrumental value of alien life would so high as to render the question of whether it also has implicit value not very practical. Intelligent alien life would offer special ethical problems, for the morality of species is influenced by their biology, and intelligent aliens would be the result of a likely different biology, and of a definitely different evolutionary history. Nevertheless we can still try to come to an ethical "understanding" with them, insofar as communication does not prove impossible, by following the advice given by Peter Singer in The Expanding Circle: namely that we cannot assume that our interests are more important than theirs just because they are ours, and vice versa, i.e. we have to take seriously each other's interests.

Towards a family resemblance definition of "Life"

Erik Persson, Lund University, Sweden
Jessica Abbott, Lund University, Sweden

Finding a good definition of "Life" is a task that has turned out to be very difficult. Some say, it is even impossible, or at least meaningless. We believe both that it is possible, and that it is in fact crucial to achieve at least a tentative definition of "Life", especially when searching for the origin of life on our earth or for extraterrestrial life. We are not sure, however, that the classical way of approaching the task of defining "Life", that is, by trying to make a list of necessary properties that together makes up a sufficient set of criteria for being alive (a *de re* definition), is the best way of approaching the task. The main problem with this type of definition is that it is inherently essentialistic. It is doubtful that life as it is understood today, that is, in Darwinian terms, can be meaningfully said to have an essence. An alternative approach would be a cluster definition inspired by Wittgenstein's ideas of family resemblance. If we use this approach to define Life, it tells us that something is alive if it has a number of properties that are associated with being alive though it does not have to have all these properties and it does not have to have exactly the same set of properties as any other living entity.

In our talk, we present an extension of the family resemblance model by combining it with state of the art methods for statistical modelling in the form of cluster analysis. That way we hope to be able to construct the kind of overlapping clusters needed to achieve an informative and practically useful definition of "Life".

To contact or not to contact? Ethics, risk, and public policy in the METI debate

Kelly C. Smith, Clemson University, USA

There are at least two major projects underway to send powerful signals to hundreds, even thousands, of neighboring star systems. The debate over Messaging Extra-Terrestrial Intelligence (METI) has historically been confined to the space science community and this disciplinary compartmentalization has skewed the debate in strange ways. For example, almost all the argument to date has been over the level of risk METI might pose. Advocates of METI argue that the risk is so low it's not worth worrying about, while opponents counter that we can't assess the risks accurately enough to make a well-informed decision. In other words, the debate has been over the kinds of empirical questions physical scientists feel comfortable with. Fortunately, this has recently begun to change as scholars in other fields realize that what's being proposed is not their grandfather's METI, but something much more serious.

Assessing the empirical dimensions of METI is a useful exercise, to be sure, but what's been almost entirely overlooked is that the empirical analysis simply doesn't address some of the most fundamental issues. In particular, if we look at METI through an ethical lens, the central question is not the level of risk, but whether those who are exposed to that risk (in this case, all of humanity) agree to take it. Of course, this is nothing new to social scientists and philosophers used to dealing with human subjects, but it's *terra incognita* for those in the traditional space science community. This paper seeks to redress this shortcoming by extrapolating principles of informed consent from medical ethics to make the case that METI is simply not an ethical undertaking at present. On the other hand, this is not, at least in principle, an insurmountable problem and I suggest how prudent public policy guidelines could be enacted that would allay many ethical concerns. In other words, METI might become ethically defensible, but only if those making the decisions realize the shortcomings of their arguments.

Entangled roots: The relationship between biology and values from bioethics to biopolitics, part I

ORGANIZER

David Suárez Pascal, Universidad Nacional Autónoma de México, Mexico

Today's biology has a very important place in societally relevant discussions which range from health policies to environmental and political concerns. Indeed, some contemporary research fields or programs – such as bioethics and biopolitics – emphasize this position. Such a situation has compelled people from humanities to ask about the prejudices, ideologies, and agendas that impinge upon biological research. On the other hand, this deep relationship between biology and society should motivate biologists' concerns about the societal implications of biological knowledge, but also about the possibility that biological research is never fully detached from values. While some values such as coherence, precision, or reproducibility are an essential part of scientific practice, other aspects which take part in valuations which biologists make regarding living systems, such as robustness, adaptability, reproductive potential, health, etc. have particular nuances when applied in the biological domain. The goal of this session is to motivate a debate not only about the negative or positive values that influence biological research but also about the nature of biological knowledge which makes it particularly liable to serve as the vehicle of such explicit or tacit valuations. At the same time, beyond condemning value-laden biology as harmful, it is necessary to ponder what are the responsibilities of life scientists and society in general if biological knowledge is typically linked to a diversity of valuations which are relevant to a society's welfare. The range of topics that this interdisciplinary organized session will explore include the value of certain biological knowledge items – such as species – , the ways in which society and life scientists themselves reflect and discuss about the implications of biological research, as well as the diversity and the impact of valuations on biological methodology.

Political regulation of recombinant DNA research in 1980s Germany: Responsibility and knowledge

Anna Klassen, Friedrich-Schiller-Universität Jena, Germany

Recombinant DNA technology was considered a key technology in the 1970s and 1980s. Having ignored the economic potential for almost a decade, the Federal Republic of Germany tried to keep up with gene technology pioneers like the USA and Japan in the beginning of the 1980s. Discussions about diverse applications of new biotechnical techniques such as breeding self-fertilizing plants, germline therapy in humans or genome analysis of employees emerged rapidly in the press, political debates and the public. Committees consisting of politicians and experts from various disciplines like medicine, theology and, of course, molecular biology were installed both by governmental ministries and the parliament. Their task was to report on the scientific, legal and ethical state of affairs and to give recommendations concerning political regulations of gene technological research and development.

In my presentation, I give an overview of the discussion of the commission of inquiry “Opportunities and Hazards of Gene Technology”

(Enquete-Kommission “Chancen und Risiken der Gentechnologie”). Worldwide, this committee was the first parliamentary group engaged in discussing the questions of gene technology in its various ways of application. In the course of two years (1984–1986) its members worked intensely on topics ranging from biological raw material supply to the release of genetically modified organisms in the environment, including recent developments in technology assessment. I present different positions on potential regulations and show how they are connected to epistemic and non-epistemic values held by members of the committee. I especially focus on the relationship between responsibility and knowledge, which was brought into the popular and political discourse mainly by Hans Jonas’ influential book *The Imperative of Responsibility – In Search of an Ethics for the Technological Age.*

The forgetting of the organism, the forgetting of experience: Values in conservation biology

Gabriela Klier, CONICET – Universidad Nacional de Rio Negro, Argentina
Constanza Casalderrey, CONICET – Universidad Nacional de Rio Negro, Argentina

In this presentation I will analyze the ethical dimension of Conservation Biology. Conservation Biology emerged in the 1980s, linked to a specific problem: the biodiversity crisis. The foundational manuscript of this area, written by Soulé in 1985 and entitled “What is Conservation Biology?”, proposes that this field of study is based on ethical principles. Soulé argues, from an ecocentric point of view, that biodiversity has intrinsic value. More specifically, we will see that this value is mostly attributed to species and ecosystems. However, in the last decades, other anthropocentric perspectives have become relevant. These perspectives consider biodiversity in terms of goods and services for humans. Although both positions are apparently opposed, they have something in common: nonhuman organisms are not considered as intrinsically valuable. This leads to some practices deviled by animal protectionists, such as the use of the “sanitary rifle” in the management of some invasive species. In this research I will try to show that the “forgetting of the organism”, characteristic of different biological subdisciplines and also present in Conservation Biology, has several implications. In particular, I will propose that in forgetting organisms, Conservation Biology also forgets the singular relationships and experiences between people and biodiversity. In this way, the environmental issues concerning biodiversity are turned into “abstract” issues, detached from the emotional and experiential dimensions. These issues are now suited for a committee of experts, who decide what is valuable from “nowhere”.

What can species do?

Matthew K. Chew, Arizona State University, USA

The biological term “species” is multifarious, inviting ad hoc redefinition in some contexts and ambiguity in others. Is that a bug or a feature? In his 2018 book S*pecies: The evolution of the idea,* Australian philosopher John Wilkins suggested species are particular “phenomena in need of explanation.” He concluded, among other things: “We arrange the data we acquire (through naïve or sophisticated techniques) in ways that make the patterns in the data tractable and useful. Species are just such patterns.” However, both scientific and popular accounts commonly refer to species as actors or agents. Species are understood to occupy ranges or territories, even to define the extents of places. They are considered threats or threatened, allies or enemies, resources, pests, keystones, umbrellas, flagships, indicators and invaders. Despite superficial similarities to aspects of natural theology, romanticism, “nature faking”, and biocentrism, it is difficult to argue that these are all just examples of a single persisting tradition. They seem, instead, to represent a recurring problem. If Wilkins is even approximately correct, biologists and their allies tolerate using “species” in disparate, even incommensurable ways extending to apparently absurd category mistakes. Strictly speaking, biological species may not do anything besides existing for awhile, making them dubious objects of evaluation or ethical obligation. Are the costs of speaking strictly unbearable? Perhaps the inconvenience? Or is it both?

Entangled roots: The relationship between biology and values from bioethics to biopolitics, part II

Value-entangledness in biology: Regeneration and adaptation

David Suárez Pascal, Universidad Nacional Autónoma de México, Mexico

The fact-value distinction is a useful one for many scientists and philosophers. Indeed, according to some of them, it provides a sort of demarcation criteria between science and other areas of culture, such as art, ethics, or religion. Nonetheless, several biological concepts seemingly occupy a middle-ground between both domains (the domain of facts and the domain of values). While this has frequently been disregarded as just a rhetorical artifact, its recurrence and the difficulties to explicate such concepts in purely mechanistic or causal terms motivates the search for an alternative explanations.

One of such explanations, which I explore in this work, is that some biological concepts, such as adaptation and regeneration, have an entangled nature – i.e. at the same time that they describe some factual elements, they also specify more or less well-defined evaluative criteria, which are not less important than the factual ones. In this way, while biological research usually focus on the more factual aspects of biological phenomena, evaluative aspects also play an important role in several contexts of scientific practice.

Such an entanglement between more factual and more evaluative aspects, which characterizes some biological concepts, has a dual impact upon biological methodology. In the first place, in order to fully understand the biological phenomena that such concepts refer to, one needs to take into account the evaluative criteria which distinguish that concept from allied ones; in the second place, objectivity in relation to those phenomena which entangled concepts describe requires not only reliability, repeatability, and reproducibility, but also some sort of reflection about the evaluative aspects, which is more alike to ethical thinking than to more usual experimental know-how.

Making science human: American biologists and the philosophical shift to ethics circa 1920

Judy Johns Schloegel, Independent Scholar

The debate over mechanism and especially vitalism is a well-known and much discussed philosophical turn that defined important aspects of biological thought in the first two decades of the twentieth century. Rigorous arguments were advanced and reacted to by Hans Driesch and Henri Bergson, among others on the Continent, and included Herbert Spencer Jennings, William Ritter, and the philosopher Arthur Lovejoy in the United States. These arguments were focused quite narrowly on mechanism and vitalism as they related to the appropriate conduct of biological science or, in some cases, as solely a matter of general philosophical inquiry.

Following the onset of the First World War, however, American biologists such as Ritter and Jennings quite notably began to shift their attention to the ramifications of biological science – and of philosophical thought about biological science – on the conduct of human life. As Ritter contended in War, Science and Civilization (1915), his new preoccupation with the plight of civilization had been prompted by public discourse that science was liable for the vast destruction of the Great War and that biology, in particular, provided the rationalization of war (as well as its repudiation). A year later, Ritter elaborated on the "The Culture Value of Science" where he argued for the need to "make science human," and he began to articulate his ideas on how biology could contribute to ethics ("Biology's Contribution to a System of Morals that Would be Adequate for Modern Civilization," 1916). During the same period, Jennings argued that his biology-based principle of "experimental determinism" could be extended to serve as a rational and just basis for human conduct. As a pragmatist, Jennings' language eschewed any universal notion of an ethics or of values, but would have appropriately been read as a pragmatist's ethics ("Experimental Determinism and Human Conduct," 1919).

This paper will explore the substantial expansion of American biological philosophical discourse to the domain of ethics in the wake of the Great War and the reasons for this shift. At the same time, it will point to a diversity of perspectives within this shift. While focusing primarily on the cases of Ritter and Jennings, who were close colleagues, it will also consider the stances of those biologists who avoided such dialogue and others who likewise found themselves engaged by the 1920s with the "humanization" of science.

Hawking evolution: How technology favors survival of the weaker

Terry Bristol, Portland State University, USA

The trans-humanist movement has begun to imagine the design of new superior humans. The new CRISPR genetic engineering technology constitutes a huge leapt forward. What is the proper ethical and policy framework for these decisions?

Engineer George Bugliarello argued that modern engineering is a natural extension of biological evolution. But consider insulin technology. Previously Type 1 diabetics died young without reproducing. Now they reproduce and survive into their 60s. The genetic weakness associated with Type 1 is now spreading through the global gene pool.

Arguably this weakens the gene pool. The insulin-diabetes example is a token of a type. People who need glasses to read, once disadvantaged, are now enabled. Consider how many modern humans would survive in a hunter-gatherer culture. Engineering advances in agriculture alone have enabled, by now, billions of competitively weaker individuals to survive and thrive.

McKeown argued that virtually all advances in health and longevity in advanced nations over the last 300 years was due to engineering advances such as advances in water-sewage systems.

Stephen Hawking is the poster child of those promoting inclusion of the disabled.

The fossil record of human evolution suggests that technological advances have favored the survival of the weaker. Berkeley paleoanthropologist Tim White argues that the path from Lucy, 3 million years ago, to the modern human form has been driven, not by natural selection of the fittest, but by technological advances (tools and rules) that also tended to allow the weaker to survive and thrive. Technological advances in general appear to oppose the imagined forces of Darwinian natural selection. And, per hypothesis, it is precisely through "the middle way", with serial inclusion of the "weaker" that the gene pool has qualitatively metamorphosed to produce modern humans.

Post-scarcity, economist Paul Romer (2018 Nobel Laureate) notes that over the last 75 years global population has doubled, while economic output has grown eight-fold. Malthus was simply wrong. Life evolves through constructive, cumulative endogenous technological development that is systemically inclusive and recursively enabling. No normally functioning bio-economic system could ever consume all, or even most, of the evolutionary potential that it creates.

Matt Ridley documents in painful detail how the erroneous Malthusian presupposition of inherent scarcity and the notion of Darwinian selection of the fittest led to the eugenics movement. There are crucial ethical and policy lessons here for those who imagine they understand how to design the superior humans of the future.

The challenges of opposing intelligent design and creationism

ORGANIZER

Martin Potschka, Independent Scholar, Austria

The question addressed in this session is: Does the opposition to misguided projects on Intelligent Design and Creationism (IDC) impede future scientific research? This question will not be addressed meta-theoretically; rather, our papers provide examples of how innovative research might be impeded. The papers will not reconsider the debate on IDC. Rather they take new approaches as to whether biological models of evolution are sufficient or depend on new hypotheses to be added. Our concern is with advances in science, basically the life sciences and in particular theoretical biology. Integrating philosophy and even aspects of theology into science is discussed, and our papers leave it open whether these perspectives should be integrated or remain interdisciplinary. Our research is not a continuation of previous debates on IDC but a variety of novel approaches.

In lieu of a definition, a few prototypical features of IDC shall suffice: It is probably fair to say that typical proponents of IDC dislike evolution and attempt to disprove neo-Darwinian Logic (NL, viz. the state-of-the-art version of Darwinism with all that it entails scientifically). For IDC proponents, creation is an alternative to NL, a position that will be questioned in this session. Moreover, IDC proponents are often less interested in science than in shaping public opinion, in particular high school curricula by means of legal action. In contradistinction this session is entirely concerned with novel research positions. The courts in the US have ruled that IDC is religion, not science. This specific context, confined to the US, easily overlooks that IDC in the past has only produced bad science, and bad religion. Most recognize that there is a hidden agenda in biological debates about NL and Creationism.

In this opposition, science has been pushed to defend a methodological naturalism (MN): i.e. the idea that purely material, i.e. non-intelligent, causes suffice (Stephen Meyer). However there is no single agreed definition of MN. This understanding of scientific methodology tends to rule out many questions for the life sciences (biology and psychology) which are instead relegated to the domain the humanities or theology. From an epistemological point of view, a Popperian attitude cannot be sustained with MN: even if antithetical concepts turn out to be wrong, they need to be developed into thought experiments, given that Popperian falsificationism works by choosing among competing hypotheses. Moreover, scientific methodology does not allow for mandatory empirical assumptions and cannot be restricted to a preferred set of naturalistic positions. The aspects of creationism that concern us here are overshadowed by other (well known) dimensions of this conflict. To be acceptable as a positive science, stringent methodological restrictions must apply: science is evidence-based, not authority-based. It is the method and the facts that are decisive to legitimize an area of inquiry as science, and not whether there is some overlap with religion. Papers in this session will explore various aspects of modern epistemology as they apply to the debate over IDC. Introducing novel research approaches to science, each paper is in itself interdisciplinary and brings together in addition to theoretical biology such diverse disciplines as mathematics, physics, psychology, philosophy, and theology, as the need arises. As physicist, Taner Edis will discuss whether core tenets of NL (the combination of randomness – chance –, and rules or algorithms – necessity) make a sufficient theory of life. Martin Potschka will discuss the evolution of primate mind, which leads to the question of archetypes. Rope Kojonen will discuss the frontiers and limits of MN. All three papers contribute novel perspectives to the old question of whether a description of nature based on rules and chance is sufficient, and what extensions are conceivable.

Can physics account for biology? Intelligent design as anti-reductionism gone wild

Taner Edis, Truman State University, USA

Intelligent Design (ID) creationism objects to materialism in science, hoping to establish a role for creative intelligence in nature that is not reducible to mindless physical and biological processes. Indeed, ID targets Darwinian evolution not just because of the difficulties it causes for conservative religious doctrines, but because Darwinian processes are central to most current ambitions to account for life and mind within a physical framework, from the bottom-up. By doing so, ID raises a question about whether data could be found that could not be accounted for by any conceivable physical process, not just our current understanding of evolution. Blind variation-and-selection is a prime example of combining randomness (“chance”) and rules or algorithms (“necessity”); ID theorists such as William Dembski have claimed that design results in artifacts that are extremely unlikely to be constructed through any combination of “chance and necessity” as understood by physicists or biologists. This claim can be made more precise through some fundamental ideas in theoretical computer science, describing those meaningful non-computable functions not accessible to combinations of rules and randomness. The result of such precision, however, is to make the case for ID even more hopeless than conventional scientific criticism would indicate. This criticism can be expanded to formulate a “chance and necessity physicalism,” according to which combinations of rules and randomness can account for everything we observe, including the phenomena of the life sciences. This version of physicalism also casts light on some traditional debates concerning reductionism and how biology relates to physics. Ruling out uncompromising forms of anti-reductionism such as ID shows how a physicalist theory can account for life while weakly constraining the evolution of life-forms.

Intelligent design would modify but not replace neo-Darwinian logic in evolution

Martin Potschka, Independent Scholar, Austria

There is a well-known tradition involving Whewell, Popper, Campbell, Simonton and others to equate evidence-based hypothetico-deductive epistemology, as well as scientific creativity, with neo-Darwinian logic (in this comparison abduction is akin to genetic variation, hypothesis to genotype, deduction to translation, prediction to phenotype; selection is due to empirical evidence and environmental pressure respectively, etc.). However, there is actually a difference: Mind as an object of cognitive science is epistemologically more akin to the theological concept of Intelligent Design than to biological neo-Darwinian logic. Popper called the stage reached with the evolution of primate mind “active Darwinism”, in contradistinction to classical neo-Darwinian logic which he called “passive Darwinism”. I will argue that active Darwinism could have emerged by arranging nested loops of neo-Darwinian logic. As will be further discussed in this talk, this most likely involves the analysis of the "search space" rather than the mere simulation of the "event space". It is very likely that mind originated by chance. There are three versions to explain the emergence of mind:

1. Interlevel theorizing makes no claim whatsoever about the material base and treats the similarity of problem solutions as cases of convergent evolution, albeit in different contexts, genomic and mental.
2. Biologism reduces mind to brain structures and brain structures to genetic determination.
3. Structuralism assumes that there is a common generative formal cause (archetype).

The source of these forms is not further spelled out (religious people would call it the Wisdom of the Creator, but for the purpose of philosophico-scientific analysis no recourse to established authorities seems necessary). My paper ultimately offers two principal solutions to the emergence of primate mind: Interlevel theorizing, which is the methodological naturalism's limit of current theoretical biology; and structuralism which is a standard concept in the humanities but excluded by methodological naturalism. The latter converges with the common critique of a materialist world view: The primacy of the logos as against mere matter means that all being is a product of thought and, indeed, in its innermost structure is itself thought. One may argue again, however, that this primordial thought bootstrapped with neo-Darwinian logic by chance. Thus a structuralist position would modify the sequence of evolutionary events without diminishing the role of neo-Darwinian logic. (So much for the results that will be presented; I conclude with a brief outlook on further studies.) It remains unclear whether ultimately these choices depend on introspective methods or could be subject to positive science, like biology as currently defined. I consider introspection legitimate evidence for hypothetico-deductive epistemology provided many "observers" have to agree; but it is not positive science. Positive science requires that its hypotheses only include entities that are either overtly observable in extenso or at least predict observable characteristics. One possibility to observe a generative archetype is a study of irreducible complexity in evolution. The prebiotic origin-of-life question is a good instance where irreducible complexity might play a role. A generative archetype rooted in neo-Darwinian logic has the advantage to bypass any limitations that material causation imposes. There are a number of reasons that make it seem worthwhile to explore these ideas at greater depth. Popper argued that a hypothesis is supported not through verification of its own consequents but rather through falsification of some of its rival hypotheses. Falsification of Intelligent-Design scenarios will therefore strengthen our understanding of the origins of being. This alone makes it worthwhile to develop alternative models. Some veritable questions may at the end be inaccessible to positive science (at least as defined here), but exist nonetheless to be solved by other means. Integrating biology with philosophy hence is timely and indispensable.

Methodological naturalism and the truth seeking objection

Erkki Vesa Rope Kojonen, University of Helsinki, Finland

Critics of methodological naturalism (MN) often argue that, while MN can be politically important to oppose the teaching of creationism and Intelligent Design in public schools, MN also unnecessarily restricts the natural sciences from evaluating (and criticizing) supernaturalistic explanations involving God and non-human designers. According to proponents of Intelligent Design and supernatural explanations, this leads to the exclusion of potentially true explanations from science, harming the truth seeking ability of science. The assumption here is that a supernatural explanation, such as the miraculous divine creation of life, could in principle be true and supported by the evidence in some possible world. The truth seeking objection is then the following: given that we could be living in such a possible world, science should not rule out the possibility before examining the evidence, and thus MN fails to stop ID from being examined scientifically. However, perhaps surprisingly, a similar criticism of MN has also been made by many critics of ID. For example, philosophers Larry Laudan and Maarten Boudry have argued that science should be allowed to consider (and to refute) supernatural explanations. Indeed, science has already refuted supernaturalistic ideas like Young Earth Creationism. Thus understood, MN is not part of the definition of science, but simply a scientific preference for naturalistic explanations, which is adopted because of the past failure of supernatural explanations.

However, it seems that these objections against methodological naturalism in the natural sciences only hold if we assume scientism, the idea that the natural sciences should be our exclusive guide to reality. This idea is rejected by most philosophers, though recently defended by some, such as Alex Rosenberg. If we acknowledge the possibility of justified true beliefs about nature outside the natural sciences (as most scientists do), then it is not problematic to restrict the natural sciences to those questions that are (based on past experience) best suited to its methods. Suppose with the creationists that we live in that possible world where God has indeed created life miraculously, rather than through natural processes like evolution. Suppose again that supernatural explanations can in principle be explanatory, and supported by evidence. Yes, in that case MN as traditionally understood would prevent the natural sciences from finding the truth. However, this does not yet mean that the practitioner of MN could not then even in principle recognize the origin of life as an event where a supernatural explanation is needed. The practitioner of MN would simply have to do this inference as part of some other discipline, such as the philosophy of religion or the philosophy of biology, interpreting the results of the sciences. Similarly, the implications of the natural sciences for religious theories like creationism can be studied by other disciplines, even if creationism is not a scientific hypothesis. On my model of MN, the borders between disciplines (insofar as they are pragmatically necessary) and the proper domain of methodologically naturalistic science should be determined based on our evidence of what kind of methods and explanations work in each case. The presented model of methodological naturalism is compatible with different worldviews from reductionistic physicalism to robust Christian theism, and can surprisingly be adopted by both critics and proponents of Intelligent Design and supernatural explanations. These thinkers will simply disagree on where the limits of methodologically naturalistic science are in practice, and what constitutes a pernicious "supernaturalism of the gaps" or "naturalism of the gaps".

Philosophy in biology and medicine: The microbiota and biological individuality, part I

ORGANIZER

Thomas Pradeu, CNRS & University of Bordeaux, France

Recent research has shown that all organisms are hosts of billions of resident microorganisms, collectively known as the "microbiota", and that many components of the microbiota participate in crucial host activities, such as nutrition, metabolism, development, immunity, and behavior (Knight 2015). The central issue raised by this interdisciplinary session is whether the microbiota should be considered as part of the biological individual that hosts it, and if so in which sense. Biological individuality is a multidimensional, multilevel, and gradual concept (Pradeu 2016; Lidgard and Nyhart 2017). It can refer to the idea of unity (under which conditions a set of elements constitute a countable, relatively well-delineated, and cohesive unit in the living world?) but also to the idea of uniqueness (what makes each living thing unique?). This double session asks whether current research on the microbiota can shed light on these various aspects, and whether it challenges several traditional views about biological individuality, including possibly the idea of genetic homogeneity (Dupré 2010), autonomy (Gilbert et al. 2012), and the boundary between the inside and the outside of the organism (Pradeu 2012). If the host and the microbiota constitute together a biological unit, is it an evolutionary unit (sometimes called, controversially, a "holobiont"), and in that case, what is exactly meant by this: a reproductive unit, or rather an "interactor" (Theis et al. 2016; Queller and Strassmann 2016)? Is it a physiological unit, and if so in which sense and according to which criteria (such as, for example, functional integration, or near-decomposability)? This interdisciplinary session gathers philosophers and biologists who are experts on the microbiota. Collectively, they will use the resources of different approaches (bioinformatics, ecology, immunology, and biochemistry, among others) to better understand the dialogue between the host and the microbiota.

Immunity, development, and the microbiota: An overview

Wiebke Bretting, CNRS & University of Bordeaux, France

Scientific and medical articles are being published every day on the multiple ways hosts and microbiota interact. Given that the microbiota can influence the development, health and behavior of the host, can the host still be considered an autonomous individual? What makes an individual one? And how can an individual stay the same, even though both host and microbiota change continuously over time? These questions have been highly debated recently, in light of our growing knowledge on the microbiota (Bosch and McFall-Ngai, 2011; Gilbert et al., 2012; Pradeu, 2011).

The European Research Council-funded project IDEM (Immunity, DEvelopment, and the Microbiota) (2015–2020) investigates the concept of individuality and how it evolves in light of recent research on the microbiota. To do this, IDEM brings together philosophers and scientists from the field of immunology, microbiology, and developmental biology, as well as medical doctors. The project has led to three interdisciplinary international workshops, an international summer school on "Microbiota, Symbiosis, and Individuality: Conceptual and Philosophical Issues" (July 2019), and many publications in philosophy journals as well as in science journals.

The overall aim of the project is to provide a new understanding of how living things are continuously constructed through time, and how they interact with their environment. More specifically, four aspects are considered:

1. *Individuality and identity:* How can philosophical accounts of individuality and identity can help us frame questions about what counts as one persistent individual host?
2. *Development:* How does the microbiota influence the development of the host?
3. *Holobiont:* How a host and its microbiota are co-constructed through time, both at a physiological and an evolutionary timescale? Is the controversial concept of "holobiont" appropriate to describe the association of a host and its microbiota (Skillings, 2016)?
4. *Immunity and individuality:* What is the role of the immune system in the maintenance and construction of the organism in association with microbes? Conversely, can some components of the microbiota be considered as part of the host immune system (Chiu et al., 2017)?

The aim of the present talk is to offer an overview of the main issues raised by IDEM concerning biological individuality and the microbiota, which will also serve as a useful introduction to all the talks of the session.

How microbes make us who we are

Rob Knight, UC San Diego, USA

The concept that we carry a "genetic blueprint" that makes us who we are is now well established in society. Members of the public with no scientific training are willing to ascribe traits that have significant societal consequences, ranging from obesity to depression, to genes that make them that way. However, even very large-scale genome-wide association studies examining hundreds of thousands of people for genetic links to these traits have often obtained very modest results, often explaining just a few percent of the variation in these traits that are considered genetic. However, despite these attempts to link traits to our ~20,000 human genes, our much larger microbial gene catalog of 2–20 million microbial genes is ignored in these studies. These genes encode the vast majority of our bodies' unique metabolic functions, and perhaps most importantly, they are genes that we can change during our lifetimes. The fraction of the variance in many metabolically relevant traits that is explained by these microbial genes in the microbiome is often much larger than that explained by our human genes; furthermore, the predictive accuracy of classifiers for phenotype based on microbial genes is often much greater than that built on human genes. Causality can be established by transfer of microbes to germ-free mice, where phenotypes ranging from obesity to cardiovascular disease to rheumatoid arthritis to multiple sclerosis to major depressive disorder can be transferred from humans to mice by transferring the fecal microbiome of subjects with and without the condition. Even jetlag can be transferred this way. Mechanisms are just starting to be worked out, but include signaling through chemical metabolites, neurotransmitters, the nervous system, and the immune system, so the debate is shifting from which of these mechanisms exist to what is the relative importance of these mechanisms in constructing particular phenotypes. These findings have profound implications for concepts of innate versus acquired phenotypes, the roles of genes whether human or microbial in contributing to these phenotypes, our interpretation of heritability (which may be transmitted as microbes rather than Mendelian inheritance), and open up new vistas in how we can take control of our phenotypes not by editing our human genes by CRISPR/Cas9 but by editing our microbial ones by gentler methods such as diet and probiotics.

Immunity and host-microbiota integration

Thomas Pradeu, CNRS & University of Bordeaux, France

Most philosophical work on the impact of the microbiota on biological individuality has focused on evolutionary aspects, particularly the transmission of microbes from parents to offspring (Godfrey-Smith 2009). An equally important issue, though, is to determine to which extent the host and the microbiota constitute an integrated physiological individual, characterized by a unity of functioning. Physiological individuality and evolutionary individuality have important connections, but an entity can be a physiological individual without being an evolutionary individual, and the other way around (Sober 1991; Pradeu 2010).

Recent research has shown the existence of an intimate dialogue between the microbiota and the immune system. The microbiota is constantly shaped by the immune system, which in turn is under the continuous influence of the microbiota (Belkaid and Harrison 2017). The aim of this talk is to explore the role played by the immune system in the physiological integration of the host and the microbiota. Three issues will be raised:

1. Why is the microbiota not eliminated by the immune system? According to the traditional self-nonself framework, the microbiota should be eliminated, because it is foreign to the host. Explaining immune tolerance to the microbiota requires a revised concept of the self, or perhaps an entirely different conceptual and theoretical approach.
2. How is the dialogue between the host immune system and the microbiota shaped during development?
3. How does the immune system cope with the uniqueness of the microbiota in each individual? Does the immune system "learn" to tolerate the unique microbiota of the host? But in that case how can the immune system cope with modifications of the microbiota through time?

Building on research done in the last four years in the ERC-funded project IDEM, I will show that the immune system plays a key role in mediating host-microbiota interactions, and that the microbiota constitutes one of the main factors shaping the host immune system. I will make two further claims on this basis. First, the immune system integrates entities of diverse origins (including microbes) into a cohesive physiological unit. Second, some components of the microbiota exert an immunological role in the organism, thus suggesting the existence of a "co-immunity" between the host and the microbiota (Chiu et al. 2017)

Philosophy in biology and medicine: The microbiota and biological individuality, part II

How should we think about microbiota structure and function?

Gregor Greslehner, CNRS & University of Bordeaux, France

"Structure" and "function" are two of the most frequently used terms throughout the life sciences, including microbiota research. However, both terms and their relations are ambiguous and can denote conceptually different things. Not clearly distinguishing between those different notions can lead to serious misconceptions and confusion, like the debates surrounding the percentage of functional DNA from the ENCODE project has shown (Germain et al., 2014). In a similar way, the microbiologist Jonathan L. Klassen (2018) recently argued for the importance of having clear definitions of microbiome function. In order to clarify statements about microbiota structure and function, I suggest the following distinction of notions of structure:

1. Structure as genetic sequence
2. Structure as biochemical agent
3. Structure as interaction network
4. Structure as taxonomic community

And similarly for function (which has led to active debates in philosophy of biology over the last forty years – see, e.g., (Godfrey-Smith, 1993)):

A. Function as potential biochemical activity
B. Function as actual biochemical activity
C. Function as causal role of these activities in biological processes
D. Function as selected effect

All these notions of microbiota structure and function raise questions about their relations, their roles in health and disease, as well as the synchronic and diachronic identity of host-microbiome ensembles, and their status as biological individuals. Of particular interest are the microbiota-host interactions, how the host – or its immune system – recognizes, and influences, the structural and functional microbiota composition, and vice versa. A common way to think of the mechanism by which the host can distinguish "self" from "non-self" is via pattern recognition receptors located on the surface of host cells and signature molecules on the surface of the microbes. However, such signature motifs are shared among symbiotic and pathogenic microbes alike. I propose that the immune system might in fact not merely operate via the recognition of signature biochemical agents (2), but rather by "recognizing" the functional contribution (B or C) of microbes. The multiple realizability of such functional features by different interaction networks and bacterial communities (3 and 4) can explain why there is such a diversity of species within the same "functional guild". It might be function rather than taxonomic composition that matters for natural selection and immunological host interactions, "function first, taxa second" (Heintz-Buschart and Wilmes, 2018, 571) – or, as the microbiologist W. Ford Doolittle and the philosopher Austin Booth suggested, what matters is the "song", not the "singer" (Doolittle and Booth, 2017).

Transmitting symbiosis: The extraordinary reproductive strategies of animal-attached bacteria

Silvia Bulgheresi, University of Vienna, Austria

For a microbial association to persist throughout generations, the host progeny must either be capable of earning a "microbial fortune" from the environment (horizontal transmission) or inherit it from its parents (vertical transmission). The former modality relies on highly sophisticated molecular mechanisms of partners' recognition. The latter modality, instead, presupposes that the microbial partners are deeply integrated into the host life cycle in order to associate with its earliest developmental stage. After recapitulating the common trends in symbiont transmission, I will focus on a complementary issue, that is on how a microbe can pass on the symbiotic lifestyle to its progeny. Host transmission is especially crucial when microbes are not endosymbiotic but, instead, thrive on the surface of their hosts. This is indeed the case in marine nematode symbioses engaging Stilbonematinae and Gammaproteobacteria (Ca. Thiosymbion spp.). I will describe the different morphologies and reproductive strategies of nematode ectosymbionts under the assumption that they were evolved to guarantee a transgenerational, uninterrupted association with their hosts. Specifically, I will show the most recent data on the molecular cell biology of:

1. the up to 120 µm-long symbionts of *Eubostrichus dianeae* and *E. fertilis* in which cytokinesis appears to be retarded without affecting the degree of ploidy;
2. the rod-shaped symbionts of *Laxus oneistus* and *Robbea hypermnestrae* which widen and divide by setting their septation planes parallel to their long axes, so that one of their poles is constantly attached to the host;
3. host-polarisation of symbiont cell molecules, organelles and processes and its putative physiological implications.

Individuality and methodology: The part part

John Huss, The University of Akron, USA

The surge of interest in microbiota and microbiomes has led to a reconsideration of traditional biological ontology. Some of the questions raised include: what is an organism? What is a biological individual? Are ecosystems organisms? Are organisms ecosystems? Should the endosymbiont-host relationship be considered one of co-dependency between distinct individuals or one of part-whole relations? In the present contribution, I will argue that one influence on the tendency toward greater holism in conceptions of biological individuality is the methods of investigation of multispecies phenomena. Systems more easily studied as wholes will tend to be viewed as wholes, even if from the standpoint of evolutionary theory they may not meet the criteria for a unit of selection. Yet an overlooked part of philosophical discussions of the microbiome and holobionts is the part part. In this paper I will evaluate several different proposals for how the endosymbiotic microbiota and its microbiome are considered parts of the holobiont and hologenome (respectively). I will argue that alternative characterizations of part-whole relations are strongly influenced by the tools and methods of scientific investigation.

Genetics and eugenics in Norway, part I

ORGANIZER

Marsha L. Richmond, Wayne State University, USA

Norway became a major center for marine natural history in the late eighteenth century through the work of the Dane O. F. Müller (1730–1784). The study of the marine biology of Norwegian fjords was continued by Michael Sars (1805–1869), professor zoology at the University of Oslo from 1854, and after his death by his son Georg Ossian Sars (1837–1927). G. O. Sars was a longtime director of the university zoological laboratory and museum. He was also a liberal who supported women's access to higher education and was pivotal in promoting the career of Kristine Bonnevie (1872–1946). One of the first women to pursue university training in zoology, Bonnevie gained notice for her work on specimens collected on the Norwegian North Sea expedition (1876–1878) and was recommended by Sars to become curator of the zoology museum in 1900. Receiving a doctorate in 1906 specializing in cytology, Bonnevie promoted the study of Mendelian heredity in Norway and particularly its application to humans and inbred populations. In 1912, with Sars's backing, Bonnevie was appointed the first female professor in Norway, first extraordinary professor and from 1919 full professor of zoology. Under Bonnevie's direction, Norway remained a leading center for marine biology, but also of genetics and eugenics. By the 1920s, Norway not only could boast of having a notable number of geneticists (several of whom had international reputations and spent time working in Britain and the US), but there was also a lively eugenics debate starting in 1914 in which the geneticists Otto Lous Mohr and Jon Alfred Mjøen had main roles. A sterilization law was introduced in 1934. Against this backdrop, the papers in this session explore the scientific concerns as well as social contexts connected with Norwegian genetics and eugenics in the twentieth century.

Kristine Bonnevie: Her roles as the first female professor in Norway and the first female professor of genetics worldwide

Ida Stamhuis, Vrije University, Netherlands
Inger Nordal, University of Oslo, Norway

When we compare Kristine Bonnevie with foreign female researchers in genetics, Bonnevie's strength and power is striking. Her most successful colleagues – Tine Tammes in The Netherlands, Elisabeth Schiemann in Germany and Edith Saunders in England – even if they succeeded to become professors, did not end as such successful and powerful scientists. In our paper we will demonstrate the success of Bonnevie and discuss how that could happen. We will see that in addition to personality, also social, economic and scientific factors contributed to that result.

First we sketch Bonnevie's life, career, teaching, research topics over time and further activities. At first she built up a solid career by visiting prestigious foreign zoologists and cytologists and by making herself indispensable through innovative teaching. She then needed the support of the influential professor Georg Ossian Sars to make the necessary career steps: first in 1900 to become curator and in 1912 to become extraordinary professor. But after that she was able to direct her career herself. She was then also able to start research in human Mendelian genetics. That was an important choice in a country in which eugenics became very popular. We will discuss the relationship between genetics and eugenics in Norway and the position of Bonnevie and the influence she was able to exert in this area. She was also very active and influential in other fields: she took care of proper student housing and for proper food during the two world wars. Politically she was not hesitant to plead for women's rights and was in the city council for the liberal party and later even active in the League of Nations. When we compare that with the life of the Dutch geneticist Tine Tammes, who became in 1919 an extraordinary professor of genetics, we see a woman who remained within the field of Mendelian genetics she first chose and was a member of the society for women academicians, but who did not draw much general attention, either in Dutch society nor in the international genetics community. Also the German geneticist Elisabeth Schiemann did not play a prominent role in the German society like Bonnevie in the Norwegian one. We will conclude by trying to make these differences understandable.

Aslaug Sverdrup, William Bateson, and the chromosome theory of heredity

Marsha L. Richmond, Wayne State University, USA

In 1910, William Bateson became director of the newly created John Innes Horticultural Institution, which soon became a leading center for genetics research in Britain. Famously, the institute's staff included a large number of women, reminiscent of the school of genetics Bateson had established at Cambridge University in 1902, who independently investigated problems pertaining to Bateson's two major lines of work--non-Mendelian phenomena and somatic segregation.

Two of the women who worked at the Innes were from Scandinavia, including Aslaug Sverdrup (1891–1955), a student of Kristine Bonnevie's at the University of Oslo. Sverdrup came to the institute in 1921, with solid grounding in genetics and cytology, as well as a familiarity with the work of T. H. Morgan and his group at Columbia University. Bateson suggested that she work on the genetics of Primula sinensis, which had lain dormant since the wartime death of R. P. Gregory. Sverdrup readily agreed, writing: "I will be very interested in seeing and working with *Primula sinensis* and I am looking very much forward to it."

Bateson has been depicted one of the few leaders in genetics to remain a "chromosome skeptic" after the Morgan school introduced the chromosome theory of heredity in the 1910s. Certainly, Bateson believed that characters were not the products of genes and chromosomes but rather were the outcome of the segregation of cells during development. But it was Sverdrup who finally convinced him of the reality of chromosomal phenomena in genetics in 1924. Unfortunately, Bateson was unable to integrate this acceptance into the research program at the Innes owing to his untimely death in 1926. After returning to Norway in 1926, she worked in the Genetics Institute in Oslo, indeed serving as the Acting Director of the Institute when Otto Mohl was imprisoned during the Second World War. She also suffered a great personal tragedy when her husband was killed during the Second World War and she had to raise their son as a single mother.

This paper will examine Sverdrup's scientific work before and after coming to the Innes and illuminate her impact on Bateson and the new orientation on cytology that arose at the Innes in the 1920s, most famously in the work of C. D. Darlington.

Kristine Bonnevie's studies on the inheritance of fingerprints, and their application for racial evaluations in nazi Germany

Amir Teicher, Tel Aviv University, Israel

During the 1920s, Norwegian geneticist Kristine Bonnevie studied closely the inheritance of human papillary ridges (fingerprints). Her work suggested that the patterns of these ridges were not only hereditary, but were determined by three independent Mendelian factors, which she denoted as V, R, and U. Bonnevie also tested the possibility that these inherited patterns varied according to race. Her studies were welcomed by German anthropologists, and after 1935 entered into Nazi racial evaluations. Jews and Jewish Mischlinge who tried to dispute their racial status often attempted to argue that their legal father was not their biological progenitor. In order to examine such claims, racial anthropologists would analyze the fingerprints of the proband, and those of his/her mother, legal father, and acclaimed progenitor, according to Bonnevie's method.

The results of such analyses could help to refute categorically the proband's claims, or to mildly support it. In my paper, I present Bonnevie's published works in this area, examine their reception among German anthropologists, and explore in some detail several concrete cases of racial evaluations where her theory was put into practice.

Genetics and eugenics in Norway, part II

The Norwegian association for heredity: Expertise, authority, and boundary work in genetics and eugenics, 1919–1940

Jon Røyne Kyllingstad, University of Oslo, Norway

In 1919 Kristine Bonnevie initiated the establishment of the Norwegian Association for Heredity (Norsk forening for arvelighetsforskning). It became a key arena for academic discussions of about heredity and thus played an important role in the rise of genetics as an institutionalized discipline in Norway. When initiating the new association, Bonnevie described it both as an association for heredity and as an association for racial hygienic research. Eugenics was on the Norwegian public and political agenda at the time, and Bonnevie was, most likely, motivated by a wish to establish an arena for academic discourse that could help clarify scientific issues related to eugenics, and to counteract the misuse of scientific arguments in the eugenics debate. The new association helped to establish a boundary between acknowledged, trustworthy science and pseudo-science in the field of genetics and eugenics. This paper takes the archive of The Norwegian Association for Heredity as a starting point, and discusses the boundary work going on at the meeting point between genetics and eugenics and between science and ideology in interwar Norway. Which persons gained membership in the association, and who were kept out, and on what grounds?

It is well known that Jon Alfred Mjøen, the foremost representative of the international eugenics movement in Norway, was denied membership in the association. I will, however, argue that the association from the beginning included members with a very wide range of attitudes to eugenics, including views that were not very different from Mjøen, who advocated an orthodox style of eugenics aimed at protecting the so-called Nordic race against racial mixing, demographic decline, and biological degeneration. Academics who favored such ideas were members of the association from the beginning. These ideas, however, saw an increasing loss of credibility among Norwegian academics during the interwar years, in particular after the Nazis assumed power and turned racial hygiene and the notion of the superior Nordic race into a key element in the state ideology of German. Focusing on The Norwegian Association for Heredity, I will discuss the changing attitudes to eugenics and struggles about scientific credibility within the Norwegian scientific community in the interwar years.

Eugenics, genetics and the sterilization law of 1934

Nils Roll-Hansen, University of Oslo, Norway

Otto Lous Mohr – medical doctor, professor of anatomy, and an internationally prominent geneticist – was a main actor in Norwegian public debates over eugenics and sterilization. He started the debate over eugenics in 1915 with a sharp attack on the ideas of Jon Alfred Mjøen – an influential figure in the international eugenics movement. Despite Mjøen's apparently solid scientific credentials (with a doctorate in chemistry from Germany and membership in the Norwegian Academy of Science and Letters), Mohr's attack effectively ostracized Mjøen from the companionship of leading medical and biological scientists.

In the early 1930s two proposals for a sterilization law were introduced, one from the Mjøen camp (organized in The Norwegian Consultative Eugenics Committee) and one from the scientific experts around Mohr (organized in The Norwegian Genetics

Society). The former was in essence a moderate version of the German law of 1933. The latter was formulated by the official government committee on criminal law (Straffelovrådet), where Tove Mohr – medical doctor and the Wife of Otto Mohr – was a member. The medical faculty of the University of Oslo was a main instance to be heard in the matter. As dean Otto Mohr wrote the statement of the faculty. The gist of this document was that eugenic sterilization made little sense in the light of contemporary scientific knowledge, but a law was needed to regulate the sterilization practice that was already developing. The big contemporary issue in family politics was not sterilization but abortion. Katti Anker Møller, the mother of Tove Mohr, was the front campaigner for liberalization of abortion.

Tove and Otto Lous Mohr and the introduction of the Mendelian-chromosome paradigm to Norway in the period after 1920, and their campaign against eugenics

Gar Allen, Washington University, St. Louis, USA

Otto Lous Mohr and his wife, Tove Mohr, were important figures in both the introduction of the Mendelian Chromosome Paradigm, as developed by T. H. Morgan and his group at Columbia University, and in combatting the growth of eugenics in Norway between the World Wars. Otto Mohr was a biologist who, with his wife, spent a sabbatical year (1918–1919) in the Morgan Lab and came to know the Morgans and their students (especially H. J. Muller) quite well. They brought back to Norway the excitement of the new paradigm, showing that Mendelian “factors” (by then commonly referred to as “genes” following Wilhelm Johannsen) could be localized to specific chromosomes in a mathematically precise way. But they also struggled incessantly against eugenic ideas of compulsory sterilization, he as a geneticist and later university Rector, and she as a medical doctor (obstetrician gynecologist) and, like her mother, an advocate of women’s rights. The talk will focus particularly on the political aspects of advocating women's rights (entrance to the universities, voting rights) in the context of opposition to eugenics, abortion, and compulsory sterilization.

Extending developmental approaches to evolution: The role of chance, plasticity, and environmental stress in evolvability

ORGANIZER

Laura Nuño de la Rosa, Complutense University of Madrid, Spain

Evolvability, or the capacity of biological systems to evolve (Pigliucci 2008), is widely recognised as a core emerging research agenda in evolutionary biology (Müller and Pigliucci 2010, Nuño de la Rosa 2017). In the short term, evolvability is a function of the standing genetic variation on which selection can act and has been relatively easily integrated into the framework of classical evolutionary genetics. However, on longer time scales, evolvability depends on the ability of organisms to produce potentially beneficial variation through mutation or other mechanisms, and thus on the structure of the Genotype-Phenotype Map that determines how genomic variation is converted to phenotypic variation (Wagner and Altenberg 1996). This proposed symposium focuses on this sense of evolvability, a research agenda that, since it was proposed in the mid-1990s, has generated many empirical findings and theoretical models that deserve further philosophical attention. One of the most interesting aspects of evolvability research is that its epistemic goals partly overlap with those of mainstream evolutionary biology, such as the explanation of adaptation and understanding the roles for the environment in evolution. Evolvability not only emphasizes the positive aspect of development as a generative (rather than constraining) evolutionary force (Brigandt 2015), but also attempts to account for how development can facilitate the ability of populations to adapt, and cannot be understood independently of extrinsic, environmental factors (Love 2003). This symposium addresses three major issues concerning the nature of evolvability and its relationship to mainstream evolutionary theory.

1. Nuño de la Rosa reassesses the role of chance in genotypic and phenotypic variation from the perspective of variational approaches to evolvability, in which propensities to vary in certain directions are taken to causally explain the non-random probabilities of being selected.
2. Villegas and Ramsey provide a framework for understanding how development – particularly in the sense of developmental channeling and evolvability – fits within the causal structure of evolutionary theory, arguing that developmental plasticity can be understood as a structural cause of evolution.
3. Love and Urmanski reflect on how recent models on the role of stress in facilitating evolutionary change might lead to a more comprehensive understanding of the nature and role of the environment in evolutionary innovations.

Chances and propensities in variational approaches to evolvability

Laura Nuño de la Rosa, Complutense University of Madrid, Spain

The role of chance in evolution has been a major focus of attention in evolutionary biology, both at the level of the generation of variation (how chancy is the production of variants) and at the level of its perpetuation (how chancy is their diffusion and disappearance) (Millstein 1997). Philosophers of biology have been classically concerned with the latest sense, the notion of chance being central in discussions over the stochasticity of genetic drift and the probabilistic nature of fitness. In contrast, the role of chance in the former sense, what I will refer to as Variational Chance (hereafter "VC") has received much less attention. The reason is the apparent consensus on the Modern Synthesis' notion of "evolutionary chance", wherein variation is defined as chancy or random in the sense that the origin of mutations is independent of their impact on fitness (see, e.g. Merlin 2010). In contrast, I believe that this restricted definition does not exhaust the different meanings of VC that were instrumental in articulating the MS, and that are currently confronted in evolutionary biology. In this presentation, I reflect on how the notion of evolvability, defined as the tendency to increase the probability of adaptive evolution, touches some crucial assumptions of the received view on VC. In evolvability models (e.g. Watson 2014), the variational properties of developmental systems account for the nonrandom distribution of phenotypic variation and the associated fitness probabilities of such distributions. I argue that the chancy character of variation in these models is better understood as objectively probabilistic, instead of as random with respect to selection. This allows one to interpret the developmental tendencies invoked as causally responsible for such probabilities in the frame of causal probability (Abrams 2017). As I will show, a propensity interpretation of variational probabilities helps in clarifying the relation between the different ways in which evolvability is defined in the literature, where causal properties, probabilities and frequencies are often confused.

Evolvability and the causal structure of evolutionary theory

Cristina Villegas, Complutense University of Madrid, Spain
Grant Ramsey, KU Leuven, Belgium

In this paper, our aim is to identify what appears to be a lacuna in the causalist picture of evolutionary theory: the causal role of development. We provide a framework for understanding how development – particularly in the sense of developmental channeling and evolvability – fits within the causal structure of evolutionary theory. In order to do so, we will take a recently-published account of the causal structure of evolutionary theory and ask how development can be added to the account. The account we will employ is that offered by Ramsey (2016). Ramsey argues that fitness and drift are structuring causes of evolutionary outcomes. His overall picture is that as organisms live their lives they realize a life history, but this life history is only one of an array of possible life histories. The set of possible life histories is not homogeneous, but instead constitutes a structured set. The structure is determined by the genetic and environmental factors in its development, and results in a heterogeneity of survival and reproductive success outcomes. This forms the basis for fitness and driftability to be considered structuring causes of evolutionary outcomes.

We argue that the set of possible lives is also structured with respect to morphology. There is a space of possible morphological outcomes that are based on its developmental properties, but only one phenotype is eventually triggered in its ontogeny. This structuration, we will argue, causally explains the evolutionary changes of form accounted for in the developmental view of evolution. We will argue that this property can be characterised as developmental plasticity (Schlichting and Pigliucci 1998). Plasticity makes the development-environment reaction norms possible and is also responsible for at least some of the rules relating mutations and development (Siegal and Bergman 2002). In the view presented here, the plastic properties of life histories are not only structural causes of ontogenetic results (phenotypes), but they are structural causes of evolutionary change as well, whose triggering causes are genetic and environmental perturbations. We will argue then that phenotypic changes are population-level effects of the individual developmental plasticity of the phenotype. In this view, evolvability, or the capacity of developmental systems to evolve, can be seen as the nature, distribution, and inheritance of the plastic forms across a population. Evolvability thus acts as a structuring cause of variation as well, and the changes introduced in reproduction (mutations, environmental perturbations, etc.) trigger this variation. In this view, the biases acknowledged in the scientific literature as "developmental constraints" are better understood as the developmental channeling that plasticity and evolvability provide for evolution.

Environment, innovation, and evolvability: Mapping the conceptual landscape

Alan C. Love, University of Minnesota, USA
Brenna Urmanski, University of Minnesota, USA

Biologists have distinguished a number of different kinds of roles for the environment in facilitating evolutionary change, including cryptic genetic variation and genetic assimilation (Ehrenreich and Pfennig 2016; Paaby and Rockman 2014). A common feature of these different roles is stressful conditions where environmental circumstances for populations change significantly and induce evolutionarily significant variation (Badyaev 2005). Given substantial empirical advances in understanding mechanisms for transcriptional change under stress (Vihervaara et al. 2018), and ongoing questions about the relationships between development and evolution in evolutionary theorizing (Laland et al. 2015), especially with respect to how new traits originate (Moczek et al. 2011), there are many reasons to generate a more systematic map of the conceptual landscape for environment, innovation, and evolvability. This paper represents our initial philosophical efforts at a comprehensive analysis of the nature and role of the environment in different forms of evolutionary change with special attention to the similarities and differences of existing models. In addition to providing a revised categorization of these models and their assumptions, a key result of these efforts is the identification of a unique form of evolutionary change – stress-induced evolutionary innovation (SIEI) – whereby ancestral stress reactions and their corresponding pathways can be transformed into new structural components of body plans, such as a cell type. SIEI is a distinct model for plasticity-based evolutionary change that results in the origin of novel structures rather than the adaptive transformation of a pre-existing character.

New historical and philosophical perspectives on quantitative genetics, part I

ORGANIZER

Davide Serpico, University of Genoa, Italy

Quantitative Genetics is the branch of genetics concerned with such complex inherited traits as height, intelligence, common mental disorders, and skin colour. Although quantitative genetics has been both influential and controversial, its conceptual and disciplinary history has received surprisingly little systematic attention from historians and philosophers of science, with the result that major questions about that history – and its legacies – have remained unaddressed. Especially pressing is the need for a more comprehensive perspective on the longstanding and apparently unbridgeable divide between quantitative genetics and developmental biology: while the first is widely understood as a science about statistical properties of biological populations, the second takes into account how individual organisms are produced by the interaction between their genotype and the environment over time. To begin to fill this gap in scholarship, we submit a session aimed at standing back from present-day debates and difficulties in order to understand the historical roots and conceptual underpinnings of quantitative genetics. The time for this endeavour is ripe: recent and forthcoming publications are leading the scientific community to a questioning of received views on a range of topics related with the conceptual, methodological, and disciplinary sources and identities of quantitative genetics – e.g., works on the long-run of the nature-nurture debate (e.g., by J. Tabery, P. Bourrat, K. Lynch) and on behavioural genetics (e.g., by H. Longino, K. Schaffner), forthcoming works on human heredity by T. Porter, and current work on the debate over Mendelism by G. Radick. The session will gather together leading senior and early-career scholars working in the many interdisciplinary aspects related to the topic (e.g., philosophy of biology, medical and psychiatric genetics, behavioural genetics) for connecting historical and contemporary perspectives on quantitative genetics.

A reanalysis of Bateman's data

Thierry Hoquet, University Paris Nanterre, France

Angus J. Bateman's foundational paper on "Intrasexual selection in Drosophila" (1948) has been the focus of much interest. It is the source of so-called "Bateman's gradients," showing greater variance in number of mates and reproductive success in males than in females of Drosophila melanogaster. Having become a textbook example of sexual selection, Bateman's paper was highly scrutinized. Patricia Gowaty launched a pioneering work on that issue before a symposium was held in 2004, on "Bateman's principle: is it time for a re-evaluation?", presented at the Annual Meeting of the Society for Integrative and Comparative Biology, at New Orleans (Louisiana) at the initiative of Zuleyma Tang Martinez. In the following years, Dewsbury or Tang Martinez & Ryder (2005) focused on the structure of what was eventually called "the Darwin-Bateman Paradigm". Bateman's published data was re-examined by Snyder & Gowaty (2007) and Bateman's experimental design was entirely repeated, using new populations of flies by Gowaty et al (2012). In the present communication, I will present Bateman's experiments based on his archival material held at the John Innes Centre (UK). Bateman's experimental design was incredibly clever. However, his results were accused of sampling biases and selective presentation of data. There is also a suspicion of the inviability of double-mutant offspring, ultimately biasing inferences of mate number and number of offspring on which rest inferences of sex differences in fitness variances. This presentation is part of a research cooperation with Patricia A. Gowaty.

The legacy of cybernetics on quantitative and qualitative issues in the post-genomic era

Flavia Fabris, Konrad Lorenz Institute for Evolution and Cognition Research, Austria

This presentation aims to show the centrality of cybernetics to the formation of the Modern Synthesis in the early 1930s. It will highlight the significant role played by cybernetics in foregrounding the intellectual legacy of key contributors to the theory of biological development. This is a missing link in the Modern Synthesis, and the talk is a positive step towards filling this explanatory gap. Drawing from the first-hand study of papers, books, and correspondence letters from the archives of D'Arcy Wentworth Thompson at the University of St Andrews and Conrad Hal Waddington at the University of Edinburgh, the presentation establishes a link between the cybernetic reasoning of Thompson and the epigenetics of Waddington. Waddington's theory of developmental systems was originally entrenched in the general cybernetic framework of communication and control. Waddington extended the work of Ashby Ross and colleagues beyond their familiar boundaries, toward a cybernetic approach to biological development, which he called “epigenetics”. Building upon Thompson's works, and then on Ross' feedback-control concept, Waddington adumbrated, and then fully presented, the process of genetic assimilation. It will be shown that this link is fundamental to understanding the conceptual dimensions of cybernetics in biology at that time and clarifying what contributions these cybernetic theories made to contemporary theoretical biology, with a special focus on quantitative genetics. The presentation will stress the presence of both quantitative and qualitative reasoning in Waddington's cybernetics, its legacy for the contemporary view of cryptic genetic variation, and the main difference from Fisher's and Modern Synthesis' assumption of additivity.

How a theory of phenotypes became a theory of genotypes and what this meant for genetics

Davide Serpico, University of Genoa, Italy

In this talk, I analyse the development of behavioural genetics from its theoretical foundation in early quantitative genetics to the present. This historical analysis will reveal the role of uncritically perpetuated conceptualizations carried over from quantitative genetics into behavioural genetics – when those conceptualisations first emerged, and when others were marginalised. My aim is to provide a historical and philosophical rationale for interpreting contemporary issues in behavioural genetics. Accordingly, behaviour genetics may not be theoretically well equipped to account for the causal relationship between the genotype and complex traits such as psychological phenotypes.

First, I analyse the so-called Mendel Wars, that is, the early 20th-century debate between biometricians and Mendelians (see

Schwartz, 2009), and highlight how scholars from the two sides conceptualised phenotypic traits and the relationship between genes and complex traits. Second, I summarise the central aspects of the synthesis between the two sides provided by Ronald Fisher in 1918, which gave rise to modern quantitative genetics. I highlight the major theoretical choices behind Fisher's theoretical model and show that Fisher combined two different types of theories: biometrics, which was a theory of phenotypes, and Mendelism, which was a theory of genotypes (see Norton, 1975). In doing so, he endorsed many theoretical assumptions about the genotype-phenotype relationship (e.g., additivity and linearity) in order to model the inheritance of complex phenotypes (see e.g., Morrison, 2007). To conclude, I investigate how scholars have interpreted Fisher's model and imported it, together with its idealisations, into scientific practice, giving rise to contemporary behavioural genetics. The transition from Fisher's quantitative genetics to behavioural genetics implied a shift in focus from statistical properties of populations to causal processes involved in the individuals' development. This shift misinterprets the original aim of Fisher's model. Here probably lies the origin of empirical issues in contemporary genetics, such as the missing heritability problem, as well as slowdowns in the study of the relationship between the genotype and psychological phenotypes.

New historical and philosophical perspectives on quantitative genetics, part II

Data madness and quantified heredity

Theodore M. Porter, University of California, USA

The inheritance of mental illness became a quantitative problem beginning in the early nineteenth century primarily for the simple reason that so many persons diagnosed with such conditions were gathered up in large public institutions. Mendelians and biometricians looked to the same sources for data on these conditions, and deployed such data in rather similar ways, mainly for eugenic purposes. Mendel's sudden celebrity beginning in 1900 encouraged the false impression of a basic science of genetics that might then be applied, legitimately or not, to humans. In reality, institutional data from mental hospitals and special schools had all along provided the principal basis for such research. This paper begins by documenting some basic continuities between nineteenth-century statistical work on inheritance and the programs of research that took off in the 1890s and 1900s. It demonstrates the continued centrality of school and asylum data to the genetic study of humans in the first third of the twentieth century, and with the indispensable expertise that doctors and psychologists brought to these studies.

I first examine Karl Pearson's reliance on educational and medical specialists, especially Scottish ones, to investigate mental and psychological traits that seemed to run in families. But the teachers and administrators who supplied his data did not accept a radical divide between hereditary and behavioral causes, and he respected their views. Charles B. Davenport also faced a good deal of skepticism from doctors and psychologists regarding simple Mendelian explanations of complex behaviors, especially educational and behavioral ones. Still, he stuck to his claim that almost every mental or behavioral condition was the result of simple, Mendelian laws. It was the doctors and psychologists, however, who performed the detailed adjustments and corrections that gave him the ratios he wanted for mental illness and feeblemindedness. In Munich, at about the same time, Wilhelm Weinberg provided the statistical expertise enabling Ernst Rüdin to put to the test his Mendelian theory of dementia praecox. The results, however, were deeply disappointing. While both men looked for secondary factors to account for the poor fit of theory to data, Rudin's group turned (or returned) to empirical, data-driven methods to quantify the decisive role of heredity in the perpetuation of psychopathy as well as real mental illness.

The talk concludes with a quick survey of contrasting used by these English, American, and German eugenic researchers of some Norwegian pedigree tables of mental illness from 1859.

Degeneration and Victorian cultural history: The surprising challenge from the new historiography of quantitative genetics

Gregory Radick, University of Leeds, UK

A commonplace about nineteenth-century cultural history, in Europe and beyond, is that it was an age characterized by increasing anxiety about biological degeneration. Like any such generalization, this one has its uses, but it also has its limits. In this talk I want to consider how differently the topic of degeneration looks when it's no longer viewed as the cultural equivalent of an irresistible force, seeping miasma, doomily enervating mood music etc. The inspiration for this exercise is Theodore M. Porter's *Genetics in the Madhouse: The Unknown History of Human Heredity* (Princeton: Princeton University Press, 2018), where, among many other things, Porter shows that the French asylum doctor B. A. Morel's claims about degeneration as the universal fate of the human species were subjected to severe criticism by his professional peers, who were able to mount their arguments thanks to painstakingly accumulated quantitative data on the inheritance of insanity. Porter's work illustrates how the new historiography of quantitative genetics, for all its specialist appeal, can cast light on subjects of much wider historical interest.

How a focus on intelligence has shaped the nature-nurture debate

Kate E. Lynch, University of Sydney & Macquarie University, Australia

Intelligence is the most widely studied phenotype in human behaviour genetics (Plomin & Spinath, 2004), and has historically been the central focus of debate about the nature and nurture of human traits (Gould, 1996). In recent years the nature-nurture debate has turned its attention to heritability estimates, a statistical parameter representing the relative causal influence of environmental and genetic differences. Intelligence is attributed as being significantly heritable, ranging between 0.5–0.8 (Plomin & Spinath, 2004). leading some to make conclusions about the larger influence of "nature" on the trait (Herrnstein & Murray, 1994). However, this conclusion has been contested on multiple grounds. One criticism is that intelligence is improperly measured or defined, with disagreements about how to understand and quantify the concept persisting to this day (Sternberg, 2000). Other criticisms focus on the heritability metric itself. These take multiple forms, including the extrapolation-worthiness of the statistic (Sesardic, 2005), and non-additive interactions of genetic and environmental variance, such as gene-environment interaction (Tabery, 2014) and gene-environment correlations (Lynch, 2017). Because the nature-nurture debate, and subsequently the heritability discourse, has historically concentrated on intelligence, criticisms about the heritability metric have tended to use intelligence as case studies and examples to illustrate wider methodological analyses. However, the intelligence concept has contestable and controversial properties, owing to the debate surrounding its definition and quantification. I argue that a historical focus on intelligence has biased the way in which heritability is analysed more generally. I show that in some cases, disagreements which are thought to be related to methodology instead stem from disagreements or misunderstandings about the intelligence concept.

Beyond mendelians and biometricians

ORGANIZER

Yafeng Shan, Tel Aviv University, Israel

The development of genetics in the first decade of the 20th century is typically characterised as a confrontation between the Mendelians and the Biometricians (e.g., Froggatt and Nevin 1971; Provine 1971; MacKenzie and Barnes 1975; Olby 1988). This confrontation account usually gives the overall impression that the development of the study of heredity in this period is basically centred on a battle between two dominating approaches. The contenders in the

Mendelian-Biometrician controversy were working hard to develop and strengthen their favourite approaches and challenge and dismiss the opponents'. However, such a historiography is to a great extent misleading and oversimplified. Firstly, not all were firmly committed to one of the camps. As Kim (1994) identifies, there are a critical mass in addition to elite protagonists and the paradigm articulators of both camps. Secondly, not all of the work at the time could be simply classified as either a defence of Mendelism or that of Biometry. There were quite a few attempts to explore the alternative approach(es) to the problem of heredity (for example, Yule 1902; Darbishire 1906). Thus, a re-examination of this historical episode seems necessary and important for our understanding of the historical development of the study of heredity and evolutionary study in general. This session aims to revisit the development of genetics in the 1900s. In talk 1, Buttolph will show that the dispute between Mendelians and Biometricians was less significant than has been claimed, and in particular that there was no clear-cut point at which Mendelism achieved some kind of ascendancy. In talk 2, Pence will unearth a question about causation and the theory/world relationship from the biometry/Mendelism debate. In talk 3, Shan will counter a traditional view that Weldon is a Biometrician and examine Weldon's approach in his unpublished manuscript.

An overestimated departure: The legendary death of Raphael Weldon

Michael Buttolph, University College London, UK

At the end of the nineteenth century Francis Galton established a research programme using mathematical approaches to discover more about the process of evolution, and specifically the mechanism of inheritance. By the turn of the century this "biometric" programme came to be led by Karl Pearson (1857–1936, based at University College London) with expert biological support from Walter Frank Raphael Weldon (1860–1906) at Oxford.

This established research programme was challenged when Mendel's work was "rediscovered" in 1900. The principal champion of the new “mendelism” was the Cambridge zoologist William Bateson (1861–1926). The mechanisms postulated by mendelism and biometry are quite distinct, but the complexities of biological processes are such that it was not easy for either school to show that its results better represented the realities of nature.

The “biometrician-mendelian debate” has been subject to extensive historical analysis. This has focussed upon the relationships and exchanges between Bateson, Pearson and Weldon, with “walk-on” parts for one or two dozen more British and American scientists of the time. It documents a dispute, at times viciously personal, continuing during the first years of the twentieth century, but ceasing on the death of Weldon in 1906.

This story is wrong in several respects. First, as Eileen Magnello (2004) suggests, the “defeat” of mendelism was not part of the biometric agenda. Biometry was a challenge in the sense that it represented a different research approach, but both Pearson and Weldon accepted the reality of mendelian inheritance at an early stage. Furthermore, mendelism was never seriously threatened by biometry; most of the evidence against mendelism at that time was provided by people who were not working within a biometrical framework. Finally, the death of Weldon in 1906 did not secure for mendelism an unearned victory by arbitrarily depriving biometry of the crucial support of the biological expertise that Weldon had provided.

Instead the debate continued uninterrupted until doubts were raised about a fundamental flaw in the biometrical paradigm around 1910. This resulted in a perceptual shift and thereafter the biometrical approach continued to be widely used, not as a theory with explanatory power but primarily as a practical instrument for improving the breeding of economically-important animals and plants, a tendency facilitated by the demands of World War I. Over the same period mendelian theory was extended and sophisticated, with the resolution of many apparent anomalies, and increasing support from chromosome studies. Outright hostilities ceased and in a calmer intellectual environment mendelian genetics became the primary framework within which to understand life-processes, and biometric techniques were widely used in breeding programmes. Then in 1918 George Udney Yule published a synthesis of mendelism and biometry. This reconciled the main features of the two frameworks to the satisfaction of most of his contemporaries; but there was never a personal reconciliation of Bateson with Pearson.

From the biological world to statistical theories: Nineteenth-century lessons for twenty-first-century philosophy of biology

Charles H. Pence, Université catholique de Louvain, Belgium

Philosophers of biology have expended a great deal of effort in the attempt to understand the broad-scale causal structure of evolutionary theory. What kind of processes are natural selection, genetic drift, mutation, and so on? What role do commonly studied properties like fitness, population size, selection coefficients, and others play within these processes? Why do all of our best theoretical systems for understanding evolutionary theory invoke statistics and probability? Often, the answers to these questions are taken to be peculiar to the biological context, and to result from contemporary philosophical reflection on issues of probabilistic causation and statistical inference.

It is my goal in this talk to offer the first half of an argument that this is mistaken. I will argue here that these kinds of questions are not a novel product of the contemporary philosophical literature, but rather have been with us since the very introduction of statistics and chance into evolutionary theory in the last decades of the nineteenth century. One of the fundamental philosophical issues underlying the debate between biometricians and Mendelians – in particular, one of the core issues that the biometrical school believed that it needed to resolve in order to offer a compelling picture of evolution – was precisely the same question currently being grappled with by contemporary philosophers of biology. What features of the biological world necessitate theorizing in a statistical manner, and how do statistical theories map onto the biological world? Reconnecting with the history of this debate, I argue, will help us construct a clearer picture of the stakes both in the historical and in the contemporary context.

Weldon, no biometrician?

Yafeng Shan, Tel Aviv University, Israel

W. F. R. Weldon is widely regarded as a leading figure of the Biometric school to rival with the Mendelian approach to the study of heredity. This view is prima facie plausible. Weldon was one of the founders of the journal Biometrika, where the name of the Biometric school came. His 1902 paper “Mendel’s Laws of Alternative Inheritance in Peas” preluded the Mendelian-Biometrician controversy. His confrontation with William Bateson constituted the central part of the controversy. It is also believed that his sudden death in 1906 somehow caused the end of the debate. However, I argue that it is unjustified and oversimplified to label or interpret Weldon as a Biometrician, like Karl Pearson. In this paper, I aim to revisit Weldon’s stance in the Mendelian-Biometician controversy and examine his approach to the problem of inheritance. Firstly, I show that Weldon’s early publications on heredity only suggest that early Weldon (1901–1904) was a critic or sceptic of the Mendelian approach. Secondly, by reconstructing Weldon’s unpublished theory of inheritance, I argue that late Weldon (1904–1906) was a synthesiser rather than a Biometrician. Thirdly, I compare Weldon’s synthesised project with G. Udney Yule’s (1902) and A. D. Darbishire’s (1906).

Genealogies of life in Germany at the end of the eighteenth century

ORGANIZER

Joan Steigerwald, York University, UK

German contributions to the development of natural history and the life sciences at the end of the eighteenth century are the subject of continual historical reassessment. These reassessments reflect shifting understandings of what is important to science – different valuations of mechanical explanations, intentional agency and teleology, different emphases on theoretical principles and empirical inquiry, and different characterizations of the interplay between science and culture. Two historical figures who have been at the center of many of these assessments are Immanuel Kant and Johann Friedrich Blumenbach. That historians return again and again to these two figures indicates the richness of their works as well as the ambiguities of their legacy. This session reconsiders Kant's attitudes to natural teleology and his relationship to Blumenbach. It reconsiders the principles and investigative media on which Blumenbach based his understandings of species variation. It also reconsiders the ways in which Blumenbach's study of the races of humankind drew on both detailed empirical studies and broad philosophical and cultural conceptions. The session explores the complex intersections of philosophy with biology, human history with natural history, and physical processes with agency and teleology that informed German contributions to the genealogy of life at the end of the eighteenth century. The reassessments of Kant and Blumenbach offered here follow from a reconsideration of what is important to a scientific understanding of living beings and their historical development.

(Mis)understanding the Kant-Blumenbach relation: Mechanism and natural teleology

Boris Demarest, Universität Heidelberg, Germany

Scholarly assessment of Kant's role in the development of biology has shifted greatly several times over in the last half-century alone. In the mid-20th century, Kant's notorious prophecy "that we can boldly say that it would be absurd for humans even to make such an attempt or to hope that there may yet arise a Newton who could make comprehensible even the generation of a blade of grass according to natural laws that no intention has ordered; rather, we must absolutely deny this insight to human beings" (AA V: 400) was widely regarded as a failed negative prophecy. As a result, Kant was considered to be on the wrong side of scientific history because of his lingering commitments to teleological reasoning. In the 1980s, Timothy Lenoir raised a controversial challenge to this judgment by arguing that Kant's specific balancing of mechanistic and teleological thinking provided the theoretical core of a very fruitful "teleomechanist" program that flourished in Germany from the 1780s until the middle of the 19th century. By the early 21st century, however, historians' judgment of Kant shifted again. In a paper from 2000, Robert Richards argued that the alliance between Kant and Blumenbach, which Lenoir regarded as the source of the German teleomechanist tradition, was based on a misunderstanding. Richards, and John Zammito with him, concluded from this historical misunderstanding that Kant was on the wrong side of history after all – only this time because of his lingering commitments to an all-too rigid mechanism which Blumenbach could overcome.

The thesis that the alliance between Kant and Blumenbach was based on a misunderstanding offered an important and much-needed corrective of historians' views on Kant's role in the history of biology. I argue, however, that the harsh judgment of Kant to which the thesis led is misplaced. In particular, I argue that it is wrong to see Kant as hostile towards natural teleology. What many readers underappreciate, I argue, is Kant's subtle stance on mechanism and teleology. They tend to think that Kant saw organisms as entities that can only be explained by assuming intentional agency, and that he saw mechanism to be opposed to any kind of explanation in terms of intentional agency. I argue that this both misconstrues the complex relationship between teleology, intentional agency, and mechanism, and Kant's appreciation of this complex relationship. By reconstructing both the complexity of the relationship and Kant's take on it, I argue that the *Critique of the Power of Judgment*'s epistemic humility is less about teleology and life than about how to conceive of teleology and life in a mechanist framework. In this way, I seek to show that, although the Kant-Blumenbach alliance may be a historical misunderstanding, it is not a historical mistake.

Blumenbach on the varieties of the human species

François Duchesneau, Université de Montréal, Canada

Johann Friedrich Blumenbach (1752–1840) has probably been the principal German biological theorist working on the human race issue at the end of the eighteenth and beginning of the nineteenth century. Simplifying to a maximum, one may say that he addressed two questions related to that issue. On the one hand, how, that is, by what mechanisms, similar with or dissimilar from those involved in animal species variations, did heritable anatomical and physiological differences come about among representatives of the human species? On the other hand, did these differences flow from a single stem species or, alternatively, did the present varieties or races originate from different stock species? Even if they had ideological and moral underpinnings, it was, at least for Blumenbach, essential to pursue the investigation on these issues as a matter of natural history, with the methods of experimental philosophy being strictly applied to them. This is not to say that speculative considerations were absent from his arguments and conclusions. On the contrary, he constantly held that the empirical data he would start from and work on, among which his pioneering observations of skulls, were to accord with a systematic conception of the living organism, animal as well as human. The main question to be addressed is about identifying and assessing the theoretical principles on which he would ground this "scientific explanation" of species varieties in the case of humans. His concept of *Bildungstrieb,* apart from meaning a principle of vital self-organization, was designed to afford a sufficient reason, a methodological key, for explaining the regular processes that unfold in an integrative fashion and yield the various functions of organic parts. Did the reliance on such a hegemonic principle and on such vital forces as derive from it represent a resource sufficient for explaining those processes, by which organisms frame up, are preserved, repaired, and consequently vary so as to produce relatively stable subspecies?

The Caucasian

Joan Steigerwald, York University, UK

Recent scholarship has given new attention to the development of the concept of race as a category of natural and human history. Much of this attention has focused on the racialization of the peoples of the world. Less attention has been given to the depiction of the Caucasian as a part of these developments. This paper focuses on Johann Friedrich Blumenbach's contribution to these depictions. Blumenbach regarded humankind as a single species with five regional varieties. He termed these varieties peoples or nations (*genti, Volk, Nationen*) as well as races (*Race, Rassen*), blurring the distinctions between natural and cultural characterizations. In his portrayal of the varieties of humankind, Blumenbach drew on his expanding natural historical and anatomical collection at the University of Göttingen. In this collection he particularly valued his specimens of skulls and his portraits of representative individuals as new media through which to study the question of race. In his study of skulls, he was concerned with their overall view or general form and symmetry. He then compared this overall view to the character of the national faces that his portraits offered. Blumenbach's category of the Caucasian was expansive; it included Arabs, Persians, North Africans, and Central and South Asians as well as Europeans. He presented the skull of a Georgian female as exemplary of the race. For his portrait he took as exemplary that of a Turkish man, Jusuf Aguiah Efendi, the first permanent ambassador to London from the Ottoman Porte. European readers of Blumenbach's work on the varieties of humankind might have seen in these portrayals of the Caucasian race their kinship with non-Europeans. Or they might have seen in these portrayals that the question of race was a matter for peoples other than themselves, as relating only to peoples other than Europeans. In any case, Blumenbach's depiction of the Caucasian complicated Europeans' self-understanding of themselves as a race.

The paleontological science of form: Between mechanical adaptation and structural constraints

ORGANIZER
Marco Tamborini, Technische Universität Darmstadt, Germany

> *"Morphology made no concrete contribution to the synthesis, but rather the reverse: the synthesis had an impact on the field of morphology"* (Mayr, 1980).

With these words, biologist Ernst Mayr allotted the place and sealed the subsequent destiny of morphology during the Modern Synthesis of Evolution. Several historians and philosophers of science have accepted and strengthened his reconstruction, asserting for instance that "morphology contributed virtually nothing to the synthetic theory of evolution" and hence "failed to contribute to the modern synthesis" (e.g. Ghiselin, 1980). The two main arguments behind this severe judgment were that early twentieth-century morphology was burdened with idealistic thinking and that morphology – as a mere descriptive and not theoretical science – makes sense only in conjunction with other disciplines like, for instance, phylogenetics. This session aims to revise this narrative by presenting a more nuanced picture of early twentieth-century morphology. By focusing on the paleontological science of form during the 1960s and 1970s, we will argue that although morphology was not taken into account from the main advocates of the Modern Synthesis, it contributed to expand and critically re-elaborate its neo-Darwinian theoretical framework. We will analyze which practices and morphological problems shaped twentieth-century science of form and consider their philosophical, historical, and technological preconditions. Particularly, we will investigate two central topics which characterized the paleontological science of form in Germany and in the USA from the 1960s onwards: the notion of mechanical adaptation and idea of structural constraints on form. Departing from the historical analysis of these concepts, we will reflect on the broader philosophical and methodological issues of the paleontological science of form, such as the relationship between necessity and contingency in morphological reconstructions. As a result, we will provide preliminary insights into a different history and theory of twentieth and twenty-first-century morphology.

Challenging the adaptationist paradigm: Morphogenesis, constraints, and constructions

Marco Tamborini, Technische Universität Darmstadt, Germany

In 1979, evolutionary biologists Stephen Jay Gould and Richard C. Lewontin published an influential article in the Proceedings of the Royal Society of London: "The Spandrels of San Marco and the Panglossian Paradigm – A Critique of the Adaptationist Programme". In this work, the authors criticized the agenda that had "dominated evolutionary thought in England and the United States" according to which natural selection is seen as an "optimizing agent". Conversely, they proposed a different standpoint on evolution, in which Baupläne (or body plans) are "constrained by phyletic heritage, pathways of development and general architecture". From this perspective, "constraints themselves become more interesting and more important in delimiting pathways of change than the selective forces". As the two authors admitted, while this different focus on evolutionary mechanisms was "long popular in continental Europe," (Gould & Lewontin, 1979) it was almost entirely absent in English-language biology. Indeed, as Gould himself noted in a report during a 1971 meeting on form in Tübingen, Germany, "German thinking about form ... differs systematically from our own in some fundamental ways. In particular, there remains a reluctance to grant Darwinian processes a complete role in the explanation of form ... thus, there is a much greater willingness to speak of the non-adaptive nature of many structures" (Gould, 1971b).

Given this background, how did this "European" perspective, so alien to Anglo-American evolutionary thought, come to form the basis for a major theoretical challenge to Adaptationist thinking? What were the sources of this alternative perspective? What broader theoretical agendas did German-language morphologists who supported this view hold?

In my talk, I show that the German morphological tradition made a major contribution to 20th-century study of form. I will present how paleontologist Adolf Seilacher (1925–2014) sought to examine morphogenetic processes in order to illustrate their inherent structural properties, thus challenging the neo-Darwinian framework of evolutionary theory.

Growth, form and evolution: Stephen Jay Gould before (and after) punctuated equilibria

Max W. Dresow, Minnesota Center for Philosophy of Science, USA

Stephen Jay Gould is one of the best-known scientists of the past fifty years, celebrated for his theory of punctuated equilibria (with co-author Niles Eldredge), for his strenuous critique of adaptationist thinking, and for his idea that contingency plays a major role in determining the pattern of life's history. In addition to stimulating scientific discussion, these contributions have made Gould a darling of philosophers of biology, who in recent decades have devoted considerable attention to all the aforementioned ideas, and several more besides. Yet for all the attention Gould's mature thinking has received, his early thinking has been mostly ignored. This is a shame, because Gould's thinking prior to and surrounding the articulation of punctuated equilibria is fascinating and complex. The purpose of this talk is to pull back the curtain on Gould's early research, as well as his precocious synthesis of D'Arcy Thompson's morphology, Martin Rudwick's paradigm method and Julian Huxley's gradal system of classification. What is revealed is a view of evolution (and an associated methodological approach) both coherent and largely opposed to the ideas for which Gould is known. But given this starting point, how did Gould come to occupy the positions for which he is now celebrated? I offer several suggestions in this regard, which highlight Gould's lifelong desire to make a distinctively paleontological contribution to evolutionary theory, as well as the changing resources available to him for this purpose. In addition, I remark on how an improved understanding of Gould's early research deepens, and in some cases, challenges our understanding of his later achievements.

The presuppositions of paleontology: Some methodological remarks on necessity, possibility, and double contingency

Mathias Gutmann, Karlsruhe Institute of Technology, Germany

The validity of paleontological reconstructions depends on its methodological starting point. This originates in valid biological ("functional") descriptions of the recent lifeworld. Paleontological reconstructions share this property with evolutionary statements in general. These are of a retrodictive nature, explaining the recent lifeworld as the result of transformation-events from a specifiable non-recent lifeworld. Accordingly, the reconstruction has a methodological starting point later in time and a conclusion earlier in time, whereas the report of the transformation itself shows a reversed order: the methodological starting point becomes the transformational conclusion, the recent lifeworld, the reconstructed conclusion becomes the transformational starting point, namely the origin.

In this paper, I will argue for a modal characterization of this type of explanation as "double contingent". The double contingency is revealed by considering the validity of the respective types of statements, which constitute an explanation:

We have to presuppose valid functional descriptions of the lifeworld, which lead to specific reconstructions of its respective evolutionary transformation. Thus, on the one hand, the validity of the reconstruction depends on the validity of the methodological starting point. The coherence of functional descriptions of the recent lifeworld, on the other hand, depends on the validity of the resulting evolutionary reconstruction.

According to the proposed analysis, the structure of evolutionary explanations displays some core features of a typical hermeneutic circle:

The – assumedly – correct explanation provides us with some further knowledge on the extinct lifeworld, which became reconstructed, as well as knowledge on the recent lifeworld, which became explained. The corroboration of this knowledge, however, refers necessarily to – assumedly – valid reconstructions, already performed as well as to further functional descriptions of the recent lifeworld. This peculiar double contingency is explicated by analyzing the logical structure of a dispute on the evolution of Enteropneusta (Hermichordata), which were quite recently revised in terms of N(ew)A(nimal)P(hylogenie).

Concepts and understanding in ecology, part I

ORGANIZERS

Rose Trappes, Bielefeld University, Germany
Philipp Haueis, Bielefeld University, Germany

Concepts provide scientists with the building blocks to construct models and explanations, which in turn facilitate theoretical understanding of phenomena in a domain of inquiry. This two-part session will discuss the connection between concepts and understanding in the context of ecology and examine the concepts and methods which ecologists use to achieve understanding. By providing detailed case studies from ecology, the session aims to both advance ongoing discussions in philosophy of ecology and provide novel insights for debates in general philosophy of science regarding the role of concepts and understanding. The first part of the session focuses on three concepts central to ecology: niche, biodiversity and hierarchy. In the first talk, Trappes compares and contrasts the different uses of the niche concept in ecology and evolutionary biology. The different definitions of niche in the two fields, broad and relatively dynamic in the case of evolutionary biology, structured and relatively static in the case of ecology, complicates the heralded unification of ecology and evolutionary biology via niche construction theory. Trappes' case study sheds light on how concepts can enable or hinder biological research in different investigative contexts. In the second talk, Justus scrutinizes the methodological status of biodiversity, a crucial concept in conservation biology. While explicit definitions of biodiversity are often missing, defining biodiversity in terms of algorithms conservation biologists use lack the appropriate criteria for implicit definitions. Justus' critical analysis of definitions in ecology links to debates about the need of alternative models of conceptual structure in scientific practices. The third talk by Haueis picks up on that topic by showing how the concept of hierarchy has failed to provide a unified theoretical understanding of ecosystems. Ecological hierarchy theory overlooks the way multiscale modeling involves scale-dependent descriptions which are often incompatible with each other and therefore resist theoretical unification. Haueis' talk supports philosophers of physics and biology who claim that scientific concepts are part of a patchwork of models, rather than unified theories. The second part of the session focuses on the notion of understanding in relation to methods in ecology. The talks by LeBihan and Wakil provide first steps towards such a dialogue. LeBihan provides a novel account to determine the cognitive value of idealized mathematical models in ecology. This account uses the modal theory of understanding to claim that mathematics allows ecologists to systematically explore relationships between different models. The talk by Wakil critically examines whether the standard method of comparing of ecosystems is a reliable guide to test ecological hypotheses. Her reconstruction of comparative claims as arguments from analogy suggests that comparing ecosystems is no reliable guide to select which hypotheses further ecological understanding.

Defining the niche for niche construction

Rose Trappes, Bielefeld University, Germany

Niche construction theory (NCT) has been hailed as a conceptual tool for uniting and transforming ecology and evolutionary theory (Odling-Smee et al. 2003; Odling-Smee et al. 2013). Yet NCT has proved a controversial proposition. Much of the debate has focused on the “construction” side of niche construction, the idea that organisms have widespread and systematic impact on their environments that may be ecologically and evolutionary significant (Laland & Sterelny 2006; Scott-Phillips et al. 2014). Less attention has been accorded to the “niche” side of niche construction: what is it, exactly, that organisms are constructing?

In ecology the niche concept has a relatively long and involved history (Pocheville 2015). These days ecologists tend to accept some version of a Hutchinsonian definition of the niche in terms of the range, for n environmental parameters, within which a population can establish or persist. Further distinctions are then drawn between fundamental and realised niche, establishment and persistence niche, and population and individualised niche (Holt 2009; Dall et al. 2009). In contrast, NCT’s chief proponents define an evolutionary niche concept as the sum of all the selection pressures faced by a population (Odling-Smee et al. 2003: 40). Contra Odling-Smee et al., I argue that the ecological and evolutionary niche concepts are not equivalent. On the one hand, the ecological niche concept allows more internal structure (fundamental vs realised, establishment vs persistence, and population vs individual). On the other, the evolutionary niche concept is more dynamic, and thus makes more sense of changes in the requirements of organisms over time. These conceptual differences have significant consequences for the way that niche construction can be defined. I explore the way each concept can be used to define niche construction, and what this implies for the potential for NCT – and the niche concept more specifically – to successfully integrate evolutionary biology and ecology.

On implicitly defining biodiversity

James Justus, Florida State University, USA

Biodiversity is a (if not the) core concern of conservation biology and plays prominent roles in several other environmental sciences. In an attenuated form, it is also the target of important ecological research. But seemingly insuperable difficulties confronting attempts to define the concept explicitly have catalyzed incisive criticisms and sown widespread pessimism about future prospects. This analysis furthers that pessimism by considering the idea that the algorithmic practices of conservation biologists implicitly define biodiversity. Taking well-known implicit definitions as the comparative benchmark (e.g. for "line", "point", "logical constant", and even "force"), divergences from it in the case of biodiversity reflect more than differences of context or incidental detail. They reflect departures from the very conditions that render proposed implicit definitions defensible. For example, unlike Euclidean geometry and Peano arithmetic, there is not a single stable set of principles or statements facilitating the proposed implicit definition of biodiversity. Rather, algorithms are supposed to be doing the defining, and they form a multifarious multiplicity, which in turn raises a family of serious concerns. The suggestive analogy between conservation biology and medicine also fails to buttress the definition. Implicit definitions unfortunately fair as poorly as explicit ones for biodiversity.

The concept of hierarchy and the problem of scales in ecosystem modeling

Philipp Haueis, Bielefeld University, Germany

In the 1980s, ecologists introduced concepts from hierarchy theory to develop a unified theoretical understanding of complex ecological systems. Hierarchy theory assumes that

a. ecological systems are organized at multiple spatiotemporal scales, that
b. entities at different hierarchical levels display response rates that differ by at least an order of magnitude and that
c. aggregate lower-level (faster) behavior asymmetrically constrains higher-level (slower) behavior (Allen and Starr 1982, O'Neill et al. 1986).

For example: in a tree, leaves and tree-rings are at different hierarchical levels because sun light changes affect photosynthesis rates on a daily basis, while affecting tree-ring width (i.e. growth rates) only on an annual basis. By allowing an such a principled decomposition of ecosystems into components, the concept of hierarchy was supposed to provide the basis for a unified theoretical framework to different fields of ecology, such as community- and function-based ecosystem science.

From a contemporary perspective, hierarchy theory failed to provide the unified theoretical understanding it promised. In hindsight this failure seems linked to the general move away from theory-driven towards data-driven ecological modeling, and to the particular issue that hierarchy theorists often simply restate known ecological explanations without adding novel insight (Sarkrar 1984). In this paper, I provide an alternative explanation which focuses on the problem of scales in ecological modeling (Elith and Leathwick 2009). Hierarchy theorists correctly saw that ignoring scale introduces errors into ecological models, but overlooked that multiscale modeling frequently invokes incompatible submodels. For example: multiscale models of krill distribution treat krill both as discrete individuals and as dynamic fluids (Levin 1992). Here, integration is not achieved by unified by unified descriptions but by techniques which homogenize data from one submodel to incorporate them into another (Wilson 2018). Furthermore, hierarchical concepts refer to different kinds of properties, depending on which scale ecologists use them. For instance, in communities of species, “constraint” refers to competition and reproduction, whereas in function-based ecosystems, it refers to constancy of biomass (O’Neill et al. 1986). Such descriptions do not afford unification if they decompose ecosystems along nonisomorphic boundaries (Wimsatt 2007). Because it lacks the resources to deal with homogenization and multiple decomposability, hierarchy theory fails to provide a unified framework for multiscale ecological modeling. Rather than unified theory, a patchwork of different models seems better suited to understand ecological hierarchies.

Concepts and understanding in ecology, part II

Understanding ecological theory

Soazig LeBihan, University of Montana, USA

Theoretical modeling in Ecology has been under fire since the 1990s. Idealized, mathematical models have been criticized on multiple grounds, e.g. for

1. their inability to meaningfully capture biological concepts,
2. their lack of scientific rigor,
3. their lack of both predictive and explanatory power,
4. their lack of applicability to conservation decision-making

(Peters 1991, Shradder-Frechette and McCoy 1993, Cooper 2007, Ch. 5). As a result, recent work in ecology has focused on bottom-up modeling. Still, the cognitive and practical value of theoretical ecology is the subject of rather recent heated discussions (e.g. Donhauser 2016, Sagoff 2017, Donhauser 2017). Levins (1966) is well known to be critical of bottom-up approaches. Weisberg (2006) describes the issues associated with bottom-up approaches, as well as the advantages of top-down modeling à la Levins. That said, neither Levins nor Weisberg account for the cognitive value of idealized, mathematical models, which they criticize for being unrealistic and hence lacking explanatory power. Some have offered non-exhaustive lists of some independent ways in which models can be useful in ecology (Odenbaugh 2005, Cooper 2007), but no coherent, systematic account has been articulated. The main goal of this paper is to show that the theory of modal understanding offers a systematic and coherent account of the intrinsic cognitive value of theoretical ecological models, which in turns explains their potential heuristic and practical value.

The main argument will be that theoretical models provide representations of the phenomena with high navigating power. Notably, the theory of modal understanding will explain the value of the use of mathematics. Under the theory of modal understanding, mathematics will be shown to be a valuable tool for a systematic and rigorous exploration and navigation of the relationships that exists between various theoretical models.

Problems with the comparative approach to hypothesis testing in ecology

Samantha Wakil, University of North Carolina Chapel Hill, USA

Most behavioral ecology textbooks present the "comparative approach" as the standard methodology for hypothesis testing. The comparative approach has been criticized by some ecologists, but the philosophical basis on which it rests has been less explored. I argue that the comparative approach is built on the notion of arguments by analogy. Concerns regarding the epistemic status of analogies invites a different kind of criticism against the comparative approach, and supports the view that it is an impoverished methodological tool.

An analogy consist of two parts:

1. the base or source and
2. the target.

The base refers to a familiar domain or process we already have good knowledge about. The base then serves as a model by which one can comprehend and draw new inferences about a less familiar domain (the target). Reasoning by analogy involves identifying "a common relational structure" between the base and the target and then generating an inference on the basis of this commonality. (Gentner and Smith 2012)

One concern about analogical reasoning is that there is significant unclarity as to what, precisely, a common relational structure is. A further problem is that there does not appear to be any criteria by which we can determine the evidential significance of any given similarity or dissimilarity we might observe between the base and target. In this talk, we will examine a commonly cited case study about the breeding behavior of gulls in relation to predation risk. This case study is meant to support the usefulness of the comparative approach. But, I will argue that the study actually reveals how the comparative approach fails to satisfy the primary criteria of testability. Namely, that testability is essentially contrastive.

Reconstitution as a more inclusive way of inheritance and its relation to current debates: Small RNAs, holobionts, and niche construction

ORGANIZER
Sophie Juliane Veigl, University of Vienna, Austria

In recent years, calls for an "Extended Evolutionary Synthesis" (EES) have been debated repeatedly. One key question is whether other processes which are not accounted for by the "Modern Synthesis" (MS) influence the trajectories of evolution. Some possible candidates for this are the process of niche construction (NC), the boundaries of a single organism as a unit of selection, and the inheritance of acquired traits (IAT). If these examples indeed turn out to require an account exceeding the explanatory power of the MS, they would support the case for an EES. In this panel, we aim at providing three case studies to put EES to the test. Particularly, we examine the conceptual problems that impede the acceptance of alternative modes of inheritance. Our case studies support the promise of "extended inheritance": forms of inheritance not obeying the neo-Darwinian/Mendelian paradigm at the core of MS. We criticize the notion that DNA replication is the only means to confer the stability of traits throughout generations and introduce the concept of "reconstitution" as an alternative to secure such stability. We define reconstitution as the processes through which phenotypic similarities in the parent-offspring line are transgenerationally maintained in a population. These processes are not homogenous and might be multiply realized due to the different nature of inheritance channels. In our talks we analyse and set some limits on the different mechanisms of reconstitution connecting it to some contemporary debates in biology. The first talk will examine the inheritance of small RNAs as an example of how the stability of traits can be conferred without the need of encoding information in chromatin and replicating it in each generation. Rather, reconstitution of information is sufficient. The second talk will show that extended inheritance through population structure provides a theoretical basis for considering holobionts as units of selection. Channels of inheritance additional to vertical transmission provide intergenerational stability of traits with sufficient fidelity for the group to behave as a unit of selection. The final talk will set the relation between the reconstitution, ecological fitness and niche construction. It will be argued that niche construction breaks the reconstitution of environmental conditions (ecological inheritance) and as result the ecological fitness of the different entities (those that live in the modified environment and those that don't) becomes impossible to compare. In conclusion, the panel will provide a philosophical analysis of concepts central to the debate over the EES. It will provide an empirical basis to explore "reconstitution" as an alternative to the paradigmatic notion of replication as the only means to confer the stability of traits. The limits of reconstitution and extended inheritance in general will also be discussed. In conclusion, we aim at contributing to the debate within both the philosophy of science and evolutionary biology by introducing a new concept and at the same time exploring its scope and empirical adequacy.

Reconstitution of chromatin modifications: Small RNAs and IAT

Sophie Juliane Veigl, University of Vienna, Austria

Inheritance of acquired traits (IAT) has become a common topic in discourses about the relationship between inheritance and evolution. Several pathways for IAT are proposed, including epigenetic, behavioral and horizontal transmission. Substantial key questions remain: How could acquired traits be inherited? Is there any "active" IAT? Or is the transmission not part of any inheritance mechanism? Reports on beneficial effects of IAT are scarce, especially in mammals. The inheritance of chromatin modifications is considered a key candidate for IAT. However, it has been shown that in organisms with a clear soma / germline distinction, chromatin modifications transmitted by the parents are erased after fertilization. Nevertheless, corresponding chromatin modifications reappear in the next generation. In summary, several questions need to be addressed before considering the role of IAT in evolution:

1. What is the mechanism of IAT?
2. What is the role, if any, of chromatin modifications?
3. Is IAT advantageous?

The possibility of extended inheritance is thus seriously challenged because of the erasure of chromatin modifications. In this talk I argue that gene-centrism and a focus on DNA as the single source of inheritance limits our conceptual resources for thinking about inheritance. In fact, it led to the view that chromatin modifications need to be replicated in order to be possible sources of inheritance that confer transgenerational stability of traits. Against this view, I conjecture that for a trait to be stable throughout generations, and thus be inherited, it needs not be replicated. This means that a specific chromatin modification need not be inherited by DNA replication. It is sufficient if it is reconstituted in the subsequent generation.

In several model organisms, it has been shown that small RNAs are transmitted in parallel to DNA and reconstitute chromatin modifications in each generation. It has thus justly been asked whether chromatin modifications are “causes or cogs?”. In recent years, small RNAs were hypothesized to be the key effectors of gene silencing, and possibly activation, as well. Small RNAs were shown to be responsive to adverse stimuli, such as viral infection, heat / cold shock and starvation. They provide a memory of the specific stressor and orchestrate the deposition of chromatin modifications, what leads to silencing or activation of targeted genes. Small RNAs are vertically inherited, as well as amplified in each generation. Subsequently, they reconstitute chromatin modifications and thus confer the stability of traits. This suggests that reconstitution is a possible mechanism of IAT.

A small RNA based paradigm illuminates how acquired traits can be faithfully transmitted, without the need for replication of chromatin modifications. In each generation, small RNAs reconstitute chromatin-modifications, after parental chromatin-modifications have been erased. Thus, small RNAs suggest an alternative pathway of inheritance, in parallel to DNA. Small RNAs transmit acquired responses to past stimuli and might have a beneficial or adverse effect on the offspring. In conclusion, considering "reconstitution" instead of "replication" as a trajectory of extended inheritance widens philosophers' and biologists' conceptual toolbox.

Extending reconstitution: Inheritance through population structure among holobionts

Javier Suárez, University of Barcelona, Spain & University of Exeter, UK

Holobionts are biological assemblages composed of a host plus its symbiotic microbiome. Holobionts are pervasive in biology and every macrobe is believed to host a huge number of microorganism, some of which are known to have a substantial influence on the phenotype of the animal. Because of this, a considerable number of biologists have recently suggested that holobionts are units of selection, i.e. entities that exhibit inherited variance in fitness (Gilbert et al. 2012; Rosenberg & Zilber-Rosenberg 2014).

Contrary to that claim, some authors have recently suggested that holobionts cannot be considered units of selection. They argue that the existence of independent reproductive regimes among the entities that compose the holobiont (the host, on the one hand; and the symbionts, on the other) makes it impossible to talk about holobiont inheritance (Moran & Sloan 2015; Douglas & Werren 2016). In other words, even if there might be phenotypic variation among different holobionts in a population, this phenotypic variation cannot be intergenerationally transmitted from parent to offspring. Or, at least, not with the degree of fidelity that would be required for natural selection to act on the holobiont. Therefore, according to them, the microbiome is, at most, an environmental factor that only influences the phenotype that the host expresses, but which cannot be selected together with its host.

In this talk, building on some recent evidence about holobionts, I elaborate an extended notion of inheritance through reconstitution for biotic conglomerates that overcomes the difficulties posed in Moran & Sloan (2015) and Douglas & Werren (2016). I argue that this notion is adequate to capture some phenomena of intergenerational preservation of variation among holobionts that could not be captured with the restricted notion that the critics use, thus widening our conceptual toolbox.

My talk will be divided in three parts: First, I will argue that critics of holobiont inheritance use a very restricted notion of inheritance that equates inheritance with DNA replication only. I argue that this notion is insufficient to capture the concept of "inheritance", since replicated and transgenerationally transmitted DNA does not exhaust the full range of factors that have an influence on the expressed phenotype. Second, I argue that the definition of inheritance should be widened to include those factors that are actively acquired and maintained for an organism to express its phenotype, and are thus net contributors to the phenotype variation in the population. This is a way of inheritance by "reconstitution", and consequently, replication is just one of the ways in which reconstitution might occur. An important aspect of the definition I offer is that what needs to be preserved to talk about "inheritance" is the transgenerational distribution of the phenotypic variation within the existing population, no matter whether this distribution is preserved among parents and offspring. Finally, I will argue that there are reasons to believe that some holobionts satisfy the suggested definition, and thus it is reasonable to considered them as cases of individuals whose traits are transgenerationally reconstituted.

Niche construction as a process of wrecking the reconstitution and its consequences for ecological fitness

Adrian Stencel, Jagiellonian University, Poland & ImmunoConcept, France

Niche construction (NC) refers to the situation when organisms substantially change their environmental conditions. It can be an important evolutionary process only when two conditions are fulfilled:

1. it leads to significant changes in the environmental factors that determine the selection pressure acting on the population;
2. those changes are inherited by future generations.

For example, byproducts of biochemical pathways of a group of organisms might change the environmental conditions and, if they are permanent for several generations, natural selection might start to favor organisms of type "A", whereas before NC it favoured organisms of type "B". In other words, NC is a process responsible for changing the dynamics of transgenerational reconstitution, since its action leads to a change in the environmental conditions in which the organisms live in (ecological inheritance).

It is important to note that NC might not proceed homogeneously and might concern only a few members of the population. The process of endosymbiosis is an illustrative example: Some bacterial species start living inside the host and thus abandon their original ecological niche, while the rest of the population keeps living outside the host. In some circumstances, this change in the environment leads to an increase in reproductive success of the endosymbionts. This raises a question: if NC increases the reproductive success of some individuals in contrast to those who are not experiencing niche change, can we then argue that it increases their fitness? Can we say that it is beneficial for them? The intuitive answer would be affirmative.

A problem emerges with this answer if one is committed to use the ecological concept of fitness. The ecological concept of fitness is often defined as: "x is fitter than y if and only if x's traits enable x to solve the "design problems" set by the environment better than y's traits do." This concept assumes that the fitness of one unit can be said to be higher than the fitness of other units only if it is measured in the same environment, since these are the only conditions where we can test whether one unit can solve the "design problems" better than another. Thus, being put in the same environment is a conditio sine qua non for understanding whether one unit has a higher ecological fitness than another.

In this talk I will argue that NC, if proceeding heterogeneously, is a process that takes some individuals from an environment “X” and puts them in environment “Y”, thus breaking the necessary conditions for comparisons of ecological fitness. I argue that in such situations NC neither increases nor decreases the ecological fitness of the individuals whose niche is being reconstructed. It simply makes their fitness incommensurable in relation to their counterparts that inhabit the unchanged niche. As result, I will argue that the relation between NC, ecological fitness and reconstitution can be fully understood only if we enrich it by the concept of fitness incommensurability. ding what astrobiologists should look for on other planets, today, to detect life, or at least biosignatures (evidence of life or of past life). I discuss these issues of reasoning with analogues in the context of examples from astrobiology, including the case mentioned above of the “hot spring” model of the origin of life and its influence in decisions about the 2020 Mars landing site.

Individual papers

Agential niche construction

Bendik Hellem Aaby, KU Leuven, Belgium
Hugh Desmond, KU Leuven, Belgium

Niche construction has often been described as a process where the organism causally changes its selective environment (Brandon 1990):

> *"[T]he organism influences its own evolution, by being both the object of natural selection and the creator of the conditions of that selection."*
> Levins and Lewontin 1985, p. 106

Yet, this results in a very broad definition, encompassing any changes that an organism might have on its physical environment, as long as those changes produce changes in selection pressures over a certain time-interval (cf. Laland et al. 2016).

While this broad definition has been defended as a consequence of the fundamentality of the concept of niche construction (Laland et al. 2005), it has also been criticized as unable to distinguish between accidental consequences of an organism's behavior and cases of niche construction where the organism may be considered a (difference-making) cause (Sterelny 2005).

More recently, the proposal has been to limit niche construction to "significant modifications" only, and "organism-mediated modifications" (e.g. Matthews et al. 2014):

1. An organism must significantly modify environmental conditions;
2. Organism-mediated environmental modifications must influence selection pressures on a recipient organism (Matthews et al. 2014, p. 247).

However, this definition raises further questions: where is the boundary to be placed between significant and non-significant modifications? And where is the boundary between organism-mediated modifications and modifications where the organism has played a purely incidental part?

In this paper we argue that these problems can only be resolved within an agential approach, where the relevant distinction lies between agential and non-agential forms of niche construction. An organism is engaged in agential niche construction when it exhibits goal-directed behavior where the modification of the selective environment is its goal of said behavior. Conversely, an organism is engaged in non-agential niche construction when the modification of the selective environment is a consequence (but not a purpose) of its behavior. We argue that this approach can better account for problematic cases, as well as explain why the paradigmatic cases of niche construction behaviors (e.g. beavers building dams) seem to involve agency.

The discovery of RNA splicing at 40: From public memory to epistemic justice

Pnina Geraldine Abir-Am, Brandeis University, USA

The discovery of RNA splicing, also known as the discovery of "split genes", in 1977, is widely seen as the 3rd most important discovery in molecular biology. (after DNA structure & mRNA function) By revealing that many eukaryotic messenger-RNAs are not co-linear with DNA but rather are the products of multiple splicings of non-contiguous segments of a primary transcript of the genome, the discovery led to a new paradigm of genetic regulation. In addition to clarifying how alternative splicing explains genetic diversity, the discovery of RNA splicing led to the current progress in understanding how the splicing mechanism is performed by the spliceosome, the largest stand alone biological assembly. The discovery also has therapeutic ramifications for diseases resulting from splicing errors.

This talk explores how the paradigmatic shift away from gene-protein co-linearity was experienced as "surprising", or as a case of a strong theory coupled with weak foundations. The synergy of several technologies (e.g. RNA: DNA hybridization, electron microscopy, DNA and RNA sequencing, gene mapping) in defining the discovery is also explored as part of an effort to interrogate its alleged simultaneity across labs.

This talk also aims to clarify how the public memory of this discovery, often highlighted as team work, still sedimented into the present, as a public memory limited to two, lab director, Nobel laureates. (1993) The role of gender bias in the 1970s, often displaying intersectionality with ethnic and age bias, is shown to have obscured the key role of women, junior, and foreign scientists in this major discovery.

The talk concludes with an interpretation of how the quest for scientific progress intersected with issues of epistemic agency, authority, and in/justice in the 1970s, or a decade which is now better understood by historians as an era of innovating science and social policies, such as the "War on Cancer", (1971) the Affirmative Action Legislation, (1972) and counter-cultural effects.

Anthropocene and the systemic dimension of biological functions. The case of epigenetics, horizontal gene transfer, and antibiotic resistance

Flavio D'Abramo, Max Planck Institute for the History of Science, Germany

To prove that weaknesses of fathers do not affect biologically their descendants, about a century ago August Weismann cut mice's tails to show that next generations not inherited these mutilations. A political, democratic conception of equality of opportunity–i.e. to all individuals should be given similar conditions to develop their talents and satisfying their basic needs–was reified within a biological model–i.e. phenotypic traits "acquired" during one's life in interacting with the environment do not influence next generation. This neo-Darwinist framework justified that no intervention for individuals and communities is required to rebalance conditions of disadvantage. In this paper I show that the political debate fuelled by scientific inquiry on the influence that social and material environments have on individuals and communities, "forget" the systemic approach needed, such as the one utilised through the model of horizontal (or lateral) gene transfer. Animal husbandry at scale, for instance, is allowed by use of antibiotics, which in turn has elicited antibiotic resistance. Bacteria and related DNA elements spread, horizontally, and contribute to the metabolism of other species in different and usually uncontrollable ways. Horizontal gene transfer is a ubiquitous process, constitutive of most of living beings. Bacteria are indeed in charge of coordinating gene expression and hence cell differentiation during the first phases of mammals' development, and other vital functions. To end, I address the questions: "What is the influence that contemporary mode of production has on scientific models?", "How can we develop a non-teleological, systemic take of the Anthropocene?"

What research practice shows about fitness and natural selection

Marshall Abrams, University of Alabama at Birmingham, USA

Causalist philosophers and biologists argue that natural selection and other evolutionary "forces" are general kinds of causes of evolutionary change. Many causalist philosophers view the basic form of biological fitness as a probabilistic, causally relevant property of actual token organisms. They then define the fitnesses of traits as simple averages of actual token organisms' fitnesses. Statisticalist philosophers and biologists, who often grant the assumption that token organisms have fitnesses of the kind that causalists postulate, deny that that causal properties of individual organisms aggregate into fitnesses of traits or into population-level causes that could be called "natural selection".

My focus in this talk is on the practice of empirical research in evolutionary biology. Developing arguments sketched in earlier work, I argue that biologists' practices show that token organisms' fitnesses, treated as forming the basis of causal trait fitnesses and natural selection as a causal factor, play little or no role in evolutionary biology. Biologists nevertheless implicitly treat trait fitnesses as causal. Research practice is therefore in tension with typical causalist and statisticalist views.

I distinguish between four categories of biological fitness concepts:

1. Causal token-organism fitnesses, which are the focus of the propensity interpretation of fitness and related views. Fitness concepts that most philosophers take as basic causal concepts of fitness usually fall within this category.
2. Causal organism-type fitness, which includes trait fitnesses that most causalists accept but that statisticalists do not.
3. Measurable token-organism fitnesses, which are easily measurable properties such as actual numbers of offspring, and are sometimes conflated with causal token-organism fitnesses.
4. Statistical organism type fitnesses, which are trait fitnesses defined in terms of measurable token-organism fitnesses. These may be what statisticalists take trait fitnesses to be.

I use a case study of empirical research on a contemporary human population, and argue that the researchers' use of multiple regression to infer selection gradients implicitly assumes the existence of causal organism-type fitness (2), estimated from statistical organism-type fitness (4), which is defined in terms of measurable token-organism fitnesses (3). This pattern is shown by details of researchers' use of data and their use of p-values, as well as their use of language.

Causal token-organism fitness (1), which has been a primary focus of philosophical discussion, plays no role in this research. I argue that this pattern is common in evolutionary biology, and that causal token-organism fitness plays little if any role in it. This supports the view that it is a mistake to think that causal token-organism fitness is important to understanding evolution, and also shows that empirical research in evolutionary biology assumes that trait fitnesses contribute to natural selection as a causal factor. I suggest that biological practice is most consistent with a view that actual organisms are realizations of properties of an underlying probabilistic system defined by the characters of a population and its environment. This conception treats fitness and natural selection as causal, without defining either in terms of properties of actual token organisms.

Pregnancy as an evolved reproductive relation

Arantza Etxeberria Agiriano, University of the Basque Country, Spain
Laura Nuño de la Rosa, Complutense University Madrid, Spain
Mihaela Pavliçev, Cincinnati Children's Hospital, USA

Questioning whether the pregnant female is a carrier of independent developing individuals or a single individual by itself has become a focus of debate in the philosophical literature (Kingma 2018). If we consider the kind of individuals involved in pregnancy from the physiological, evolutionary, and interactive perspective it is evident that pregnancy challenges current philosophical views on biological individuality. Besides, received views of reproduction conceal the complexity and diversity of the relations involved: reproduction is not just replica or copy making and maximising evolved strategies, whereas the notion of "self-reproduction" is problematic in that it assumes the self-sufficiency of reproducing entities. Therefore, to advance in a relational understanding of biological reproduction, abstract models and generalisations drawn from specific taxa should be replaced by empirically motivated evolutionary accounts. Here we attempt an account of pregnancy that will look into some common assumptions about biological reproduction and individuality for evolution. Recent work in evo-devo supports a view of the evolution of mammalian reproduction as a merging of female and egg involving major innovations at various scales of organization (morphological, physiological, developmental, genetic). Thus, from this reproductive perspective the pregnant female can be considered a developmental stage tantamount to a evolutionarily novel kind of temporary individual and this view of therian reproduction has crucial implications for the status of the pregnant female. Understanding the evolved relations, distributed agencies, and emergent individualities in the case of pregnancy (and biological reproduction in general) requires considering material continuities/discontinuities, forms of multiplication and strong developmental interactions. As conclusion our claim for individuality in the case of eutherian pregnant females is presented as a step towards elaborating on the properties of biological reproduction as evolved kinds of relations.

The genesis, reception and development of the tumor angiogenesis research program

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Angiogenesis (i.e. the formation of new blood vessels from pre-existing ones) is considered now a hallmark of cancer, and inhibiting angiogenesis a promising strategy for the treatment of cancer. The first formulation of the hypothesis that tumor growth is angiogenesis-dependent and that inhibition of angiogenesis could have therapeutic implications for treating cancer was made in 1971 by Judah Folkman, a surgeon at Children's Hospital in Boston. This article uses Hans Jorg Rheinberger's analytical framework on the oscillation of epistemic things and technical objects to describe the evolution of the experimental system that led Folkman to his seminal observations on tumor angiogenesis. A particular attention is given to the social context that shaped the evolution of this experimental system. The article also examines Folkman's use of illustration practices common to the field of surgery as persuasive representations of the scientific relevance of his hypothesis. These drawings were presented as depicting factual phenomena observed in the laboratory, but they were also material instantiations of epistemic objects that were still unfolding, as the level of evidence provided by Folkman in support of his hypothesis was not high enough to attract the attention of cancer biologists. The tumor angiogenesis research program, although initiated in the seventies, only became attractive around the world in the mid-nineties. The article describes the reception and slow diffusion of this therapeutic strategy and examines narratives of resistance put forward by early adopters as well as Folkman himself by putting angiogenesis research in the context of the landscape of theories and therapeutic pathways that were explored at the same time in cancer research.

A model of phenotypic architectural changes to account for selective and non-selective processes of evolutionary changes

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The last decades have seen the flourishing of accounts of evolutionary forces other than selection, many of which have been collected under the name of Extended Evolutionary Synthesis (ESS) (Laland et al. 2015). The range of phenomena targeted by these accounts spans from genetic mechanisms (e.g. Cherniak & Rodriguez-Esteban 2013, Kimura 1983, Wagner 2015) to developmental (e.g. Maynard Smith et al. 1985), systemic (e.g. Kauffman 2000) and neo-Lamarckian (e.g. Koonin & Wolf 2009). Although almost none of them denies the importance and even preponderance of selection in the history of life, and they rather aim at integrating non-selective phenomena into neo-Darwinism (a view known as "pluralism"), they are highly criticized by main-stream biology, that either limits or completely denies their evolutionary importance, often underling that their contribution to fitness is immaterial. We believe that classical neo-Darwinism and the pluralistic view are compatible and suggest two tools that can help building a unified vision of evolution.

In the first place, we believe that a fair analysis of the relative importance of selection and other non-selective forces to the shaping of phenotypes should first acknowledge that the range and diversity of types of evolutionary phenomena is wide, and that each type might involve the action of one or several different evolutionary processes. We propose a classification of evolutionary phenomena based on the changes in form and function that each entails, suggesting that selection is behind some but not all of them.

In the second place, we suggest that fitness, being an intrinsically selective measure, should not be used to judge non-selective phenomena. We propose instead other selective-indifferent variables to map the contribution of non-selective forces.

Finally, based on these two tools, we present a model of phenotypic architectural changes that could help unifying selection and non-selective forces in a pluralistic account of evolution.

Error repertoires and the role of negative knowledge in biology

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Debate continues on the significance of publishing statistically negative results from medical trials and other research. At the same time, less attention has been given to the epistemic role of documenting errors or negative knowledge in general. Here, I discuss the use of informal catalogs of domain-specific mistakes, or error repertoires (Mayo 1996). Such knowledge of past error can help in interpreting unexpected experimental results and in raising evidential standards for subsequent research—as illustrated in the history of oxidative phosphorylation. Error repertoires can also function on a deeper conceptual level, in raising the bar for explanatory arguments. For example, recurring forms of biological essentialism/biological determinism tend to exhibit several by-now-familiar flaws. This error repertoire can facilitate timely debunking and could potentially guide more effective study design. Error in science is a powerful tool to leverage learning, and memory of error is, ironically, a critical component of progress in science.

Abel Salazar's contributions on the structure (and function) of the Golgi region in mammalian cells

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The present paper looks at the research developed in the early twentieth century by the histologist Abel L. Salazar (1889–1946) aimed at a better understanding of the structure and function of the Golgi region of biological cells. Medical doctor, professor, scientist and visual artist, Abel Salazar is a multifaceted figure of the Portuguese cultural setting of his time. Expelled from academia by political reasons in 1935, and though later he had the possibility to return, his research career has been relatively short and deeply marked by the difficulties of scientific isolation. Methodologically, his research work is based on the implementation and the successive adaptations/improvements of the tanno-ferric method for the staining of mammalian tissue slices for optical microscopy, looking at both normal and tumoral biological samples. Those studies provided evidence on a specific highly tannophilic area in the Golgi region and, even though his interpretation of the obtained data had not prevailed, those data disclosed part of its structure as it became later understood. The fact is historically illuminating. Building upon published texts and archival sources, my analysis addresses the role of visual representations in Abel Salazar's research work (spanning the staining of biological samples and the drawing to record observations) and more broadly in the dynamics of scientific knowledge production, and also the limiting role of instruments. Finally, I will present and discuss how this case is deemed significant for the curation of a series of public events trying to show and raise awareness to the dynamics of science.

The concept of the cell as an active conception of life: The case study of Haeckel, his monism and his monera

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The Cell Theory was established by the axioms of Schleiden and Schwann (1838) and Virchow (1858); it claimed that the cell was the fundamental living building block, the minimal vital unit. Consequently, as it allowed to distinguish living/biological from non-living/non-biological beings, the conceptual establishment of the cell concept played a major part in the foundation of biology as a full-fledged scientific field. But since the investigation on the cellular components and the molecular biology has developed, the cellular object tended to be less considered for itself; this led to a vague boundary between what is alive or not, and generally between biology and physics. In a sense, the cell is still the concept that distinguishes biological from non-biological entities, but de jure, life should be reduced to non-living components. However, if we focus on the German-19th-Century context when the Cell Theory developed, there were several scientists – from the Naturphilosophen such as the naturalist Oken (1779–1851) to the biologist Haeckel (1834–1919) – who considered at the same time life as something inherent to matter in a monistic framework and as something that is not reducible to un-living components (Zammito 2018, Cunningham & Jardine 1990). In that context, life was characterized by activity. For instance, Virchow emphasized the intrinsic dynamicity of the cell (Duchesneau 1987).

Therefore, I aim to analyse this conception of life as something active in the specific case of Haeckel. Virchow's former student, Haeckel was simultaneously an admirer of Goethe and a major defender of Darwin in Germany. He inherited at the same time the speculative views of Naturphilosophen and the main theories of his time (i.e. the Cell Theory and the Theory of Evolution by natural selection) (Richards 2008). From this scientific background, it resulted a monistic interpretation of life where life was not reducible to physical elements even if biological entities were only made of physical components. He called "moneron" the simplest living being, simpler than the cell since it had no nucleus. In this moneron, life was enabled by plastidules, i.e. "active factors" inherent to the chemical composition of the protoplasm (Haeckel 1876). In this presentation, I will analyse such notion of active factors and to see the part they played in the Haeckelian conceptualisation of living activity as being capable of nutrition, reproduction, sensibility, and minimal motility (Haeckel 1876). How do we assume matter as the only substance and how do we simultaneously keep aliveness as something special? How do we unify a kind of reductionism and an acknowledgement of living matter? In focusing on Haeckel, the point is to redesign how life, matter and activity were connected in his monism and to show that this active conception of life said something from its Cell Theory background.

History of the symbiogenic theory of evolution

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A concise, critical and specifically focused proposal on the history of the symbiogenic theory of evolution is presented, despite the existence of valuable exegeses on the subject, but certainly more general in treatment or too short. This story rather punctually initiates with the discovery of the dual nature of lichens by Simon Schwenderer in 1867 and ends with the hypothesis of serial endosymbiosis advanced by Lynn Margulis in 1967, covering a time lapse of one hundred years. To accurately reconstruct this specific story, some primary sources of Americans as well as second sources to English language of Russian and German authors were used.

The long-lasting tradition of investigating the nature of the eukaryotic cell (started two centuries before Schwenderer by Hooke and Malpighi) culminated in efforts to explain and probe the origin of the cell itself. Therefore, the scientific speculation as well as experimentation were at their highest level when the discovery that lichens were composite organisms formed by an association between a fungus and an "alga" was announced. The descriptions of more symbiotic associations between different organisms followed immediately, as were the invention or implementation of new terms and concepts to refer these associations. Hence, the inclusion in Biology of terms such as consortium, symbiotismus, symbiosis, mycorrhiza and other became common. Once symbiosis was accepted (1878) as a universal phenomenon, there was a general tendency amongst researchers to foresee the implications of such associations, for it was noted the amazing resemblance between mitochondrion and chloroplast with certain types of bacteria and algae, and by the fact that those organelles did not arise de novo, but form from preexisting ones. Consequently, it was hypothesized that these organelles were once free-living organisms. Although many Botanists, Cytologists, Zoologists and other researchers from Europe and America stood out by their contributions to symbiosis and Cell Biology, three Russian scientists are considered the founders of what now is called the symbiogenic theory of evolution: Famyntsin, in the

1860s, was the first in separating the lichen endosymbionts, giving no explanation of his results; Mereschkowsky, in 1905, proposed the term symbiogenesis to explain the origin of new, more complex organisms by the association of two or more simpler, different organisms in symbiosis, and stated that chloroplasts were indisputably symbiont cyanobacteria; Kozo-Polyansky proposed symbiogenesis as a new principle of evolution and of origin of evolutionary novelties. In America, Wallin, independently, advanced his hypothesis of symbionticism to explain the origin of new species based on his studies of mitochondrion. A time period of 40 years followed this intense educated speculation; the hypotheses of evolution by symbiogenesis were rejected or forgotten by the scientific community. Those years were dominated by the ideas of Oparin on the chemical origin of life, as well as by the notion that mutation, recombination, Mendelian genetics, natural selection and population genetics were the best, in not the only, explanations for the origin and evolution of organisms (e. g. de Vries, Haldane, Fisher, and Dobzhansky), and by the "Modern Synthesis" of evolution constructed by Huxley. The impasse was finished by Margulis´s relevant paper of 1967 exposing her own ideas on endosymbiosis. As Margulis worked towards the symbiogenic theory's redivivus, she also went further with the serial endosymbiosis hypothesis and fought to include all these ideas into the Extended Synthesis of evolution.

Lessons from embedding in animal behavior science

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Biology, like life, is filled with amazing diversity and complexity. Yet much philosophy of biology has focused narrowly on what is thought most "fundamental" to life and the life sciences: genetics and evolution. Have philosophers of biology been considering a caricature of the life sciences all along? Certainly not: No more than, say, geneticists consider a "caricature" of life in their own focused field of study. That said, philosophy of biology ought not to simply be a philosophy of genetics and evolution. One way to expand our collective field of view is to take a cue from the life sciences themselves. Philosophy of biology can diversify and see what else is out there to explore. Relatively recent enthusiasm for philosophy of ecology is a welcome addition, but there are still fields of the life sciences that are largely unexplored by philosophers. My support for the view that it is time for philosophy of biology to explore new fields is informed by a year spent as an embedded philosopher among biologists in the animal behavior sciences. This diverse collection of biological fields includes behavioral ecology, traditional ethology, behavioral genomics, comparative cognition, animal welfare, behavioral endocrinology, animal communication, and more. The theories, models, and practices within these fields have significant implications for our philosophical understanding of biology, and our understanding of science more broadly. Choosing just one example, the implied and applied ontologies found in active research programs within animal behavior sciences are often quite different from the ontologies described by philosophers. One can find genuine ontological commitments to such things such as "information", "subjective mental states", "life-history stages", and "animal personalities". Such unusual entities play explanatory and predictive roles, but are largely unconsidered by philosophers concerned with "fundamental" ontological entities like objects, processes, or structures. Furthermore, the animal behavior sciences draw upon and inform theories, models, and practices within anthropology, conservation biology, ecology, neurology, biochemistry, psychology, physiology, medicine, and agricultural studies. The interconnection and reliance on common theories, models, and practices among these sciences suggests that considering a broader range of the life sciences has implications for our understanding of science more generally. The diversity within the animal behavior sciences presents a largely untapped resource for philosophers of biology to increase our understanding of the life sciences and their subject matter. I suspect that other overlooked fields will be equally fertile. It is time for philosophy of biology to grow.

Does the scorpion sting itself to death? The history and philosophy of an "easy" question

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The tale of the scorpion encircled by flames choosing to turn its deadly sting on itself is one of the most striking images of animal self-destruction. It was made famous by Byron in his poem the Giaour, although the story predates him by several centuries. But do scorpions actually commit suicide? Or at least sting themselves to death? The question seems eminently resolvable by empirical inquiry, yet experimental investigation dates to at least 1731 and persists for almost 200 years before there is a widely accepted answer. I use the history of these investigations to explore the complex intersection of factors required to address even putatively straight forward questions. Salient factors include skepticism of the historical naturalist tradition, British colonialism providing access to scorpions for new scientists, international science journals facilitating communication on animal anecdotes, and the advent of evolutionary theory sparking interest in self-destructive instincts. Yet even though much of the scientific community came to a general conclusion by the early 1900s, the present day persistence of the tale of scorpion suicide, on YouTube and Reddit, on Yahoo Answers and pet shop owners forums, and even in non-biology academic papers, reminds us of the patchwork nature of not just the development, but also the distribution, of scientific findings.

Microbial signaling

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In the last two decades there has been a growing interest in bacteria and other microorganisms. Philosophy, however, only recently started to pay close attention to the microbial world. Recent work has investigated what bacteria can tell us about life (Parke, 2013), cooperation (Lyon, 2007), individuality (Clarke, 2016), species (Franklin, 2007) or general questions in philosophy of science (O'Malley, 2014). Some surprising theses have also been put forward, such as the idea that some bacteria aggregates (biofilms) are superorganisms (Shapiro, 1988; cf. Clarke, 2016) or that there is such a thing as bacterial cognition (Shapiro, 2007). In this essay I would like to focus on a different aspect of microbes that has been receiving an increasing amount of attention by scientists: the capacity of certain bacteria of producing signals.

The goal of this essay is twofold. First, this paper aims to establish whether expressions such as “signal” or “communication” used for bacteria are simply employed in a metaphorical sense, or whether there are some reasons for taking it seriously. This approach might also contribute to iron out our theory of microbiotic signaling, which might help us to assess which of the attributions of signals are justified and which are not. A second motivation is to investigate whether any of the philosophical theories on the nature of signals can accommodate communication between bacteria. Paying close attention to bacteria might help us to test and articulate more powerful theories of signaling. Note that these two goals should be addressed in tandem. In order to assess whether bacteria produce signals, we need a theory of what signals are, and in order to develop a plausible theory of signals we need to confront it to current scientific explanations and intuitions. Accordingly, I will proceed as follows: first, I will lay down the scientific evidence and take the scientist’s expressions at face value (which includes words like “cell-to-cell communication” and “signaling”) and I will argue that this talk can be partly vindicated by a particular theory of signals. Secondly, I will defend that this (approximate) fit also lends support to this theory of signals. Finally, I will derive some interesting consequences for a general theory of communication.

Classifying evidence and representation: Two status types of cell biological data images

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This practice-focusing study seeks to disambiguate the meaning of “evidence” in cell biology from the philosophical perspective. I argue that the representational status and the evidential status of cell biological data images can be philosophically classified. As the majority of wet-lab biological data are produced in visual forms such as photographs and chart graphs, this study focuses on the epistemic role that data images play in the development of explanations for cell phenomena. This study will show the problematic ambiguity in the use of the term “evidence” and propose an ad-hoc definition of cell biological evidence. In biological expressions, things that practitioners refer to as “evidence” seem to support explanations to various extents. Moreover, the nomenclature of visual evidence is normally technique-based, such as “histological evidence” and “immunostaining evidence”. Nonetheless, these names suggest more the technical means of producing representations of something that happens inside the cell than the evidence for specific arguments. It should be noted that I do not challenge the practitioners’ terminology. Instead, I seek to show that the cell biological reasoning process and the rich meanings of data images can be appreciated within the abundantly growing scholarships of representation and evidence.

In the process of reasoning about cell phenomena, data images are given two types of status, which serve two separate yet complementary functions at different stages of the development of explanation. Upon having obtained new data, researchers determine its evidential validity. Here, the data is used to prove that an event really occurs after experimental intervention and within the hypothetical spatiotemporal framework. Once the experimental intervention has been proven relevant to and effective for producing an event, the data becomes a representation of a specific mechanism component. This study argues that the representational meaning of the data cannot be separated from the practice of intervention. The representational data gains a candidate position within a coherent explanation and is used for surrogative reasoning. Such a use informs the researchers of ways to organise components of the mechanism in question.

Overall, by drawing on an analysis of cell biology, this study seeks to contribute to both the literature of evidence and the literature of representation. While they are both important topics in philosophy, previous studies have neglected the possibility that the two concepts may have complicated relationships in some sciences and contribute differently to the epistemology of those sciences.

Vindicating metaethical naturalism: The case for final causes in the life sciences

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The central claim of metaethical naturalism is that moral facts or properties just are natural facts or properties, where what it takes to be a natural fact or property is to be an appropriate object of study for our best natural science. Those who oppose metaethical naturalism have argued, therefore, that moral properties are somehow inappropriate objects of study by our best natural science. One such line of attack put forward famously by Jean Hampton (1998) says that metaethical naturalism has trouble dealing with the intrinsic motivating force of moral properties, since allowing for such properties would necessarily commit one to Aristotelean final causes wholly unacceptable to natural science. In what follows, I argue that this line of attack is predicated on an outdated picture of science. Specifically, I argue that recent advances in many areas of biology show that final causes play an indispensable role in our best life science.

My strategy for showing this will be to identify the three central characteristics of final causes set forth by Hampton:

1. “there is a certain place, state of affairs, or kind of motion that is appropriate or “fitting” for an object”. It has a “compelling rightness”.
2. “the object whose movement or state is to be explained is in some way able to respond to this compelling rightness”
3. “the object’s state or movement could be explained by appealing to its sensitivity to this compelling rightness”

I will then go on to show that there is a plausible sense in which a wide range of biological phenomena studied by evolutionary biology, immunology, ecology, and molecular biology meet these characteristics. I conclude that, even if final causes are essential for understanding moral properties, this poses no problem for metaethical naturalism since we can find them in our best science too.

Mapping experimental biology: From the laboratory to the biological world

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To say that the main aim of experimental biology is the description of living system as they occur in nature may sound like something trivial. However, anyone who has seen the operation of a laboratory will realize that it is a highly complex task that never occurs in a direct way, where even skeptical positions could be assumed as to whether we are really knowing a "natural world" independent from the highly artificial environment of the laboratory. In this work we propose to tear down any possible skepticism by taking serious attention to the real practices that are performed in the biological laboratories and proposing a general outline of the process of generation of knowledge in experimental biology.

To achieve this purpose, we argue that the experimental activity in biology can be mapped through four principal landmarks:

1. constrained action,
2. standardization,
3. epistemic "tightening" and
4. extrapolation.

All together, the four landmarks compose a dynamic system that we call the Epistemic Experimental Space (EES), i.e. the space in which experimental knowledge is produced, justified and finally extrapolated to the world "out there".

The first landmark consist in the action of biological theories, background knowledge and different assumptions that, together, constrain the possible actions undertaken in the laboratory and also orient the experimental practices. The second consist in the construction and optimization of stable and reproducible experimental systems that are constituted by a set of highly standardized elements such as instruments, materials, samples, techniques, etc. The third consist in the production of knowledge about epistemic objects (proteins, cells, model organisms or whatever) and its properties, acquired through the operation of experimental systems. To justify the reliability of this knowledge, scientist use many methods, being epistemic robustness one of the most important. Then, finally, this reliable knowledge produced within the walls of the laboratory can be extrapolated to the world outside and eventually used for delivering representations of the "biological nature". Such representations, in the form of biological theories and models, constrain further experimental actions, generating a new cycle inside the EES.

The scheme we are proposing implies that in each of the four landmark different kinds of knowledge are produced. Also each landmark assumes diverse epistemic and ontological assumptions, presents its own theoretical problems and offers its own strategic solutions. And finally, each of the four depends on the other three for its justification and correct attainment. With this map we intend to understand the generation of knowledge in experimental biology in all its complexity and, most important, understanding how scientists manage to justify it.

Pain in psychology, biology and medicine: Some implications for eliminativist and physicalist accounts

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Eliminative materialism states that terms postulated by folk psychology, including subjective experiences, beliefs and other mental states, fail to refer and therefore should be eliminated. This paper provides an analysis of arguments for pain eliminativism from the perspective of contemporary pain research in medicine, biology and psychology.

Although not always explicitly distinguished, three distinct claims are associated with pain eliminativism:

i. pain as measured by self-report tests should be eliminated;

ii. pain concepts postulated by folk psychology and other theory-theory approaches should be eliminated;
iii. pain as a natural kind should be eliminated.

Given the dissatisfaction of eliminative materialists with folk psychology, it is safe to assume that their arguments are primarily meant to support (ii). Some eliminativist arguments are effective in undermining some folk psychological explanations and the pain concepts attached to them. However, since measured, or reported, pain is not clearly distinguished from a folk-psychological concept of pain, (i) is often implied as well. Claim (iii) is supported by arguments stating that what we commonly call "pain" is in fact a complex phenomenon that dissociates into distinct components underpinned by distinct biological mechanisms. What is suggested here is that "pain" is a heterogeneous class lumping together distinct natural kinds.

Arguments for elimination can be classified as follows: analogies with cases from the history of science; conceptual inconsistencies associated with folk intuitions about pain; and the failure to identify pain with biological mechanisms. I object to the first two types of arguments on the grounds that the term "pain", as understood in biomedical research, is not an explanatory concept. Rather, the term is partially operationalized and its extension is empirically defined by means of psychometric tests designed independently of any particular psychological or biological explanation. Thus, even if there are reasons for doubting the explanatory value of pain concepts or for rejecting them because of their incompatibility with accepted explanatory frameworks, this has no bearing on pain as a measurable phenomenon. I reject the third type of arguments by challenging the assumption that biomedical research assumes an identity model of reductive explanation. Instead, I argue, scientific inquiry aims to explain the phenomenon of pain by elucidating its causal mechanisms. If mechanism and pain stand in a relationship of cause and effect, then it is not clear how pain could be identified with or replaced by its causal mechanism.

Finally, I provide a methodological rationale for resisting extreme versions of claim (iii) stating that each instance of pain is underpinned by a singular mechanism. My objection hinges on the notion that empirical research requires a minimal degree of generality in order to describe phenomena, as well as to correctly interpret experimental interventions.

Generalized Darwinism revisited: How a new synthesis changes our view on cultural evolution

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Theories of cultural evolution, dual inheritance theory or generalized Darwinism have been around for some decades now. The idea is that cultural systems obey the same abstract principles of variation, selection and reproduction in their development as biological systems – organisms, genes and populations – do. As well as heavy enthusiasm, like the ability to provide a long expected scientific synthesis for the social sciences (resembling the "modern synthesis" for the life sciences, cf. Mesoudi 2011), such approaches faced severe skepticism and critiques from various directions. Exceptional aspects of cultural transmission – like conformist bias, blending inheritance or guided variation – led some researchers doubt that cultural evolution is truly "evolution". Furthermore, the identification problem of cultural units or variants (memes) and of cultural "generations" seemed to undermine the application of population dynamical or phylogenetic methods for the study of cultural phenomena. But meanwhile, our biological understanding of "evolution" itself has evolved in various directions as well. Aspects like phenotypic plasticity, epigenetic regulation, inclusive inheritance and niche construction seemingly change our view on evolution in direction of an "Extended Synthesis" (cf. Pigliucci/Müller 2005). In this paper, I am going to show that most approaches in the field of cultural evolution today still adopt and assume a very classical notion of evolution as e.g. given by population genetics. I want to argue that many critiques are loosing grip, when we involve a more fine grained notion of cultural "evolution", which takes into account these new findings and makes evolutionary models much more applicable to the study of sociocultural systems. I am going to demonstrate that in three case-studies.

Indigeneity within datasets: DNA sequences journeys and genomic representations about the Karitiana people

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In this talk we describe and analyze the practices and processes through which blood samples from some members of the Karitiana people, an indigenous group in the Western Amazon (Rondônia, Brazil), were transformed into digital DNA sequences, datasets, and increasingly are reused for analytical and comparative purposes in multiple human evolutionary and biomedical studies. In other words, we track the sometimes disembodied but interconnected social lives of tissue, digital data, and Karitiana donors in order to pose important questions about contemporary bio-mapping technologies and indigeneity, understood here broadly as ways of being "indigenous" through time and space. We offer a model about how the materiality of human genomic data enables and silences certain forms of representation (scientific, cultural, and political), while compromising both the epistemic and bioethical robustness of human population genomics. We use the model to propose an alternative mode of governance of genomic datasets between this indigenous community and life-scientists that we call informed co-participation. In this framework, past DNA donors and their descendants play an active role in sanctioning the re-use of stored digital bio-data for new purposes, and also in re-assessing provisional results and population metadata according to their self-fashioned notions of indigeneity. This is a much needed strategy for testing the robustness of datasets and the cultural assumptions that makes them more "real" and less epistemic objects. This mode of governance and collaboration could benefit other ethnic minorities and researchers beyond the field of human genomics.

Meta-parsimony

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My paper introduces meta-parsimony as a means of evaluating both singular and multiple parsimony claims, which are bound to particular context. I begin by laying out first-order parsimony, proceed to introducing the concept of meta-parsimony, and conclude by applying meta-parsimony to two case studies: the first is on non-human animal mindreading debate and the second is on the neutral theory of ecology.

Parsimony is ubiquitously appealed to in the sciences because data routinely underdetermines the task of theory selection. Ambiguity regarding the way in which specific parsimony claims should be used to settle cases of underdetermination however, has lead to error and confusion in a variety of research contexts.

One theory is more parsimonious than another if its simplicity is relevant in a way that gives one reason to prefer it. The relevant simplicity of theory, and the way of counting that comes with it, are both contextually obtained. In this sense parsimony claims are local (Sober 1994). In addition to this, parsimony claims are multiple in so far as they can have distinct aspectual relevance or varying degrees within a singular context (Sober, 1994; Dacey, 2016).

This analysis of parsimony serves as a starting point for the introduction of an evaluative tool that I call meta-parsimony. Meta-parsimony has two primary tasks:

1. to evaluate singular parsimony claims that made in a definite context, and
2. to evaluate multiple parsimony claims that are made in a definite context.

In fulfilling 1), meta-parsimony evaluates the strength of a singular parsimony claim by means of its degree of quantificational restriction in combination with its evidential basis. In fulfilling 2), meta-parsimony adjudicates between multiple parsimony claims that appeal to distinct aspects of a given system by means of the respective parsimony claim's degree of quantificational restriction in combination with its evidential basis. Put slightly differently, in 2) meta-parsimony dictates that, ceteris paribus, the parsimony claim that is the most quantificationally restricted and holds the most evidential strength should be favored.

In the second half of the paper, I formally define meta-parsimony and apply this to two case studies.

This first example pertains to the non-human animal mindreading debate, which centers around the question of whether or not animals can identify and use the mental states of other creatures. Within this context I put the second task of meta-parsimony to work and evaluate multiple parsimony claims that are made within a particular context. This second task pertains to the debate on the neutral theory of ecology, which aims to determine whether or not an analysis of the distributions of relative species abundance should include the influence of selection (Hubbell 2001, 2006). Within this context I put the first objective of meta-parsimony to work and evaluate the strength of a singular parsimony claim.

Dynamic natural kinds

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Recent scientific results on data-driven classifying by clustering are philosophically interesting because the clusters and their associated classifications are dynamic and change over time. While traditional classifications are constructed by human experts, the new cluster-based classifications of technologies critically rely on sophisticated computational tools sifting for patterns in huge data sources. For example, Packard et al. (2018) classify how technology evolves by analyzing millions of digitized patent records with Google's software for real-time natural language translation (Le and Mikolov 2014). This cluster-based classification of technology illustrates the ontic and epistemic implications of the smart, data-driven computational tools that produce contemporary scientific classifications. The classes in traditional classifications are fixed and have a static set of essential characteristics, but the clusters in the new classifications are dynamic; some persist, others disappear, new ones arise, some divide, and others merge and fuse. These clusters share important epistemic properties with traditional natural kinds; for example, locating something in a particular cluster can help us to explain and predict certain things about it. But the clusters differ from traditional natural kinds precisely because they are dynamic. The dynamic ontology implied by these clusters is much more contingent and open-ended than the static ontology implied by traditional natural kinds.

The new cluster-based classifications differ in important respects from previous approaches to classifying by clustering. For example, the approach to biological classification called phenetics (Sneath and Sokal 1973) aims to classify organisms according to the overall similarity of their properties. However, when assessing overall similarity, it would be naïve to give the same weight to all properties, and in practice there is no consensus about the proper weight to assign to individual properties. The new classifications have no analogous problems because the properties are chosen and weighted for principled reasons with few theoretical presuppositions and minimal human bias. A second problem with phenetics and related views is that classifying organisms based on overall similarity would create separate "species" for males and females, and separate "species" for juveniles and adults. The new classification methods side-step these problems because the clusters exist in an abstract feature space that allows nearby entities to have many different properties.

There is little consensus about natural kinds today but one of the most prominent positions is Richard Boyd's view that natural kinds are "homeostatic property clusters" that are stabilized by internal "isolating mechanisms" (Boyd 1991, 1999). The homeostatic property cluster (HPC) view is attractive because cluster membership can be a matter of degree and because clusters can overlap, and the new dynamic cluster-based classifications share these virtues with HPC, but they also have important differences. One is that, while HPCs are typically described in terms that are quite abstract, vague, and hypothetical, the new dynamic cluster-based classifications are grounded in very specific, empirically measurable properties. But the most important difference is that, where Boyd emphasizes the stability and "homeostasis" of property clusters and the HPC view presumes that each specific natural kind has a specific internal mechanism that creates and preserves its cluster's stability, the dynamic cluster-based classifications stress that the clusters are dynamic.

The womb and the war: The construction of women's body and the conscription of women to military service

Erela Teharlev Ben-Shachar, Bar-Ilan Universit and Open University, Israel

This lecture will delineate an example of the co-production of the feminine/women physiology and the Israeli society in wartime. The lecture is based on Science and Technology Studies (STS) theories that assume that medical and biological conceptions of the human physiology are entangled with conceptions of society. Specifically, the perception of the body is co-produced with the ideal of man (and woman), with the historical and political context, with power relations between men and women and more. This lecture will focus on the way the conception of Israeli medical doctors regarding the women's womb changed as the expected role of women in the army changed. This would be described through the writings of Dr. Shulamit Tolchinsky, a female sport-medicine doctor that was active in Israel during the 1940's. The texts Dr. Tolchinsky has published along this decade, a decade that was full of disputes about the part women should take in the military effort, reveal a transformation of the conception of the female body. This body that was regarded most of the Pre-state era as fragile, gentle, not fit for pioneers' jobs and for nation buildings' activities have seem to change as the Independent War was approaching. All along the 40's as the belief that women should be recruited grew stronger, and their part in the militia (the Palmach) got larger, the feminine body was thought to be less fragile, more plastic (being able to get stronger with exercise) and its internal organs – mainly the womb, were captured as more sturdy. This case study shows how medical perceptions are interwoven with conceptions about women's roles and the part they are supposed to take in society.

Explaining body's disruption and natural death. A late-medieval paradigm shift

Chiara Beneduce, University Campus Bio-Medico of Rome, Italy

The explanation of ageing, body's disruption, and corporeal death has been a long-lasting theoretical issue at the intersection of philosophy and science [De Ceglia 2016]. In the pre-modern thought, the topic was specifically addressed in natural-philosophical and medical debates on the biological aspects of living organism. Since the Greek Antiquity and throughout the Arabic and Latin Middle Ages, two key-concepts were at the very basis of the explanation of bodily deterioration and death: "radical moisture" *(humidum radicale)* and "nutrimental moisture" *(humidum nutrimentale* or *cibale).* Radical moisture is a corporeal humidity (proper to living beings from conception) that plays the role of fuel in the consumption of the body's natural heat. Nutrimental moisture is a humidity acquired by food assumption, which has the role to restore radical moisture as a remedy to its consumption. Natural death occurs when nutrimental moisture becomes ineffective in its restorative role. The origin, characteristics, and ways of interaction of radical and nutrimental moisture have been widely debated and variously interpreted in the pre-modern science. Nonetheless, they stand as a widespread general paradigm to explain body's disruption and natural death for many centuries [Crisciani and Ferrari 2010, Crisciani 2005, Dunne 2009, Ferrari 2013, Hall 1971, Jacquart 2006, Marinozzi 2010, McVaugh 1974, Moreau 2015, Reynolds 1999].

In this paper, I formulate the following hypothesis: in the discussions of bodily deterioration and corporeal death, a different explanatory paradigm started occurring in the Late-medieval and Renaissance biological teachings on the living organism. Another conceptual couple substituted the radical and nutrimental moistures: "fluid moisture" *(humidum fluens)* and "consolidated moisture" *(humidum consolidatum)* are found in the medical and natural-philosophical explanations of natural death, especially in the commentary tradition of the *Parva Naturalia,* at least starting from the fourteenth century and well into the sixteenth century. With this substitution of concepts, the explanatory model to account for bodily deterioration and death also changed in a evident way. While previous explanations were based on the description of the interaction between two substances (radical moisture and nutrimental moisture), in the new explanatory paradigm fluid and consolidated moistures are taken as different viewpoints to describe natural death as a unified phenomenon, in terms of a general drying up and consolidation of the body.

This paper is a case-study within a broader research plan: a throughout study of models of medical explanation in late-medieval and Renaissance science. This historical-philosophical research agenda could especially provide a stronger theoretical background to the flourishing debates on "explanations in medicine" as they are currently set up in contemporary Philosophy of medicine [Reiss and Ankeny 2016].

Evolution's invisible hand? From Adam Smith to contemporary evolutionary biology

Nicola Bertoldi, University of Paris 1 Panthéon-Sorbonne, France

Coined by Adam Smith (1759) and tightly associated with both classical and neoclassical economic thought, the metaphor of the "invisible hand" visualises a recurrent topos in the history of ideas, i.e. the assumption that any form of order and harmony at the collective level results from interactions among individuals pursuing their purposes. Such a motif also seems to be found in Charles Darwin's (1859) argument for natural selection, i.e. that new biological species and higher taxa emerge from the progressive accumulation of spontaneous individual mutations, which are better adapted to changing local environments, across many generations. Although such an analogy appears warranted by Darwin's sources of inspiration (Bowler 1983), its meaningfulness remains questionable. Since the image of the invisible hand was first devised to explain the unintended consequences of voluntary actions, to which extent does it apply to natural phenomena? This paper aims at answering this question by outlining criteria for comparing the way in which the "invisible hand analogy" can be formalised in economic theories with the way in which this same analogy can be rigorously applied to evolutionary biology. This question is all the more relevant that economists such as Johnson, Price and Van Vugt (2013) have attempted to redefine the notion of the invisible hand precisely within a Darwinian framework, which relies on multi-level selection theory. Our analysis will thus focus on E. O. Wilson's (1975) sociobiology, and Stephen Jay Gould (2007) and Niles Eldredge's punctuated equilibrium theory, i.e. two attempts to revise Darwin's theory by addressing the problem of the emergence of collective properties (social behaviour and speciation) from individual ones, which ascribe very different roles to the action natural selection. More precisely, this analysis will aim at identifying the conditions under which the analogy with Smith's invisible hand is meaningful within the framework of both theories.

Stability and the looping effects of human kinds

Riana Betzler, University of Cambridge, UK

How to distinguish natural kinds—and whether there exists a substantive difference between natural and social or human kinds—is a longstanding problem in the philosophy of science. Recently, there has been a trend of thinking of natural kinds as grounded in scientific practice; these kinds of accounts place emphasis on the epistemic value of attributing natural kindhood to entities. They capture what "natural kind" is supposed to be doing—that is, enabling reliable inference. In this paper, I focus on one such account—Matthew Slater's (2015) Stability Property Cluster (SPC) account of natural kindness.

This account has many virtues. It foregrounds—rightly, I think—the issue of stability as central to natural kind ascriptions. It avoids widely-acknowledged problems with traditional essentialist accounts, thereby framing itself as ripe for use within the life sciences. It also advertises itself as being more flexible than Boyd's

Homeostatic Property Cluster (HPC) account—which has enjoyed a kind of orthodoxy in the life sciences—insofar as it is able to find stability without reference to mechanisms. It is also domain-relative, or able to be tuned to the specific requirements of different areas of inquiry. While this does not provide us with a universal notion of "natural kind," it does help to account for the plurality of natural kind concepts currently existing within the field; it does so by explicitly acknowledging that there are specific aims, interests, and norms being captured by the use of "natural kind" across different disciplines. These features, I argue, indicate that the account holds promise.

I ask, however, how it fares within the human and social sciences, especially in the face of Ian Hacking's (1995) "looping effects." Hacking's central worry about looping effects is that they are destabilising; because the targets of the human sciences change in response to classification, they are "moving targets." This undermines the potential for stable knowledge about them. Given that stability is the central feature of Slater's account, it seems as though the existence of such looping effects within the human sciences would preclude its applicability there. If human kinds truly are "moving targets" in Hacking's sense, they cannot count as natural kinds for Slater. I suggest that this is a potential pitfall of the account, since there are good reasons for resisting a sharp division between natural and human kinds (see e.g., Cooper, 2004). I then go on to consider ways in which we might deal with such looping effects.

You can be Jane Goodall: The history behind today's far-reaching campaigns encouraging K-12 girls to pursue biology careers, 1960s–today

Amy Sue Bix, Iowa State University, USA

One of today's most notable aspects of education is the rapid spread of high-visibility campaigns to draw more young women into biology and other STEM careers. Across the US, volunteers with "Young Women in Bio," wearing pink labcoats, host dozens of workshops, tours, and demonstrations to stimulate girls' interest in genetics, molecular biology, plant-sciences, and more. Parents can enroll daughters in multiplying special initiatives, such as the University of Illinois's NSF-funded "Girls Explore Biology" camps, Minnesota's "Girls Solve It! With Mathematical Biology," Wheaton's "Bioengineering for Girls," and Missouri's "Women in Wildlife." The Girl Scouts heavily promote new environmental learning and "naturalist" badges. Children's biographies of Jane Goodall, Temple Grandin, Maria Merian, Rosalyn Yalow, Mary Anning, Gertrude Elion, Eugenie Clark, all promise to inspire girls' enthusiasm for biology. Commercializing the message of helping K-12 girls embrace an identity as future life-science professionals, Lego sells female oceanographer minifigures, the UK's Lottie offers female paleontologist dolls, and Disney promotes DocMcStuffins.

Starting in 2016, the United Nations began marking February 11 as the annual International Day of Girls and Women in Science, emphasizing the urgency of "dismantling barriers" to gender parity and helping "girls to believe in themselves as scientists." Reaching worldwide, groups such as the UK-based STEMettes gather adult women in biology and other sciences to mentor younger girls, promote girls' STEM potential, and run STEM camps in Nambia, Peru, Malawi, and beyond.

Though widespread today, few such efforts to encourage girls' aspirations to ambitious careers in biology and other STEM fields existed just a few decades ago. This paper analyzes the history of how, when, and why scientific societies, educational institutions, non-profits, and other actors began devoting intensive effort to girls' outreach. The story of this dramatic shift is complex, both reflecting and driving changes in gender relations, plus escalating concern for girls' psychological well-being and personal opportunities.

The history of girls' STEM advocacy underlines the significance of unpacking disciplinary divergences. In the US and certain other nations, under-representation of women persists far more severely in physics, computer science, and some engineering disciplines than in biology. Nevertheless, current conditions in life sciences still spark concern. In Norway, the US, and elsewhere, girls-education advocates direct attention to ongoing "leaky pipeline" problems and stereotypes that result in female under-employment, particularly in academic biology ranks. Observers have particularly noted gender gaps in certain specialties, such as neuroscience. The gendering of environmental studies and biomedical engineering programs represents especially significant historical and present-day case-studies.

This paper focuses on such case-studies in biological sciences, past and present, connecting this history of biology to a broader account of the girls' STEM advocacy movement. The talk draws on archival material from the NSF, AAUW, Girl Scouts, plus primary-sources from other countries, exploring the origins, explosive growth, and limits of programs to encourage girls to enter biology and other STEM fields.

Artificial and natural reconstructions of evolution in the study of lateral gene transfer

Cédric Blais, University of King's College & Dalhousie University, Canada

The material character of science has been of growing concern to historians in recent years, as scholars look to its instruments, sites, collections and practices. This paper contributes to a material history of biology by examining the intermingling of instrumentality with evolution in the laboratory development of lateral gene transfer (LGT) research. Far from simply being an abstract theory underpinning systematics, evolution has become over the past century an instrumental process whose biological and epistemological standing has evolved with the material methods of scientists. The relation between artificial (instrumental) and natural selection inaugurated by Darwin has long underpinned the division between laboratory work and fieldwork, wherein the former was delineated as the site for the study of genetic mechanisms and mutations, whereas the latter investigated "natural" evolutionary events. The mid-century rise of molecular biology and the subsequent ascent of "genomics", documented by Edna Suárez-Díaz and Michael Dietrich, have transformed this division and styles of labour. The new molecular science brought both artificial and natural evolution into the laboratory, thanks to the construction of new objects and instruments such as genomes, gene trees and molecular clocks. The material organization of the new evolutionary science is exemplified by the research carried out in the laboratory of John Archibald, one of the leading sites where the genomic study of lateral gene transfer is participating in “cutting down the tree of life”. As this paper will show, LGT provides a rich case study to examine the new instrumental methodologies of evolutionary studies, allowing us to watch in real-time as researchers re-negotiates existing material practices. Indeed, the core of LGT research, genomics, is a site of contention. Critics argue that LGT may be an artefact of genome analysis, and that genomic data alone is not sufficient to establish its occurrence. This controversy points to the contemporary ramifications and transformations of the founding debate of molecular biology, which pitted organisms against molecules as the fundamental site of evolution. Researchers in the Archibald lab do not re-iterate the old debate so much as they negotiate anew the relation between organisms, molecules, and the instruments that underpin evolution. Central to this effort is their attempt to go beyond genomic data by “artificially” recreating lateral transfer events in lab-based organisms, which may then act as biologically significant reconstructions of “natural” evolutionary processes. Bringing a participant observer account of this still emerging – and unresolved – research in conversation with a material examination of the history of LGT and molecular biology, this paper will explore the shifting relationship between “artificial” and “natural” evolutionary events in the laboratory. Doing so, it will highlight the instrumental character of evolution in laboratory research.

A feeling for the neuron: The status of the “discrete-gating picture” in Hodgkin and Huxley’s model of the action potential

Andrew Bollhagen, University of California, USA

In “What was Hodgkin and Huxley’s Achievement,” Arnon Levy identifies what he calls the “discrete gating picture” – a highly underspecific physical interpretation of the differential equations that constitute HH's model of the action potential. Importantly, for my purposes, the discrete gating picture was never explicitly presented in HH's published work. Nonetheless, it figured significantly in their own ongoing research program and had a considerable influence on neuroscientific research that followed in their wake. In short, while it was never made part of the publicly available paraphernalia of science, it nonetheless served to structure HH's work and research to follow. In this paper, I inquire into the status of the discrete gating picture and its relation to HH's explicitly formulated and published differential equations. I suggest an account on which the discrete-gating picture served as an underspecific and non-discursive sense of the neuron's mechanical dynamics. The discrete-gating picture, on my account, is a "feeling for the neuron" that was articulated and communicated in the form of HH's differential equations.

Whither the biosocial? Local epistemic goals and collective interests in integrative biosocial research

Olesya Bondarenko, University of Cambridge, UK

In the last decades, integrated biosocial theories and models have proliferated in various fields of science, reflecting the "interactionist consensus" on the importance of both biological and socio-environmental causes in the development of many human traits. However, Keller (2016) has recently expressed the worry that scientists engaged in such research have largely ignored the causal importance of sociocultural factors, "hijacking" biosocial integration in a way which suits the purposes of biological sciences. How can we respond to this problem? One way of approaching it is to maintain that the "biosocial" will always remain a highly local project (or, rather, a number of highly local projects) attuned to the epistemic goals in specific areas of science. In this paper, I argue that this is not a satisfactory response for two reasons. One is that such goals may be historically contingent and do not necessarily reflect the interests that the broader socio-epistemic community may have with regard to biosocial integration. I outline who the participants in this socio-epistemic community may be and what interests are relevant here. By using a rather broad definition of "interests", I aim to do justice both to the value of theoretical research and to the usefulness of specific lines of biosocial inquiry for policymaking. The second reason is that the biosocial approach inevitably loses its potential as a source of scientific novelty if it becomes caught up in the existing disciplinary paradigms. I end by illustrating the above reflections with a case study of biosocial research on human behaviour.

Evolution in contention: The mobilization of scientific creationism in Mexico (1973–2000)

Jorge Armando Romo Bonilla, National Autonomous University of Mexico, Mexico

Since the 1980s, philosophers, historian, and biologists have become increasingly concerned about the surge of creationism in the United States. Most of the scholarship on this subject has suggested that creationism an American phenomenon, though others, like the historian of science and religion Ronald Numbers, have warned that the movement is a more global phenomenon. Creationism and creationists activities have reached countries as diverse as Brazil, South Korea, Saudi Arabia, and Mexico. It is an adaptable movement, one that travels across many borders.

Numbers' work, however, addresses the topic of creationism in Latin America as a decontextualized phenomenon, and as a chemical substance diffusing across the globe. A contextualized history of creationism, in contrast, requires us to understand the sociopolitical and religious context in which creationist actors and their tools (leaflets, public conferences, and workshops) move, regardless of the absence of factors that have been seen as necessary conditions for its growth –for instance, evangelical churches and a tradition of literal Biblical reading supposedly absent in Catholic countries.

My research recognizes that that Creationism is not an isolated phenomenon, and it has arrived in Mexico: actors and practices are mobilizing across the permeable border between the United States and Mexico, and taking roots in the southern country. In this presentation, I will focus on the strategies adopted by creationists in order to move creationism across the Rio Bravo/Rio Grande border. To do that, I focus on two influential representatives and fellow travelers of this movement: Mexican creationist Rubén Berra and John Morris Pendleton, who have dedicated their lives to organizing conferences, national congresses, and mobilize creationist ideas through the writing and translation of magazines, brochures, and websites. My aim is to show how these actors have configured creationist's ideas and practices in Mexico, but in doing so, they have become part of itinerant creationism which is fit to confront the secular tradition in Mexican stated-ruled education. Finally, I will give some element to open the discussion and pose an important question: can we talk about a Mexican Creationism?

A historical epistemology for contemporary phage therapy

Thomas Bonnin, Université de Bordeaux, France

Bacteriophages (or phages) are viruses that have bacteria as their hosts. Discovered a century ago, and rapidly used as therapeutic agents to treat bacterial infections, they were nevertheless eclipsed by the massive rise of antibiotics from the 1940s onward. Faced with today's major public health scourge of antimicrobial resistance, some scientists and physicians are attempting to rekindle and develop therapeutic phages, encountering considerable difficulties along the way. The "Anthropo_Phages" research project, designed and led by Charlotte Brives at the University of Bordeaux, aims to track the variety of factors (epistemic, economic, regulatory, cultural …) at stake in the renewed interest about this type of therapy in western European countries.

In this talk, I present my contribution to the project, which aims to elucidate the historical foundations to contemporary phage therapy. Where do these contemporary practices come from and where did contemporary practitioners learn their trade? Where did they get their material, instruments and protocols? To answer these questions is to unravel the role of different actors involved in the survival of phage therapy through its eclipse in Western Europe in the second half of the 20th century. Potential actors include (a) research and medical centres from the former Soviet Union countries (especially the Eliava Center in Tbilisi, Georgia); (b) research centres studying phages as a model organism for molecular biology; (c) research centres studying the physiology of phages.

To carry out this jointly historical and philosophical work, I develop a framework inspired by historical epistemology and recent works in the philosophy of scientific practice. This includes Leonelli and Ankeny's work on "repertoire", Rheinberger's "experimental systems" and Chang's "systems of practice". These approaches provide me with conceptual tools that help me defining the subject of my historical investigations. My work is also "indirectly empirical", in the sense it will benefit from the rich ethnographic work carried out by other members of project. I conclude this presentation with a sketch of some of the initial results.

Gender and the measurement of fertility: A case study in critical metrology

Marion Boulicault, Massachusetts Institute of Technology, USA

Human fertility is in an apparent state of crisis. In July 2017, scientists reported that sperm counts among men from North America, Europe and Australia have decreased by 50–60 % since 1973, with no sign of halting (Levine et al. 2017). For women, the story is bleak and familiar: women's fertility decreases with age, yet women are waiting longer than ever to have children (Kincaid 2015). In this paper, I investigate this apparent fertility crisis by analyzing the seemingly mundane practice of measurement, i.e. the standards, methods and instruments by which the phenomenon of fertility is quantified. By comparing two widely-used fertility measures – semen analysis in men, and ovarian reserve testing (ORT) in women – I argue that socio-cultural ideas about gender play a significant role in constructing fertility as a measurable phenomenon. Different temporal assumptions implicit in semen analysis and ORT reflect and enforce a view of women as more responsible for – and therefore more to blame for – infertility than men. I conclude by arguing that, in the case of semen analysis and ORT, it's not just fertility that's being measured, but degrees of adherence to entrenched norms of masculinity and femininity (Almeling 2011).

This paper also has a methodological aim. Significant philosophical attention has been paid to measurement as a metaphysical and epistemological phenomenon (see Tal (2017) for an overview). Following philosophers like Ian Hacking (1999) and Anna Alexandrova (2017), this paper calls for greater attention to the socio-political and ethical dimensions of scientific measurement. What role does measurement play in the creation and maintenance of social norms and, conversely, how are social norms reflected in our measurement practices? How can we best conceptualize and investigate the intersection of measurement and oppression? Answering these questions, I contend, requires an interdisciplinary approach that conceptualizes measurement as a social and material practice. This approach – which I call "critical metrology" – is what I develop and aim to demonstrate through the case study of fertility measurement.

The chimerical nature of scientific theories

Michael Bradie, Bowling Green State University, USA

In her 2000 book, *Who wrote the Book of Life?: A History of the Genetic Code,* Lily Kay argues that the fact that the "Book of Life" is characterized as a "Book" and that the DNA-protein connection is taken to be a "code" is somewhat of a historical accident. The biological particulars, DNA, RNA, the 4 bases and the 20 amino acids, were known in the 1920s. But the correlation was not a pressing problem because the prevailing view was that genetic specificity was due to proteins. Had the correlations been investigated and resolved in the 1920s, the resulting characterization would likely not have been in terms of information, messages, or codes because such a framework did not exist then. It was only after WWII and the cybernetic revolution that such language became the dominant lens by means of which to characterize biological processes. So, our "informational" understanding of genetics is a cultural artefact and this gives credence to Kay's characterization of the Book of Life as a Chimera – a culturally constrained characterization of some natural processes. The use of the informational metaphor to characterize the processes of DNA replication and transcription has fallen somewhat out of favor and been replaced, often, by the metaphor (de jour) of "mechanism". So, the Book of Life, as currently understood, is not so much a collection of "codes" as a collection of "mechanisms". I want to suggest that Kay's point can be generalized. Scientific theories, as characterizations of natural phenomena, all invoke metaphors to describe and explain. As such, I will argue that all scientific theories are chimerical, amalgams of natural and cultural factors. To the extent that this model of understanding blurs the distinction between nature and culture, it promises, among other things, to provide a new twist to one of Thomas Kuhn's more controversial claims, namely, that scientists who work in different paradigms live in different worlds.

Shark attack! The sensationalizing of ecological issues

Martin Bremer, Florida State University, USA

Scientific issues surrounding the environment can be misunderstood and politicized to the detriment of all. Perceptions of environmental issues are susceptible to individual bias which can lead to distrust of scientists and educators. Visceral attachment to sentiment undermines scientific evidence. Shark attacks provoke a guttural fear of the unknown and unseen, yet they only account for 6–15 deaths per year, globally. Shark attacks provoke an unnecessarily large and destructive response including shark culls and the deaths of thousands of sharks. Anthropocentric climate change is gradual enough that people do not notice the day-to-day effects creating an apathy toward and confusion regarding the serious threats to environmental, global health. Using Florida as a focal point, this presentation will explore the public perception of the environment and the lack of educational focus on the environment; and distrust of scientific data. Ultimately, I argue for active engagement with the environment as a means of educating people about environmental concerns locally. Discussion will include historic examples of environmental engagement in Florida leading to important scientific work, as well as the current status of environmental engagement in Florida.

Types or traits? Typal personality disorder constructs in DSM-5 as natural kinds

Danielle Brown, University of Alberta, Canada

In response to conceptual, empirical, and practical challenges regarding the status and diagnosis of personality disorders in the DSM-IV-TR (2000), the section on personality disorders in DSM-5 (2013) has been revised to include two approaches of classifying and diagnosing personality disorders. The first approach is largely consistent with categorical, symptom-based model of the DSM-IV-TR. The alternative model for personality disorders (AMPD), included the "Emerging Methods and Models" section of the DSM-5, is a hybrid dimension/categorical model that represents the six clinically recognized typal personality disorders as specific pathological variants of a totalizing personality structure organized according to the trait-based Five-Factor Model. While the shift towards a dimensional understanding of personality disorders has achieved considerable empirical support, concern has been raised that the hybrid-model of the AMPD may present additional conceptual and empirical challenges. One of these challenges concerns the present status and significance of the six retained typal disorder categories represented on the AMPD's dimensional-trait model. Proponents of the move toward a purely dimension-trait model (Livesley, 2012) suggest that these "types" should be viewed as holdovers from a deficient taxonomy, and that if personality disorders are to be understood as "types" at all, they should be continuous types organized with respect to the underlying personality dimensions affected. On the other side, proponents of the DSM-IV typal categories (Shedler et al., 2010) maintain that these types are meaningful clinical constructs that describe not only reoccurring clusters of traits, but deeper psychological processes, etiological patterns, and prototypes against which all other cases of personality dysfunction can be compared. In this paper, I examine the conceptual issues bearing on this classificatory controversy, specifically focusing on the introduction of the concept of personality as a structural category in DSM-5 and how this development has affected (and may continue to affect) the foundation upon which we divide the terrain of mental illness and pick out clusters of symptoms thought to constitute disorder kinds. In particular, I argue that one of the challenges confronting an account of personality disorders as natural kinds are issues arising from the conflicting conceptual frameworks of the DSM-IV categorical model and the AMPD.

Extrapolation and cascading uncertainty across dynamical scales in modelling: From ecological modelling to climate downscaling

Kimberly Brumble, University of Calgary, Canada

The articulation of and propagation of irreducible and heterogeneous uncertainty in climate modelling is a fundamental challenge for climate modellers and for those who use climate models to make science-informed decisions to mitigate climate change. However, methods currently employed in climate modelling to articulate and reconcile uncertainty between model scales (global, regional, and local) rarely present uncertainty in forms which can be handled productively as climate information is downscaled through the modelling process. This dissertation uses the tools of philosophy of science and philosophy of modelling to create a taxonomy of the sources of uncertainty encountered by climate modellers at each of these modelling scales. Considering advances from decision theory and environmental sciences in categorizing and handling heterogeneous uncertainties for policy, this project analyzes the form of scientific inference involved in climate downscaling. Philosophy of modelling allows for the analysis of and identification of best practices for extrapolating information under heterogeneous types of uncertainty and across spatial scales. I suggest that extrapolation inferences from spatial scaling in ecological modelling as a novel statistical, conceptual, and inferential approach to this problem. I suggest that climate downscaling follow localized ecological impacts studies and hydrological impacts studies in adopting the co-production of knowledge structure; collaborations between climate modelers, impacts studies, and decision makers are presented as ways to bridge the gap between specializations and reduce many of the sources of heterogeneous uncertainties which arise across scales.

Thou doth process too much: Why process ontology of biology should halt the war on machines and learn to love technology

Tyler David Price Brunet, University of Cambridge, UK

Recent years have seen growing contributions to Process Ontology (e.g. Dupré 2013; Nicholson and Dupré 2018). One persistent source of justification for a process ontology of biology is that it can displace the (wrongheaded, entrenched, Cartesian) idea that organisms are, or should be understood as, complex machines. This takes the form of arguing for a fundamental distinction between machines and organisms: unlike machines that are understood as mechanisms, organisms can only be understood as processes. This argument might seem to bolster process ontology of biology. Instead I argue that it threatens it. If machines cannot be understood as processes, then process ontology fails as a general metaphysics of the sciences. To keep the metaphysics behind process ontology of biology, we also need a process ontology of technology. I will argue that process ontology fails to distinguish machines from organisms. First, I show that the arguments for a process based distinction fail to properly account for technological and biological diversity. The fluidity and dynamicity of some machines is often underestimated, while that of some organisms is overestimated. Second, I will provide a sketch of a process ontology for machines. The features sometimes assumed specific to process ontology of biology, such as the invocation of underlying change to explain surface-level stasis, and the role of hierarchical processes of stabilization, apply equally well to many modern machines.

Religious signalling as an evolutionary explanation: What formal modelling can add

Carl Brusse, University of Sydney, Australia

In this paper I discuss three questions raised by the application of signalling theory to religion; outlining formal modelling approaches and presenting simulation results which attempt to address them.

Many naturalistic explanations of see religion as maladaptive at the individual level, the result either of indirect evolutionary forces (such as group selection or cultural evolution) or else the accidental by-product of traits selected for in different contexts. Not so the signalling theory of religion, which posits that religious practices arose to help solve coordination and assurance problems with respect to cooperation – upregulating positive assortment (and fitness) of prosocial individuals. The prediction is that religious practices co-evolved with complex sociality, in a runaway process driven by individual-level fitness advantages.

However, despite its explicit appeal to evolutionary signalling theory, proponents of religious signalling theory seldom delve deeply into the recent formal literature on signalling (in biology and elsewhere). This has arguably led to some conceptual and terminological confusion, but also to missed opportunities: there is scope for more precise and target-apt signalling models to be investigated, and this paper aims to demonstrate ways forward in this regard.

I will provide a brief overview the application of signalling theory to religion, motivating three worries that formal modelling can address: i) asymmetries in sender-receiver evolutionary dynamics, ii) the conditions under which different signal forms are likely to evolve, and iii) the plausibility of the signalling-cooperation co-evolutionary explanation. Finally, I present the results of some relevant simulation work. While these results are far from definitive, they at least offer a case study of how the modification of abstract models to better fit their target systems can offer alternative insights into evolutionary theories and their explanatory potential.

B. Spinoza and J. P. Müller: How the Dutch philosopher inspired the father of contemporary physiology

Filip Adolf Albert Buyse, CSMBR, Pisa

It is hard to believe that, in recent publications, nobody has really examined yet why “the father of contemporary physiology” quotes so explicitly from Spinoza’s work and refers to it at different stages of his impressive career. This is even double remarkable, given the fact that during the last decades there is much interest in Spinoza’s philosophy among contemporary biologists such as Antonio Damasio, Henri Atlan and Jean Pierre Changeux who argue that the Dutch philosopher (1632–1677) anticipated modern biological thinking. Likewise, it is amazing that Spinoza’s name is completely absent in several important biographies of Johannes Peter Müller (1801–1858).

This paper aims at filling this striking lacuna by investigating the relation between Spinoza’s sensory philosophy and Johannes Peter Müller’s sensory physiology. After having resolved some misunderstanding concerning Johann Müller’s name, it examines in the second section, when and where precisely J. P. Müller mentions Spinoza (1632–1677) in his works. In a third section, it tries to find out why Müller applies the ideas of the Dutch philosopher rather than those of other influential early modern philosophers This part explores several elements of Spinoza’s philosophy and claims that especially his innovative ideas on memory and his views on the affections of the body played an important role. However, this paper argues that also elements from Spinoza’s metaphysics were playing an important role even though the 19th-century physiologist only seems to quote from his epistemology and his theory of emotions, being afraid to be accused of Spinozism.

Müller’s main work Handbuch der Physiologie des Menschen (1837 & 1840) was in 1845 translated in French and between 1838 and

1842 in English so that his ideas spread rapidly in Western Europe. This paper will help not only to clarify the relationship between the Copley-medal winner and Spinoza but also that between Müller and the myriad physiologists who were subsequently inspired by his work.

Self-organization as level property: Towards a non-eliminativist reducctionist approach to organizational closure

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One of the key concepts to describe biological complex systems is self-organization, understood as a process in which local interactions among the components of a system produce emerging behavioral patterns without any external coercion (Anderson 2002, 248–249). This notion of self-organization has led several authors to argue that a distinctive characteristic of living beings is that they performs an organizational closure, whose theoretical description necessarily involves the postulation of ontologically irreducible emerging properties. The identification of an organizational closure in the organisms presupposes the performance of a coordinated constrictive action of the component entities of the system that, seen only from a macro perspective, can be interpreted as giving rise to biological self-maintenance (see, for instance, Mossio, Bich, y Moreno 2013).

The goal of this paper is to address organizational closure as a level property from a perspective that interprets the levels at which a complex system can be analyzed as intervals of quasi-decompositionality (Simon 1961, Cáceres & Saborido 2017, 2018). Thus, we defend that, according to this interpretation, the organizational approach can be seen as a very fruitful research program to explain living systems, and other complex systems, but without the metaphysical burden that is often glimpsed.

To do this, we will first develop an approach based on the idea of level as interval of quasi-decompositionality, which serves to describe level features as modeled properties of the entities that make up a system at a given level. Second, we will clarify how emerging properties can be treated as level properties and how interlevel causation can also be explained from this perspective. Thirdly, we will relate the ideas of organizational closure with that of level properties and we will argue that self-organization is not really an emerging characteristic of biological systems, but a macroscopic consequence deducible from the microscopic properties of component elements.

In conclusion, we claim that the concept of interval of quasi-decompositionality is a theoretical tool that allows us to characterize the organizational closure as a reducible level property, and which lays the basis for developing a non eliminativist reductionist approach to the organizational features of living beings in philosophy of biology.

The exposome as a postgenomic repertoire: Exploring scientific change in contemporary epidemiology

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In the last decade, a new notion has emerged in epidemiology: the "exposome". The exposome is a way to describe and characterise the totality of exposures experienced by individuals, distinguished between: generic external (e.g. social capital), specific external (e.g. environmental pollutants) and internal exposure (e.g. oxidative stress). The exposome is considered and presented as a highly innovative, a new paradigm for epidemiological research.

However, I argue that the innovation of the exposome is better captured by the notion of repertoire. In this framework, scientific innovation is connected to conceptual, institutional, material, technological, organisational and economic elements of scientific research. I use the framework to argue that the exposome is based on the alignment of conceptual, material and social components. At the conceptual level, the repertoire is built on a commitment to understanding exposure as a dynamic and multi-layered issue, which implies an expansion of the notion and a broad characterisation of environment. At the methodological, technological and material level, the repertoire employs omic technologies developed in the genomic context and the study of biomarkers, which have significant influences on the size of datasets and interdisciplinary. At a social and institutional level, the repertoire is organised in short-term projects with the funding framing of public and environmental health and disease risk.

The specification of the components of the exposome allows me to show how many of these components have been transferred from other lines of research, including: the sequencing repertoire, that emerged in the genomic context and has since then increasingly spread in the life and health sciences; exposure science, i.e. the discipline that studies human contact with external agents; and the biomarkers approach, which studies elements or characteristics that can be precisely measured and used as indicators of various processes. I show that the exposome repertoire is thus the result of the repurposing of these approaches for new audiences.

The analysis of the conceptual and material background of the exposome leads me to engage with discussions on innovation in the life and health sciences. I specify my claim and argue that the exposome can be considered a "postgenomic" repertoire. I use the term with a historical meaning, to describe research that employs genomic-based technologies, is increasingly aware of the complexity in interpreting genomic results and has a critical engagement with gene-centric approaches. On this basis, I discuss conceptual implications on notions of exposure and environment and the epistemic impact of large omic datasets, thus connecting my account to discussions on the innovative character of postgenomics at conceptual and methodological levels.

What is evidence for sustainability? Engaging theories and shaping practices in sustainability science

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Christopher Luederitz, University of Waterloo, Canada
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Sustainability science is an emerging interdisciplinary field dealing with wicked problems of our time, from anthropogenic climate change to loss of biodiversity, pandemics, and rapid urbanization. One the main aspirations of this field is to create evidence-based knowledge that can contribute to achieving more sustainable futures. This knowledge should be action-oriented as it aims to support and inform interventions towards sustainability, rather than just explain the causes of (un)sustainability. In recent years, sustainability science has emphasized the importance of real-world sustainability experiments that take place at the science-society interface and include multiple academic and societal actors. These experiments initiate change towards sustainability and aim to generate knowledge and evidence about processes of social change towards more sustainable futures. However, in sustainability science, we still lack transparent and systematic ways to deal with evidence in the context of sustainability experimentation. For instance: it is still unclear what criteria we can use to assess evidence or how we can account for the way evidence is generated in the first place or utilized in ever changing, highly contextual, and collaborative settings. Hence, in this talk, I ask: What notion of evidence can support sustainability scientists and practitioners in achieving more sustainable futures?

In answering this question, I will present the results of an interdisciplinary project that included sustainability scientists and practitioners as well as philosophers, ecologists, and social scientists. I will show how we have engaged with recent theoretical works on evidence (ranging for instance from evidence-based policy, public health, and medicine) as well as with empirical work from sustainability experiments in so-called real-world laboratories. I will point out the challenges emerging when trying to balance scientific rigor and the role of contexts and people as well as normative values and goals in shaping a notion of evidence that could be useful for sustainability scientists in their work. I will present two main results. First, I will argue for the importance to move beyond more traditional criteria to assess and evaluate evidence, such as validity, replicability and generalizability, and incorporate considerations of (i) effectiveness of interventions in realizing normative goals while keeping into consideration long-term perspectives; (ii) meaningfulness of interventions for the multiple actors involved in the process of experimentation that can support agency; and (iii) appropriateness of implementation in considering the complexities and uncertainties characterizing local socio-ecological contexts. Second, I will argue for the importance of having a processual approach to the notion of evidence that considers its entire life cycle from its generation and validation in one context to its circulation as well as adaptation and utilization across different contexts.

The observation of animals throughout history: The descriptions of snakes

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Maria Elice de Brzezinski Prestes, University of São Paulo, Brazil

The focus of this presentation is the observation of animals throughout history, taking as a case study the morphological and anatomical descriptions of serpents. Whether by its wide geographic distribution, or by the different types of relation with the human being, mentions to this animal appear in works of natural history since Antiquity. In this presentation were selected passages from works of the occidental tradition such as Aristotle *(De Partibus Animalium* and *Historia Animalium),* Pliny the Elder *(Natural History),* Saint Ambrose *(Hexameron),* Ann Payne *(Medieval Beasts),* San Epifanio *(The Physiologus),* Albertus Magnus *(Questions Concerning Aristotle's On Animals),* Francesco Redi *(Letter to sir Lorenzo Magalotti),* Willem Piso and George Marcgrave *(Historia Naturalis Brasiliae).* The comparison has the intention of discuss some epistemological and methodological aspects that guided the observation and correlated description of animals in Antiquity, Middle Age, Renaissance and early Modern Age. Thus, another goal is to discuss the importance of the longue durée historical studies as pointed by Jo Guldi and David Armitage in *The History Manifesto* (2014) as a way to contribute to the methodological and epistemological discussions of the present biological sciences in the light of the past.

Noise in gene expression and the power of chance in explaining behavior at molecular and cellular levels

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In biology, the stochastic variation of gene expression that results from low numbers of molecules, thermal agitation, and quantum effects is generally described as noise (Kærn 2005; Pipel 2011). Within these processes, noise is historically conceived by biologists as mere nuisance (Heams 2014). Indeed, in the mid-twenty century some internal stochastic instability was supposed to affect the normal course of intracellular processes, thus producing stochastic variability in cell phenotype even in the absence of any genetic and environmental change. Starting from the 1990s, this hypothesis has been established thanks to theoretical and experimental investigations: cell-to-cell non-genetic variability is due to stochastic fluctuations during the process of gene expression, what has started to be called "noise" (McAdam & Arkin 1997). For example, cell-to-cell phenotypic variability among isogenic cells is thus considered as simply an error, a random deviation with respect to what is expected when one knows their genotype and the environment they grow in. In other words, chance is conceived in this context as a mere nuisance to the regular, deterministic, and predictable progress of molecular processes taking place inside cells, in particular gene expression. Recently however, noise has been recognized as having a positive function (McAdam & Arkin 1997; Elowitz 2002; Eldar and Elowitz 2010). Nevertheless, the epistemological status of noise remains fuzzy: despite some biologists recognizing its functionality, there is no consensus around what exactly it explains. In the presentation, we argue that stochasticity affecting various biological processes involved in cell functioning may actually play a positive, constructive role, contributing to the explanation of these processes, and should thus be conceived as more than just noise. More specifically, our objective is dual. First, we aim at showing that the way noise is currently conceived in the biological literature is ambiguous because it mixes up ontological and epistemological considerations. Second, we argue for a positive conception of chance, which is intended to enrich and augment the current, mostly negative, epistemology of chance that has characterized the biological discourse about molecular and cellular processes since the 1970s. According to the augmented epistemology we argue for, chance can be conceived as a “theoretical operator” (Morizot 2012) with a biological, and even functional, relevance. When it is shown to play a role in the functioning of the cell as well as in the development of individual organisms throughout time, chance can be conceived as a behavior of cellular processes, and has to be taken into account in models and explanations as such.

Misconceptions behind visual representations in the teaching of evolution in Mexico

Jordan William Cruz Castillo, Universidad Nacional Autónoma de México, Mexico

Many of the students’ misconceptions about evolution are very similar to ideas held by scientists from the past. In this way we speak of a parallelism in the history of science and the teaching of a certain subject. This work deals with two fundamental concepts for the teaching of evolution, on the one hand, visual representations as an object of study and, on the other hand, epistemological obstacles that have a direct relationship with misconceptions. Some of these obstacles can be understood by studying the history and trajectory of representations. For example, many of the images that are used today in teaching evolution in Mexico are obsolete because they are inspired by the works of Marsh in 1870 and Zallinger in 1964, among others. Nowadays, these images are part of the collective imagination of Mexicans about biological evolution and they have been used since 1970. In order to historicize visual reconstructions (what they sought to communicate and under what theory and in what context they were used), as well as to clarify their trajectories (how these images circulated from academic to public spheres), it is possible to understand why these representations are currently a source of misconceptions. This is how this work takes as a central assumption that in the visual representations of evolution some epistemological obstacles can be identified. Since the visual images -understood as any representation or figure in two dimensions- can be the product of the socialization of science, they synthesize many of the problems and controversies regarding a particular topic. What is interesting is that the images of evolution are the observable part of deep thought structures, both in students and teachers. Given that misconceptions are persistent, they tend to be similar to ideas that are supposed to have been overcome in the history of science and that ultimately are personal and/or shared conceptions. For this reason, the aim of this work is to present and discuss a method to deal with these obstacles using visual representations as an identifier of misconceptions and as a starting point to change them.

3D/4D metaphysical equivalence: Lessons from the species debate for the metaphysics of change and persistence

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Vanessa Triviño, University Rey Juan Carlos, Spain

In a recent paper, we explored the consequences that the species-as-individuals thesis together with the species concept problem have for metaphysical theories of persistence (Triviño and Cerezo 2015). In particular, we addressed the question whether the species-as-individuals thesis together with the species concept problem threaten the thesis of metaphysical equivalence (ME) between three-dimensionalism (3D) and four-dimensionalism (4D). Reydon (2008) has offered a positive answer to this question. He claims that 3D/4D ME finds a counterexample in the species debate. Conversely, in our previous work, we gave a negative response by challenging one of Reydon's crucial assumption, namely that the term "species" is homonimous and refers to two different entities in different biological disciplines (evolverons in evolutionary biology and phylons in systematic biology). On this occasion, we aim at showing that, even if we accept his assumption that "species" is homonimous, 3D/4D ME still holds.

In our argument, we challenge the strong association between a synchronic view of species (i.e. evolverons) and a 3D theory of persistence, and a diachronic view of species (i.e. phylons) and a 4D theory of persistence. In doing so, we present two arguments, a metaphysical one – the process argument, and a biological one – the gene-flow argument.

In addition, our theoretical research stresses the importance of distinguishing two different issues: the issue about the temporal consideration of an organism/species (synchronic and diachronic) in relation to other organisms/species, and the issue of the persistence of an organism/species (endurance or 3D and perdurance or 4D).

Finally, we show how this debate concerning the persistence of species helps to illustrate some misunderstandings behind contemporary analytic metaphysics of change and persistence.

What can we learn from how a parrot learns to speak like a human? A model for referential communication learning

Shereen Chang, University of Pennsylvania, USA

In this paper, I propose a model of how animals learn to communicate referentially. In proposing my model for the acquisition of referential communication, I aim to highlight the importance of social and ecological context when thinking about communicative behaviours and capacities. If the context in which an animal lives does not demand linguistic communication, linguistic behaviour is unlikely to arise. When the animal's context demands referential communication, such behaviour is likely to be found in animals that survive.

My model represents four key factors in the acquisition of referential communication without presupposing any capacities for recursion. The model's four dimensions emphasize the importance of motivation in the form of social and ecological incentives, demonstrating the usefulness of referentiality to the learner, learning within a socially interactive context, and sufficiently exposing the individual to the form of communication being learned. When a capable animal is trained under conditions that fully realize the four dimensions of my model, we should expect that animal to learn to communicate referentially. Under conditions that satisfy the dimensions partially or not at all, we should expect a corresponding decrease in success in the animal's learning.

I present evidence that my model applies to mammals and parrots, who are cognitively capable of acquiring referential communication. My analysis examines the research of Irene Pepperberg and Nicolas Giret et al. Both the Pepperberg and Giret labs trained grey parrots to communicate using words. While parrots in the Pepperberg lab successfully learned to use many words referentially, parrots in the Giret labs did not. Pepperberg's subjects learned to communicate referentially via various training methods that emphasized social context and interaction. To introduce new words, Pepperberg primarily used a Model/Rival technique in which two human trainers demonstrate the reference and functionality of target words, while providing social interaction. After the parrot attempted to vocalize a new word in the presence of the referent object, trainers would repeat the word in different sentences to clarify its pronunciation, reminiscent of how human parents talk to young children. In this way, parrots acquired the referential use of words through techniques similar to how humans learn to speak. I show that the model applies also to other species trained by humans to communicate referentially, as well as to the referentially specific communication of animals found in nature.

What can cultural selection explain?

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Despite claims by some cultural evolutionists that progress in the social sciences has been painfully slow, it is undeniable that there already exists a very substantial body of work in disciplines, such as anthropology, sociology, and history, that study cultural phenomena and cultural change, using their own frameworks and methodologies, and with their own explanatory goals. The challenge, then, for advocates of cultural evolution is to show that there are significant aspects of culture lacking explanation, that these lack explanation due to the shortcomings of other frameworks, and that an evolutionary approach can make meaningful contributions to that understanding.

Cultural evolution is a diverse field, and various authors have explored the potential explanatory benefits of aspects of the cultural evolution project, such as broad "population thinking", or cultural attractor theory. Here I focus on cultural selection in particular, a significant research programme within cultural evolution, which makes claims about the ability to understand large sets of cultural phenomena as adaptations that are the result of cumulative selection.

I argue that a lack of attention has been paid to the precise explanatory, predictive and practical gains we should expect from utilising cultural selection frameworks, over (for example) historical or anthropological ones. For example, arguments for cultural selection frequently rely on the Lewontin conditions, only demonstrating that selection models can be applied to culture, without explicitly demonstrating the explanatory dividend that arises from their application (Mesoudi et al, 2007; Richerson et al, 2016). This is a particularly important when considering the potential practical payoffs: it has been suggested that employing cultural selection models could bring tangible benefits in terms of explaining innovation and sustainability science (e.g., Waring et al, 2017). Understanding what unique explanatory gains we can expect from cultural selection is crucial, if we wish to realise these practical benefits.

In this paper I offer a clarification of the explanatory targets of cultural selection, and how the modes of explanation differ from non-evolutionary approaches. I use a case study of the application of cultural selection to sustainability science to illustrate the dangers of applying selection models with little explanatory power. I argue that we need to find evidence of cumulative selection in cultural phenomena in order for selection frameworks to give meaningful explanatory benefits.

Bichat’s two lives

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In Recherches physiologiques sur la vie et la mort (1800), Xavier Bichat, a medical doctor at the Hôtel-Dieu in Paris, distinguishes between the “organic” and the “animal life” of humans and animals. The organic life is directed towards the inside of their bodies. It is composed of organs which maintain cycles of assimilation, consumption and excretion. The animal life is directed towards their outside. It is composed of sense organs, nervous systems, brains and locomotor muscles. In this essay, I will focus on four aspects of Bichat’s distinction: first, on the role of both lives within the “animal series” from the first animal, the zoophyte, to the last animal, the human, second, on the difference between animals and plants, third, on various forms of interactions of both lives within organized bodies and between these bodies and their surrounding world, and, fourth, on the relation of both lives to “social orders”. Further on, I will discuss the position of Bichat’s thesis of two lives between medicine, anatomy, physiology, philosophies of human and animal subjectivity and anthropology.

Kuhn’s scientific objectivity: The role of anomalies in revolutionary science

Daniel Choi, Independent Scholar

For Kuhn, objectivity is characterized as sensitivity to evidence, especially to the evidence associated with “anomalies,” experimental results that prove inconsistent with the scientific paradigm that produced them. Given Kuhn’s views on the incommensurability of paradigms, there is some question as to whether he is entitled to assume the paradigm-neutral nature of anomalies. While Meiland, in response to Scheffler, argues that Kuhn’s belief in anomalies and their power to remold theories renders him a proponent of objectivity, specifically “independent standard” objectivity, Siegel contests this characterization, stressing that the incompatibility of paradigms ultimately undermines anomalies associated with theory-change under a paradigm-neutral view. All three appear to concede that Kuhn's notion of scientific revolution precludes the possibility of scientific objectivity obtaining outside of normal science. Nevertheless, it is precisely in moments of theory-change that we would expect the epistemic virtues associated with objective evidence-sensitivity to be of maximal import. Given that scientific revolutions are difficult to identify contemporaneously, and considering that Kuhn's definition appears to limit objectivity precisely to moments of revolutionary paradigm change, it follows that a general Kuhnian notion of objectivity is difficult to discern. As such, Kuhn's notion of objectivity appears to be of little value in application to a universalizable scientific methodology governing ordinary scientific observational and inductive practices; the extreme context-sensitivity of Kuhn's objectivity undermines the very epistemic virtues for which one would normally appear to that notion.

Does cultural selection have to be blind?

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In theories of natural selection, cultural selection and evolutionary epistemology it is often assumed that selection takes place only if the agent of selection is blind, rather than acting with intelligent foresight. I show that the assumption is needlessly restrictive, and that selective effects are compatible with intentional design. This implies that the empirical base for evaluating cultural selection theory is much wider than is usually assumed, and it also removes one serious impediment from the project of evolutionary epistemology.

Darwin's causal argument against special creation

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In *The Origin of Species,* Darwin presents his "one long argument" against the thesis of special creation (SC) and for his alternative hypothesis of evolution by natural selection (ENS). His objections to SC come in two, perhaps contradictory, forms. First, Darwin sometimes argues that some observations, such as imperfect traits, seem to provide evidence against an omnipotent and benevolent creator because SC predicts that traits should be perfect. More specifically, using the Law of Likelihood, the claim is that for some observations, Pr(O|SC) < Pr(O|ENS), so O is evidence that favors ENS over SC.

However, in other places, Darwin argues that SC makes no predictions and confers no likelihoods at all, that "on the ordinary view of the independent creation of each being, we can only say that so it is;—that it has so pleased the Creator to construct each animal and plant" (Darwin 1859, Ch. 13). Because the goals and intentions of an all-perfect God are unknowable, we can't assign precise likelihoods to various outcomes on the hypothesis of design. Worse, if we make favorable assumptions about the creator, we can generate a high probability for any outcome whatsoever.

This latter possibility has come to be known as the Preference Problem (Sober 2008). I explicate a way out of the Preference Problem that Darwin himself found compelling, using the modern tools of causal modeling frameworks. In frameworks obeying the Causal Markov Condition, probabilistic dependencies between two variables are indicative of a causal relationship between them (or between them and some common cause). The Preference Problem states that the design hypothesis can accommodate any probabilistic dependency between observed traits and the designer and hence preserve a causal connection between the two, come what may.

However, Darwin himself held that the most persuasive evidence against the design hypothesis was a particular probabilistic independence, namely, that the variations that occur in a population are probabilistically independent of what would be good for those organisms to possess (in modern terminology, mutation is random with respect to fitness) (Beatty 2006). Given certain assumptions, probabilistic independencies indicate the absence of a causal connection between two variables. Darwin's insight is that if there were a designer that is a common cause of both variation and natural selection, then we would predict a probabilistic dependence.

While this gives Darwin a kind of evidence against SC that does not fall victim to the Preference Problem, there are several complications of the causal modeling framework that provide an “out” to the design proponent. I argue that the probabilistic independence Darwin identifies doesn’t merely put theological pressure on our conception of a designer, but in fact, standard causal reasoning justifies the inference that there is no such designer.

An exploration of the role of technology companies in cultural evolution: A case study of PCR

Louis Scott Cole, University of California, Davis, USA

William Wimsatt, who advocates for a developmental view of cultural evolution, recently presented a research framework for studying cultural evolution that emphasizes the importance of human population structure (Wimsatt, 2018). Wimsatt believes that to make significant progress in understanding cultural evolution, we must eliminate a simplifying assumption typically made in dual-inheritance and other replication-centric models of cultural evolution: the assumption of a homogeneous human population. Population structure is an essential component of models of biological evolution, he argues, and it is likely even more important in models of cultural evolution given that the transmission of cultural entities is more complex than that of biological entities (being horizontal as well as vertical). In this paper, I make a preliminary attempt to support Wimsatt’s claim by examining an aspect of population structure present in all modern societies: groups of technically-fluent individuals employed by technology companies. My focus is the manner in which these companies interact with and respond to two types of cultural entities in the service of furthering their goals: artifacts and ideas. The artifacts of interest are new products commercialized by other companies that are within the same technical domain as the company’s products. The ideas of interest here are the technical concepts embodied in those other products. To explore how these cultural entities are sought out and used by these companies, I will present a recent case study from the bioinstrumentation industry. It focuses on both the invention of, and some of the subsequent inventions influenced by, the polymerase chain reaction (PCR), a DNA sample preparation technology that is ubiquitous in modern life science research. PCR was invented and commercialized in the mid-1980s by Cetus Corporation (Emeryville, CA). Following PCR's introduction, other companies developed products that leveraged ideas borrowed from PCR but that addressed different research needs. I'll focus on two. The first is cycle sequencing, a DNA sequencing approach introduced by Applied Biosystems (Foster City, CA) in the early 1990s. The second is TaqMan (also known as "quantitative PCR" or "qPCR"), a technology developed jointly by Roche Molecular Systems (Alameda, CA) and Applied Biosystems in the mid-1990s for quantifying gene expression levels. The case study suggests that technology companies—examples of non-homogenous population structure—might be viewed as accelerators of technological and cultural evolution since they have both the ability and the desire to actively seek out new technical concepts (ideas) and to evolve their own product offerings (artifacts) as quickly as possible.

Materializing trans identities. A dialogue between the new biology and the new feminist materialisms

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In 1964 Robert Stoller coined the term "gender identity". By introducing this new term, Stoller was redefining the very category of gender and positing that every subject had a sense of self and belonging to a particular sex.

In light of this, gender was dichotomized between, on the one hand, a gender identity (psychic interiority) and, on the other, a gender role (corporal expressivity of masculine and feminine conducts).

This dichotomy within the category of gender had its foundations in a second dichotomy, the sex vs. gender one, which was already structured by the nature-culture opposition wherein sex was understood as nature and gender as culture.

This cartesian binary led to a disembodied understanding of gender identity by considering it a mental/internal property or as a cultural trait residing within the mind.

Since then gender identity have been at the centre of numerous debates and several questions regarding its its metaphysics and etiology have been raised. Nevertheless these debates have been framed within sex-gender and nature-culture dichotomies.

Be this as it may, different accounts of gender identity have proliferated. Among these we find the biologically inspired models, John Money's environmental model, and last but not least Judith Butler's performativity account.

Butler advances a metaphysics of gender identity and gender in which these are ensambled in the process of iterating social norms. Sex would thus emerge as a consequence of gender.

Certainly, Butler's account is these days the most popular in feminist studies. Nonetheless it has been been criticized given its lack of attention to the materiality of bodies. Numerous critics have asserted that the butlerian body has no prediscursive elements and its entirely produce through culture, more specifically by language and discourse.

Having said this, my objective in this paper is to explore gender identity from a perspective that recovers the materiality of bodies in the constitution of gender identity. I consider that a metaphysics that explains gender identity only as an intrapsychic unidimensional phenomenon, as only a discursive, linguistic phenomenon will fail to include the material processes underlying the embodiment of gender identities.

I locate at the center of my reflection the trans body because in it we observe the co-production of several aspects such as:

1. body-identity,
2. sex-gender and,
3. biology-culture.

This occurs in a non dichotomous way through the reshuffling of material logics (being these biological, psychical, and social) that constitute gendered social ontologies in our current society.

To explicate how this happens this talk follows the New Feminist Materialisms and the New Biology (DST, EvoDevo, etc.). Both share not only their novelty but their commitment with explanations regarding human nature and the world that overcome dichotomic conceptions in which the social is severed from the natural and, thus, explained either through biological determinisms, from natural sciences, or cultural determinisms, from social sciences and humanities.

Population, metapopulation and metahabitat

Gregory Cooper, Washington and Lee University, USA

As we face increasing modification of environments as a result of anthropogenic forces, metapopulation ecology has emerged as an important focus of conservation biology. However, the concept of a metapopulation has not received sufficient attention from philosophers of ecology. To the extent that it has been addressed it is often as an addendum to work that is primarily devoted to explication of the concept of a biological population. This is unfortunate for several reasons. First, the metapopulation concept presents a distinctive set of conceptual issues. Second, analyses that might be relevant are rendered less so by a nearly exclusive focus on the concept of population as it features in evolutionary biology. Population ecology is either ignored or it is assumed that a definition of population that works for the study of evolutionary change will work for ecology as well. Third, to the extent that ecological populations are addressed, the definitions tend to overemphasize the extent to which demographic phenomena are determined by the interactions of the organisms within the population. I will argue that the concept of population relevant to the study of demographic change is distinct from the concept relevant to the study of evolutionary change. The latter enterprise must keep track of gene flow in some sense (though spelling out the details has proved controversial). The key to identifying populations from a demographic perspective is the concept of a habitat. I will not defend the conceptual adequacy of this idea here. Instead, I want to explore the significance of this central role of the habitat for the concept of a metapopulation. The general understanding is that metapopulations are populations of populations. Yet, not just any collection of populations constitutes a metapopulation. The populations in question must share what we might call a metahabitat (i.e. a collection of habitat patches such that each habitat patch has the capacity to be colonized by individuals from at least one of the populations in the metapopulation). The metahabitat is typically incorporated into the metapopulation perspective under the concept of metapopulation structure. But this approach to the metahabitat is inadequate for at least two reasons. First, it is ambiguous. Sometimes metapopulation structure is about the properties of the local population, not the metahabitat at all (e.g. the ages of the local populations; their propensity to generate dispersers, etc.). Second, in metapopulation models, metapopulation structure (hence the metahabitat) is often treated in a quite idealized manner (e.g. in the original Levins model the metahabitat is infinite; the matrix between suitable habitat patches is often ignored, etc.). In general, attempts to understand metapopulation dynamics tends to focus on demographic processes not environmental change. This, of course, is not a crazy thing for population ecologists to do. However, in this age of human domination of the planet, where habitats are pervasively modified by direct intervention in the landscape and by global processes such as climate change, it is time to pay more explicit attention to the dynamics of the metahabitat.

Biology and the lawlike

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It has been claimed, to use a distinction of Windelband's, that biology is a historical science rather than a science of laws. Moreover, the claim goes on, there are no genuinely biological laws. This last claim can be and has been disputed by arguing that there must be at least some weak statistical laws of variation if evolutionary theory is to give any account of the origin of new species, and these laws must therefore be distinctively biological. This paper extends this argument for the presence of laws in biology. The key feature of laws is their emphasis on non-accidental connections among events. I shall call this key feature of laws "lawlikeness", and I show that it pervades biology in many, and possibly all, of its sub-domains. While biology is undoubtedly a historical subject in many respects, the lawlike pervades even this. There may be no grand historical laws of a sort once imagined. And the history of life is certainly contingent all the way from its grandest features to its minutest details. But such a contingent history is not only compatible with the lawlike, it presupposes the lawlike. We need not choose between the historical and the lawlike. Biology is everywhere both.

From the Cold War to Genomic Era: visual representations of genetics in Mexican high school textbooks

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The events that took place in the Cold War period (1945–1989/91) were not only restricted to European and North-American local geographies, they also reached the Latin-American continent. The great global polarization between the United States and the Soviet Union promoted advances in many scientific fields, more specifically, in biomedicine and the natural sciences on the effects of radiation in natural populations. Mexico was not the exception and was involved in major developments in science thanks to international collaboration networks such as the creation of the National Nuclear Energy Commission (CNEN) on December 31, 1955 under the government of the President Adolfo Ruiz Cortines and that later would become the National Institute of Nuclear Investigations (ININ) following the world requests for peace and the emergence of the International Atomic Energy Agency (IAEA). In addition, different international organizations were created such as the World Bank (WB), the United Nations Educational, Scientific and Cultural Organization (UNESCO), the Organization for Economic Co-operation and Development (OECD), the Inter-American Development Bank (IDB) and the Economic Commission for Latin America (ECLAC) that become relevant in the global discussion on economic and social policies, allowing the debate on the internationalization of educational trends, formulating since then, the global standards they must comply with the curricula of high school education. In the local context, this work addresses the case of the College of Sciences and Humanities (Colegio de Ciencias y Humanidades, CCH) textbooks in the 1970s that followed the plans and syllabuses under the guidelines given by the previously mentioned international institutions whose objectives and main concerns pertain to the high school level in the middle of the Cold War. As a case in point, the teaching of genetics has proved to be a challenge within the scientific community not only for the effects of the nuclear race on the genetics of natural populations, but also for the impact that the development of genetics had on society. One way in which those who are studying the high school level can understand more adequately the subject of genetics could be the scientific representations because the images are an important tool of the investigations that are carried out in the laboratories. These images can be diagrams, photographs, drawings, maps, graphics or computer simulations capable of transmitting certain information. Since the 1990s scientific images have acquired great interest from the social studies of science and technology due to the diverse range of images produced and the analysis of these in the construction of knowledge. Given the importance of genetics and the scientific representations, this work explores the images that are frequently used as communication channels and are usually captured in peer-reviewed publications and, eventually, in textbooks, also, this work seeks to show how images of genetics have changed in Mexican high school textbooks from 1970 to 2010, and the contexts in which these images have spread.

How to be unique

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It is occasionally argued that some biological lineages are special—”unique”—and none more so than our own. Epistemological implications seem to follow from such claims. In particular: if a lineage really is unique, then it must be of limited use in understanding evolutionary history. Studies of truly unique lineages are unlikely to produce results generalizable to new cases. The symmetrical claim would also seem to be true; that comparisons with other lineages will be of limited use in understanding unique ones.

But the notion of uniqueness and its epistemological implications are more vexing than this initial assessment might suggest. Adopting an evolutionary perspective seems both to over-generate uniqueness and deny that lineages are unique. According to our best accounts of evolutionary systematics, all lineages are distinct—so aren't they all unique? But if this is so, then why make a fuss about particular instances of uniqueness? Further, an evolutionary perspective also undermines the idea that lineages are unique; since every lineage must trace its ancestry back to a common ancestor. If there is a sense of uniqueness here, it is just in the sense that life—considered as a whole—is unique, in having only arisen once. This leads headlong into a dilemma: to say that humans or other lineages are unique is either vapid (because all lineages are unique) or spooky (because appealing to factors that clash with evolutionary biology).

But we think this dilemma takes us too far too fast. We develop a respectable account of biological uniqueness that doesn't fall prey to vapidity or spookiness. Our account identifies uniqueness not as a property of lineages—and thus hostage to claims about the placement of that lineage in a tree of life—but about the organisms that constitute lineages and their traits. Uniqueness is also a contrastive claim: the unique features of a (set of) organisms is unique by contrast to a set of other features.

We identify two kinds of possible discontinuities between traits held by lineage constituents. First, discontinuities in evolutionary history. Here, uniqueness tracks specific evolutionary cascades: selection pressures and evolution events across time leading to traits are due to specific, distinctive, and likely complex environmental pressures. Second, discontinuities in affordances. On this understanding, uniqueness is a contrastive claim about what specific trait(s) enables the organism to do in a relevant environment.

Together we claim that this account accommodates both the connotations of “uniqueness” as employed by empirical researchers, while remaining consistent with our best accounts of evolutionary biology.

Evidence in default

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Experiments in comparative (animal) psychology typically aim to test a default model against an alternative. For instance, Morgan’s Canon dictates that researchers prefer models that posit the simplest processes. This is often interpreted by analogy to null hypothesis statistical testing (NHST), the dominant statistical approach in psychology: the “simpler” model should be the default. Morgan’s Canon has faced considerable criticism lately, and the two proposed replacements in the literature set up the central tension of this paper. One replacement, contextual null choice (Mikhalevich 2015, Mikhalevich, Powell, & Logan 2017), accepts the general default model framing while choosing nulls/defaults case by case. The other, evidentialism (Sober 2005, Fitzpatrick 2008, 2017), rejects defaults altogether in favor of a more holistic inference to the best explanation. I develop and argue for a version of evidentialism over the default model framing (even if one wishes to retain Morgan’s Canon in a weaker form). We should never treat one model as the null or default. First, I attack the analogy that supports the default model framing: The analogy between default models and NHST fails to respect the difference between statistical hypotheses and substantive hypotheses. Statistical hypotheses specify a distribution of a certain feature (the thing to be measured); substantive hypotheses are models of the target system that motivate the statistical hypotheses and, potentially, explain them. The inferential gap between statistical and substantive hypotheses looms large in comparative psychology, because in comparative work any model can be consistent with many specific experimental outcomes. In such cases, the failure of any statistical hypothesis does not entail the failure of any substantive hypothesis. This argument undermines motivation for the default model framing. I then attack the default model framing directly, by arguing that it distorts the weighting of evidence, and systematically biases experimental practices. In the process, I show how evidentialism can square with NHST as a statistical approach to individual experiments. We can have null statistical hypotheses without default models.

The evolution of moral belief: Support for the Debunker's causal premise

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The causal premise of the evolutionary debunking argument contends that human moral beliefs are explained by the process of natural selection. While it is universally acknowledged that such a premise is fundamental to the debunker's case, the vast majority of philosophers focus instead on the epistemic premise that natural selection does not track moral truth and the resulting skeptical conclusion. Recently, however, philosophers have begun to concentrate on the causal premise. So far, the upshot of this small but growing literature has been that the causal premise is likely false due to the seemingly persuasive evidence that our moral beliefs are in fact not the result of natural selection. In this paper, I argue that this view is mistaken. Specifically, I advocate the Innate Biases Model (IBM), which contends that there is not only compelling evidence for an evolved cognitive capacity for acquiring and implementing norms but also for the existence of an evolutionarily instilled set of cognitive biases that make it either more or less likely that we adopt certain moral beliefs. I go about arguing for this in the following way. In the first section, I explain the evolutionary debunking argument and introduce my thesis. In the second section, I explicate the IBM, which consists of explaining what it would mean to have innate biases and a cognitive capacity that enables and encourages us to acquire and implement certain norms. In the third section, I show why previous arguments attempting to show that our moral beliefs are not the result of natural selection are unconvincing and in so doing present evidence and argument in support of the IBM. In the fourth section, I discuss how the differences between the IBM and Street's evolutionary account might affect her version of the evolutionary debunking argument.

Ecology of orchid pollination and scientific explanation: The case study of deception strategy from Darwinian botanists till the current scientific results

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As from the second half of the XVIII century botanists who studied Linnean Œconomia Naturae interpreted the action of pollinating insects in fertilization of orchid flowers as evidences of a finalistic order of nature created by God and in the light of such philosophical and theological considerations Christian Konrad Sprengel wrote Das entdeckte *Geheimniss der Natur im Bau und in der Befruchtung der Blumen* (1793). In this work we find the first description of orchids that have a well-developed nectar-bearing spur, in which there is, however, no nectar. In this case, if the insect will not receive any food reward, how we can explain that nectarless orchids are visited by insects that contribute to their pollination?

Sprengel, observing carefully many flowers of *O. latifolia* and *O. morio*, called them sham-nectar-producers and maintained that these orchids deceived insects by the shape of their flowers, similar to that of orchids secreting nectar.

Charles Darwin in *Fertilisation of Orchids* (first edition 1862; second edition 1877) broached this thorny subject from a view-point unknown to Sprengel: common descent and natural selection permeated his explanations about relationships between flowers, pollinating insects and their marvellous reciprocal adaptations. He examined and experimented with *O. maculata*, *O. pyramidalis*, *O. morio* and *O. hircina* and pointed out the utilitarian nature of insect visits and the intelligence of pollinating insects. On the basis of these observations he rejected the idea of deception, arguing that seemingly empty spurs of orchids might contain a "fluid" inside their walls that was released only when insects penetrated the lower part of the nectaries.

Herman Müller and Federico Delpino considered the darwinian explanation not conclusive and carried out further observations and experiments on nectarless orchids.

Müller cooperated to Darwinian researches on fertilization in Germany and in *Die Befruchtung der Blumen durch Insekten* (1873) corroborated Darwinian explanation. However Delpino's scientific studies on nectaries of the genus *Orchis* were inspired by teleology and led him to ascertain that insects visited flowers at the beginning of the flowering season and then, discovered the "imposture", they stopped their visits. Consequently in *Osservazioni sulla dicogamia* (1874) Delpino supported Sprengel's explanation.

The historical debate in connection with Sprengel's discovery was solved in the second half of XX century, thanks to the works of Anders Nilsson (1980; 1992), Amots Dafni (1983; 1992) and Salvatore Cozzolino et al. (2005).

In this paper I intend to show how the modern ecology of orchid pollination developed on Darwinian tradition of international research that was born on the reception of *Fertilisation of Orchids* to understand the floral morphology and ecological interactions between pollinating insects and plants from an evolutionary point of view.

I will try to demonstrate that the current scientific explanations of biology of orchid pollination derives benefits from the different philosophical orientations underlying the explanatory approach of the scientists who belonged to Darwinian botanists.

To substantiate my argument I will focus on the methodological and scientific requirements that from botanical sciences of XIX century have been inherited in current botany to define the cases studies.

The human cognition at the era of the holobiont

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It has been recently proven that the influence of microbiota on human brain exceeds the impact of nutritive behavior and extends to the mood, stress response, decision-making and even to the development of some brain structures. These facts lead to new insights on the human sociality and the human cognition.

Against the brain social theory and the parasitic theory, which respectively explains the cognitive evolution as the result of sociality or as the result of the parasitic stress, we propose that neither sociality nor parasitic stress are selective pressures but evolutionary steps leading to the cognitive development:

We link the cognition to the symbiosis and show that:

1. human metabolism, nutrition and microbiota show a strong evolutionary link;
2. some recent brain areas implicated in evolved cognition are related to microbiota.

We explore the interference of microbiota with the immune-brain circuit and present a cognitive perspective of the immune behavior. We propose that the sociality is a consequence of cohabitation and coadaptation of human organisms to their microbiota. We offer justifications that sociality is an evolutionary strategy that allows the human *holobiont* (i.e. human host organism and his microbiota) to adapt to the fluctuating environmental condition.

We argue that the cognition results from the evolution of the behavioral immune system by the extension of the defense against pathogens to the promotion of cooperation and to sociality as a consequence of symbiotic coadaptation. Symbiotic tolerance authorizes the coexistence and the mutualistic cooperation allowing symbiontic transmission between conspecifics. Interindividual relationships enhance confidence and sharing knowledge and ideas. The result is a collective brain with higher adaptive abilities.

We conclude that the evolution of human cognition resulting from the cooperation of collective brains is the consequence of symbiotic coadaptation.

Epistemic injustice in psychiatry

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Attention to epistemic injustice in psychiatry has so far focused on the context of patient involvement in revisions to the Diagnostic and Statistical Manual of Mental Disorders (DSM). Other related work has attended to the way various forms of epistemic injustice arise in healthcare more generally, with a focus on somatic illnesses. Still other work has examined the difficulty people with mental illnesses have in communicating their experience and/or being taken to be credible speakers in everyday contexts. In this paper, I expand on this literature in two ways. First, I will examine a wider range of contexts within psychiatric practice (broadly construed) in which people experiencing mental illness often encounter forms of epistemic injustice. These include diagnostic interviews, decisions about treatment modalities, resolution of complaints about mental health professionals, and within the context of treatment (both individual and group therapy). Importantly, this latter context, in particular, shows the extent to which the conceptions of different mental illnesses in the social imagination produces a hierarchy among patients according to which some groups of patients are significantly more marginalized than others. Second, where most of the literature in this domain has identified either epistemic injustice in general, or has focused on testimonial and hermeneutic injustice, I attempt to provide a finer-grained analysis of the varieties of epistemic injustice that tend to be found in these settings. The end result of this is a fuller map of the terrain of epistemic injustice in psychiatry, one which will, I hope, lay the foundation for more detailed examinations of specific domains within this area.

A process-oriented metaphysics of the Anthropocene

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The concept of Anthropocene has been fraught since its origin with the foundational ambiguity behind the greek notion of anthropos, which can be interpreted, as in the discipline of anthropology, both with a cultural approach (freeing itself from biological determinism) or as a living being that can be explained through the lens of natural sciences (mainly biology, genetics, ecology). Therefore, the debates about the origin, the nature and the key factors of the anthropocene amount only to a new battlefield in the same old science war. However, as the Anthropocene constitutes an unprecendented moment in human and Earth history and defines the new human condition in a broad sense (ecological, moral, political), it seems highly desirable to go beyond disciplinary quibbles in order to think out a synthetic and evolutionary concept of the Anthropocene.

We propose to rely on Gilbert Simondon's (1924–1989) philosophy of technics in order to underline the importance of technical artifacts which cannot be reduced neither to biological nor to cultural phenomena. The development of technical object lineages follow an independent pathway, what Simondon calls an "individuation", that is necessary to grasp in order to figure out how the human species became the most powerful ecological engineer of the planet. The Anthropocene should thus be understood as a special evolutionary situation in which interrelated multi-adaptative problems (cultural, ecological, social, technical) have to be solved However, there is only one process taking place, even at different hierarchical levels, the process of individuation. This individuation takes place at the interface between an individual (organism or society) and its milieu as a kind of adaptation. Simondon's concept of adaptation goes back to Lamarck and in his own allagmatic metaphysics (i.e. process-oriented and operative) should be understood as a two-way and emergent relationship between an organism and its associated milieu which gives birth to a novel (or transductive) and singular pathway. Interestingly, this metaphysical stance looks like one of the best candidates (with Dennis Walsh's organism's centered metaphysics) to make sense of the evolutionary significance of the phenomena of niche construction and cultural inheritance as an individuation process.

Drawing upon Simondon's metaphysics, we defend the three following ideas about the Anthropocene :

1. Technical artifacts are independent and essential features of human niche construction that cannot be reduced neither to internal biological factors neither to external cultural factors

2. Following the allagmatic approach of Simondon, the Anthropocene should be understood as an evolutionary process of « anthropocenisation » driven by a dissociation between the process of social individuation and its associated milieu (the biosphere).
3. The Anthropocene amounts to a total fact where knowledge, ethics and action are converging to make sense of humanity's global fate.

What is a mental symptom?

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During the two past decades, much of the literature in philosophy of psychiatry has been focusing on the concept of mental disorder. By contrast, the concept of mental symptom has received little attention. This gap in the philosophical literature may derive from the implicit assumption that the concept of mental symptom is simpler, more intuitive and less problematic than the concept of mental disorder. In this presentation, I will argue that this assumption is faulty and that the philosopher has an important role to play in order to clarify both the nature and the structure of symptomatology in psychiatry.

In the first part of my presentation, I will characterize the concept of mental symptom as it appears in classical psychiatric textbooks. I will argue that a mental symptom is conceived as the surface feature (a subjective complaint or a behavior) of some underlying pathological mechanism. Until the early twentieth century, this indexical conception of the mental symptom has been widely accepted by clinicians, despite the fact that it raises several theoretical difficulties (e.g., the nature of phenomena that should count as mental symptoms; the problem of demarcation in psychiatry between mental symptoms and physical signs; the decisive role of the observer in the clinical assessment of mental symptoms…)

In the second part of my presentation, I will show how the DSM [Diagnostic and Statistical Manual of Mental Disorders], which has become increasingly influential worldwide since the 1980s, relies on a conception that departs on several points from this indexical conception of the mental symptom. I will then present two more recent theoretical models which attempt to address the weaknesses of the DSM approach: a) The Cambridge model for symptom-formation proposed by G. Berrios and his colleagues (Berrios 2012; Aragona & Markova 2015); b) the Network theory to psychopathology put forward by D. Borsboom (see, e.g., Borsboom & Cramer 2013; Borsboom 2017). These two models have in common the ambition to shed light on the various causal pathways that produce mental symptoms (within a mental disorder or between two disorders). More generally they both help to clarify the complex relationship that exists between nosology (classification) and semiology (clinical description) in psychiatry. I will pinpoint some of the strengths and limits of these two models and will examine their respective relevance in the light of some recent research programs launched in clinical psychiatry.

Into the next stage of the microbiome revolution: impact assessment of microbiome interventions

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Brent Sinclair, University of Western Ontario, Canada
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Researchers from all walks have claimed that microbiome research, i.e., the analysis of microbial communities associated with a host organism or an environment (Douglas 2018), is revolutionary and opens new frontiers in biology. The reasons for claiming a revolution are diverse, but generally unified in their promises that the inclusion of the microbiome in ecological, medical, and agricultural studies has "the potential to transform many scientific disciplines, to impact scholars in the social sciences, and to benefit the lives of citizens around the globe" (Blaser et al. (2016). Much of the recent microbiomic research thus encompasses instrumentalist goals, and much of the "revolutionary" rhetoric extends beyond understanding the holobiont to harnessing or manipulating the phenomenon. What frameworks do we have for making decisions about the widespread use of microbiome-based interventions? On the one hand, these interventions may not differ appreciably from non-microbiome interventions, such as treating a patient with antibiotics or probiotics, which both modify the microbiome in rather uncontroversial ways. SImilarly, one might expect that widespread spraying of a microbiome-based biocontrol agent is similar to using a persistent toxin such as insecticides. Like any analogy, this one has limitations and one of the dangers of endorsing this type of reasoning is that we tend to think that anything engineered will include some sort of kill switch allowing it to be reversed. Unfortunately, more often than not, there is no killer switch when dealing with living material. Moreover, the scale of (suggested) microbiome interventions ranges widely, from modification of nutrient uptake by individual plants to proposals for global-scale manipulation of climate, and in many cases we cannot say whether the effects of an intervention will be reversible or whether the sphere of influence will be circumscribed or not. This paper presents various types of microbiome-related interventions and propose a framework within which to evaluate their impact that avoids a simplistic engineering reasoning trap.

What does it take to be a psychological primitive? Separating innateness from foundationalism

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This paper is part of a broader project on primitive concepts and whether they can play any role in a psychologically and biologically plausible theory of meaning in natural language. The first aim of that project is simply to get clearer on what it would take for statements like “x is a primitive concept” to be true. The second aim is to bridge the use of primitives in linguists’ theories of meaning with the psychological and biological facts about concept acquisition. This paper is centered on the first aim: getting clear on the view that there are primitive concepts. It focuses on Susan Carey’s (2009) view, according to which we have a stock of innate “conceptual primitives”, defined as primitive mental representations that are neither sensory nor perceptual, which lay the foundation for the rest of conceptual development. I will argue that analysing some of the key concepts here, especially the notion of “innateness” (widely acknowledged to be problematic, see e.g. Mameli & Bateson 2006), reveals that there are several independent claims at work in a proposal like that of Carey's. In particular, I argue that some representation (or any psychological entity) having a foundational role in learning is distinct from it being innate, and that these two claims require partly independent kinds of evidence. For example, the first requires evidence for the representation emerging prior to others in the same domain. Yet evidence of this kind has no bearing on the second claim, which instead requires evidence that the representation is not acquirable solely via domain-general learning mechanisms. I also argue that in this case (if not more generally) the claim to innateness entails a claim about the specifically genetic contribution to the development of the trait.

The paper is structured as follows. I first introduce Carey's (2009) proposal that there are innate "conceptual primitives", and point to some of the developmental evidence she uses to support two particular proposed primitives, OBJECT and AGENT. I briefly set out Carey's view that these primitives form part of "core cognition", which in conjunction with a bootstrapping learning mechanism, can explain our acquisition of novel concepts. Then I move on to argue that the claim about the proposed primitives' foundational role in learning is distinct from the claim to innateness, but that these are independently interesting. I also briefly point to uses of primitives in linguistic theories of meaning, such as in Jackendoff's (2002) Conceptual Semantics, arguing that to the extent that such a theory succeeds in its aim to be a fully naturalistic – i.e. psychologically and biologically plausible – account of the semantics of natural language, it needs to be hooked up to some specific claims about what the primitives are, and thus must answer to the issues discussed here.

From dancing bees to step-counting ants: A productive tradition of finding meaning in the actions of insects

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In the course of investigating animal behavior, researchers regularly attribute semantic content to the actions of animals. Often, they do so by attributing informatic properties to animal behavior or by equating a behavior with an intentional act. For instance, an animal behavior researcher might claim that a wolf's howl conveys "information about" the wolf's location, or that a migrating sea turtle "recognizes" its destination by scent. The practice has been a perennial concern of animal behavior researchers; introductory textbooks warn students about the pitfalls of anthropomorphic reasoning while historically, subfields have distinguished themselves according to their stance on the epistemic value of attributing semantic content to animal actions (e.g. behaviorism and cognitive ethology).

To gain a philosophical and historical understanding of how this controversial scientific practice has or has not helped researchers answer scientific questions about behavior, I trace the practices and pronouncements of a particular lineage of ethological researchers who regularly attribute semantic content to the navigation behavior of insects. The lineage begins with Karl von Frisch's work on honeybee navigation in the 1910s, extends through von Frisch's student, Martin Lindauer's, research on honeybee communication and orientation, and ends with Lindauer's student, Rüdiger Wehner's, current work on desert ant navigation in the 2010s. In analyzing this lineage of researchers, I uncover a productive set of norms for attributing semantic content to insect behavior that follow a consistent logic and contribute to researchers' common goal of producing physiologically-based explanations of insects' navigational capacities. More specifically, my analysis shows how the norms governing researchers' attributions of semantic content to insect navigation reflect

1. the peculiar advantages of ants and bees as objects of behavioral research in the lab and field,
2. the research lineage's strong grounding in experimental physiology, and
3. the research lineage's ethological emphasis on understanding how behaviors contribute to the fitness of an organism in its naturally-occurring environment.

This paper represents a pragmatic departure from more systematic attempts to build a general theory of semantic content that naturalizes meaning by grounding it in evolutionary processes. Viewing the problem of semantic content through the lens of scientific practice, this paper forwards a descriptive account of the circumstances under which researches belonging to certain tradition attribute semantic content to insect behavior. Furthermore, the pragmatic approach adopted in this paper underscores how practical considerations surrounding research shape and are shaped by the abstract notions animal behavior researchers employ in their work.

How to look at burrows and dams? Proposing an artistic field experiment to engage with the beaver question

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European beavers have for centuries suffered not only wholesale eradication but also from a bad name. As opposed to their industrious American counterparts *(Castor canadiensis),* the Eurasian beaver *(Castor fiber)* was suspected to lack the collective constructive abilities of their new world cousins. Some, like the pioneering anthropologist and beaver expert Lewis Morgan, author of the comprehensive *American Beaver and his Works* of 1868, benignly speculated it was due to European beavers suffering from the proximity of humans that impeded their ability to "form associations", due to which "the once skilful builder degenerates into a burrowing hermit". This was a contribution to a debate on a set of key questions generated by beavers and their constructive skills that had already occupied French naturalists such as the Comte de Buffon and Frederic Cuvier and that has continued into contemporary scholarly discussions, such as between anthropologist Tim Ingold and cognitive ethologist Donald Griffin.

Do beavers live in an "endless now", merely performing a timeless action programme inscribed in their genes, rendering them and their works part of the biotic background of human culture? Or are they actively and intentionally writing the biographies of our riparian landscapes, with their continuous collective interventions in our river systems that build on earlier work and seem to actively plan for an uncertain future? This recurring beaver question -and associated issues of animal agency, cognition and culture- has a renewed relevance in Europe, and not just for philosophical arguments that seek to ground or undermine claims of human exceptionalism based on our constructive abilities and mental skills of contemplating future events.

Since the mid-20th century, in a number of European countries the beaver has made a comeback, after a series of successful reintroduction programmes. For instance, in the Netherlands the beaver and his/her works are now thriving to such an extent that, three decades after their reintroduction, regional governments have started to displace and even "cull" what are deemed to be "problem families". An elaborate practice of beaver management has been organized around the dual aim of protecting the beaver and controlling its impacts.

This paper traces the ways in which these management practices offer a fresh occasion to delve into the historical debate on whether beaver building projects are driven by blind instinct and mindless strivings, or the product of environmentally sensitive collective decision making and multigenerational learning. Their reintroduction involved the preparation of human-made burrows to instruct the newly arriving beavers on their way of life. And current management practices entail the identification of "problem families" and decisions on whether to respect their adaptive interventions into the flow of rivers and streams. Finally, this paper will sketch a set of experimental artistic interventions to create ways of multispecies river planning for uncertain futures. Thereby aiming to explore possibly emerging forms of shared beaver-environment-human intelligence. And perhaps even to help make claims on behalf of the industrious abilities of the European beaver.

Paper care: Animal research applications as genre

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This paper seeks to provide a better understanding of the relationship between care practices and legal requirements in animal research. In the last decade, requirements for transparency and accountability in animal research have strengthened in the public and in government. In Norway, which forms the empirical site of this analysis, the animal research application and its ethical review is placed at the core of the system of governance regulating animal research. While such applications provide spaces for articulating care, there exist inherent tensions in the tools and techniques for articulating care on paper and engaging paper care. The argument developed in this article suggests that animal research applications can be approached as rhetorical spaces for caring that is oriented around balancing between harms and benefits of animal research, and that is engaged in shaping the culture of care in animal research. Investigating animal research applications as a genre of care is an effort to bring “care” as an analytical and empirical into conversation with new empirical sites and analytical categories. It is also an effort to provide insight into a specific practice of governance that seeks to facilitate care and witnessing of animal research, and the tensions inherent in such governing strategies.

Shifting ranges, shifting meanings

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Biologists studying the geography of animals and plants have long produced range maps demarcating regions where species (and other taxa) have been recorded. Range maps have a dual nature. On one reading, they exemplify natural history of the sort Rutherford called “stamp collecting”—that is, data at best, but at any rate a product that is marginally scientific. On another reading, however, they represent fully-scientific, causal hypotheses, conjecturing where species might occur, based on integrated information about their behavior and physiology, together with habitat, climate, geology, meteorology, and other geographical properties. Furthermore, hypotheses about range constructed from such information become not merely descriptive, but also normative. The express where a population could be, or even what places are right for it, and in that way can approach suggesting where a species belongs. This last idea is especially interesting because it contradicts contemporary conventional wisdom. Writers like Emma Maris, embracing the "anthropocene" and human-structured nature, would have it that no organism belongs anywhere more than anyplace else (or by the same token, ever fails to belong someplace on Earth). In any case, this is to say that, far from "mere" natural history, range maps can express a range of meanings with deep, normative implications, and that their means are tied to the choices involved in their construction. This project aims to capture some of the changes in their assumptions and consequent meanings, as they are tied to how methods for constructing range maps have shifted since the twentieth century (as well as before and during it). This short presentation will likely foreground bird maps, though the larger project ranges across other animals and plants, as well.

Students' attitudes towards new genetic technologies: Is there a relationship with students' knowledge of modern genetics and genomics?

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Niklas Gericke, Karlstad University, Sweden
Charbel Niño El-Hani, Federal University of Bahia, Brazil
Rebecca Bruu Carver, Norwegian Institute of Public Health, Norway
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A series of new genetic technologies have become relevant for people's lives in recent decades, given the advances in those technologies as applied to new areas of contemporary societies. Therefore, it is important to investigate how the public understands and to what degree they accept these new gene technologies. In this study, we investigate students' attitudes toward new gene technologies such as gene therapy, genetic testing (including prenatal testing), and personalized medicine and pharmacogenomics. These technologies were chosen according to what has been recognized as important for the literate citizen to be informed about now and in the future (Bowling et al., 2008; Dougherty et al., 2011; Hurle et al., 2013; McBride et al., 2010). An attitude can be viewed as “an association in memory between a given object and one’s evaluation of that object. This definition implies that the strength of an attitude, like any construct based on associative learning, can vary” (Fazio, 1990, p. 81). Measuring an attitude is important because attitudes are relevant factors to predict behaviors. Some empirical studies have shown a strong relationship between attitudes and behaviors (Conner et al., 2015; Roczen et al., 2014). Thus, it seems possible to estimate to what extent these technologies are accepted by the population, and how this acceptance is related to knowledge of modern genetics and genomics. We used the PUGGS questionnaire (Carver et al, 2017; Gericke et al, 2017) to investigate if knowledge in genetics and genomics influence the attitudes towards these technologies. We applied the PUGGS questionnaire to 446 Brazilian students in the first year of an Interdisciplinary Bachelor Program at the University of Bahia, because they are representative of Brazilian who have completed high school, reflecting the level of knowledge we may expect to find in a large proportion of the population. The results were analyzed using PCA, Pearson Correlation and ANOVA. The statistics show that:

1. the students show very positive attitudes towards genetic technologies, especially when they involve treatment of medical disorders, but attitudes are not so positive when this technology is used to enhance physical attributes or for economic purposes as in the case of their use by insurance companies and future employers;
2. more knowledge of modern genetics and genomics do not lead to positive or negative attitudes towards genetic technologies;
3. other social aspects, such as religiosity or area of studying, could contribute to changes in these attitudes, as students influenced by religion and respondents studying health showed less positive attitudes towards these technologies than less religious students,

and respondents studying humanities, arts, and science and technologies.

These results support previous studies indicating that people generally show positive attitudes towards genetic technologies that benefit human health (Barnett, Cooper, & Senior, 2007) and that the correlation between knowledge and attitudes is small, as evidenced by studies of other science topics (Allum et al., 2008; Sturgis et al., 2010).

Behavioural studies of humans and non-human primates: Crossed influences

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The science of ethology is the study of animal behaviour. In this discipline, we identified two opposite trends in the methodology of researchers. First, the interpretation of the data brings the ethologists to make assumptions on why and how the animal behaves, which may include using human related concepts to do so. This phenomenon is known as anthropomorphism. Second, findings in animal behaviour may bring researchers to draw conclusions regarding human behaviour. The two crossed influences, human concepts projected on animal behaviour as well as animal behaviour projected on humans, were considered in our study.

We focus on the behavioural studies of non-human primates. Indeed, primates are our closest cousins in nature, thus we easily identify ourselves with them and we might interpret their behaviour giving them human characteristics. Additionally, due to our phylogenetical proximity in the tree of life, non-human primates are often used as models for studies in cognitive behavioural sciences and neurosciences about humans.

Our study aims at clarifying the way non-human primates' behaviour is observed and interpreted by and in relation to, humans in behavioural studies. We mainly focus on case studies concerning social behaviours (such as friendship and dominance) and emotional states (such as fear, anxiety and stress).

We notice that there is a complex relation between humans and non-human primates that seems confused in the use, or non-use, of shared cognitive and behavioural traits. For instance, there seems to be an asymmetry in the way each influence is perceived: anthropomorphism is often considered in a negative way, while using non-human primate models to understand humans is more widely accepted. Even though the crossed influences can be an obstacle to observation and interpretation of non-human primates' and humans' behaviour, they are also an excellent heuristic to behavioural studies. In light of the theory of evolution, stating that human cognitive capacities and behavioural patterns are unique to our species is a fundamentally anthropocentric position, as if humans would have a privileged place in the world of the living organisms.

Hence, we emit and test the hypothesis that crossed influences are essential to reach an understanding of human and non-human primate behaviours and that this approach seems to be scientifically justified.

The extended evolutionary synthesis debate: Some ontological, epistemological and historical dimensions

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Within the plural landscape of contemporary evolutionary biology, a public debate is gaining ground: whether a "new" conceptual framework, i.e. the Extended Evolutionary Synthesis (EES), is needed to extend or go beyond the boundaries and explanatory power of the Standard Evolutionary Theory (SET). For the proponents of the EES, the narrow and "gene-centric" stance of the SET fails to capture the full gamut of causal processes entangled in the evolution of biological diversity (in particular, developmental bias, niche construction, developmental plasticity, and extra-genetic inheritance). In that sense, the EES identifies an incomplete ontology of evolutionary processes in the SET. Here, I argue that the EES can only be thought of as an "extension" on ontological grounds. As a conceptual framework that emphasizes organismal causes of development, inheritance and differential fitness, the role of constructive processes in development and evolution, and reciprocal representations of causation, the EES delivers an "extended ontology of evolutionary processes", including those that generate novel variants, bias selection, modify the frequency of heritable variation, and contribute to inclusive transgenerational inheritance. Additionally, I discuss two far-reaching dimensions of the EES debate: a) epistemological: by focusing on the explanatory goals of this framework, the centrality of the "organism", interdisciplinary integration, and tensions subtending its conceptual apparatus; b) historical/ historiographical: by briefly discussing i) the history of previous attempts to extend the Modern Synthesis (from the 1960s onwards), ii) organism-centered perspectives in the early decades of the twentieth century (in both hegemonic centers of knowledge production and sidelined countries), and iii) what does it entail to write about "syntheses" in the history of evolutionary biology. I conclude that some of the most important historical/historiographical dimensions raised by the EES debate lie in the intersection of these three issues.

Multiple realization in systems biology

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Polger and Shapiro (2016) claim that, unlike artifacts created by craftsmen, cases of multiple realization (MR) in naturally occurring systems are uncommon. Based on cases from systems biology, this article argues that, first, the gap between artifacts and naturally occurring systems is not as sharp as Polger and Shapiro envision, and second, cases of MR are very common in naturally occurring systems from the perspective of systems biology. Finally, this article examines the scope problem of MR, namely, the question that how common MR is common enough.

Many attempts to tidy up the MR thesis and evaluate its evidence have been made, both for and against it. However, the most remarkable development regarding the thesis during the last two decades is perhaps due to Lawrence Shapiro's work (2000, 2004, 2008; see also Polger and Shapiro 2016). Based on what Shapiro and Polger have accomplished during the last two decades, a well-articulated official recipe for judging cases of MR is put forward (Polger and Shapiro 2016).

With this recipe, Polger and Shapiro claim that cases of MR in naturally occurring systems are not as common as in artifacts made by humans. In response to their claim, I argue through detailed analysis of concrete cases from systems biology that MR is no less common in the biological world than in artifacts. The reason I select examples from systems biology is partly because the thriving new discipline enjoys both an engineering perspective where design principles (called network motifs in systems biology) are being discovered and a biological perspective where the target of investigation is the biological system. The interdisciplinary nature of this new area also shows that the gap between artifacts and naturally occurring systems is in fact not as large as many would imagine.

The case of MR examined in this essay involves two kinds of network motifs: negative autoregulation network (NAR) and incoherent type-1 feed-forward network (I1-FFL). These are building-block patterns that recur in different organisms or species, which appear more often than random networks (due to the selection advantages they endow to their bearers). One remarkable thing about these two kinds of motifs is that they both are able to fulfill the function of boosting the response time of the transcription network. This, therefore, constitutes a case of MR in terms of Polger and Shapiro's recipe because two different (causal) networks accomplish the same (or at least similar) function.

Having established a case of MR, the essay then considers if MR is very common in the biological world. Given the fact that the case of MR involving NAR and I1-FFL occurs in many different species, and that other pairs of network motifs that accomplish the same functions (e.g., robust patterning in development) can be easily found in the biological system, the essay concludes that MR exists commonly in naturally occurring systems.

Genetic engineering, synthetic biology and reductionists explanations in philosophy of biology

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Recent developments in genetic engineering derived from CRISPR/Cas9 technology – published in 2012 – caused an increase in the experimentation and manipulation of biological systems. At the same time, the reductionist conceptions of genetics and evolution that formed the basis of biology in the 20th century are being reconsidered and giving way to new non-reductionist conceptions of representation of biological systems, such as Extended Evolutionary Synthesis and the attempts to redefine gene.

However, genetic experimentation and synthetic biology using reductionist and interventionist tools create new biological phenomena. The simple manipulation of DNA segments, without manipulation of epigenetic structures, without environmental changes or other non-reductionist considerations has generated a whole range of new organisms, new effects, new biological phenomena, changes in phenogenesis, changes in inheritance patterns and the creation of artificial life forms. All of this from reductionist and interventionist conceptions and practices, firmly based on the neo-Darwinian Synthesis paradigm. This is the experimental argument in defense of reductionist explanations in biology.

Would the experimental argument be a possible defense of reductionist a gene-centric stance? It is evident that returning to the classic concept of molecular gene – in which there is still a direct relation 1 to 1 between genes and phenotype traces, between DNA segments and mRNA/polypeptide – is inconceivable. Epigenetics is immensely important, and one of the most exciting fields of biology research today.

Thus, this study proposes the need to return to the debate about reductionist explanations in biology, taking into account the new developments in genetic experimentation and highlighting the importance of understanding the two aspects of scientific work, i.e., science as representation and science as intervention.

Empirical support and relevance for models of the evolution of cooperation: Problems and prospects

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Recently it has been argued that agent-based simulations which involve using the Prisoner's Dilemma and other game-theoretic scenarios as a means to study the evolution of cooperation are seriously flawed because they lack empirical support and explanatory relevance to actual cooperative behavior (Arnold 2014, 2015). I respond to this challenge for simulation-based studies of the evolution of cooperation in two ways. First, I argue that it is simply false that these models lack empirical support, drawing attention to a case which highlights how empirical information has been and continues to be incorporated into agent based, game-theoretic models used to study the evolution of cooperation. In particular I examine the work of Bowles and Gintis and show how they draw upon ethnographic and biological evidence as well as experiments in behavioral psychology in their models of the evolution of strong reciprocity (2011). Ultimately, I take Arnold's misdiagnosis of the empirical support and relevance of these models to result from too stringent standards for empirical support and a failure to appreciate the role the results of these models can play in identifying and exploring constraints on the evolutionary mechanisms (e.g. kin selection, group selection, spatial selection) involved in the evolution of cooperation. Second, I propose that a modified version of Arnold's criticism is still a threat to model-based research in the evolution of cooperation: the game-theoretic models used to study the evolution of cooperation suffer from certain limitations because of the level of abstraction involved in these models. Namely, these models in their present state cannot be used to explore what physical or cognitive capacities are required for cooperative behavior to evolve because all simulated agents come equipped with the ability to cooperate or defect. That is, present models can tell us about how cooperation can persist or fail in the face of defection or other difficulties, but cannot tell us very much about how agents come to be cooperators in the first place. However, I also suggest a solution to this problem by arguing that there are promising ways to incorporate further empirical information into these simulations via situated cognition approaches to evolutionary simulation. Drawing on the dynamics of adaptive behavior research program outlined by Beer (1997) and more recent work by Bernard et al. (2016), I conclude by arguing that accounting for the physical characteristics of agents and their environments can shed further light on the evolutionary origins of cooperation.

Preserving the evolvability of what? Biological conservation and the objects of persistence

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Conservation biologists have increasingly called for measures aimed at preserving the capacity of biological systems to evolve. The preservation of this capacity to evolve, hereafter “evolvability”, is generally seen as a way to achieve the persistence of certain biological features by enabling biological systems to adapt in response to environmental change. In this paper, I consider what thinking about the preservation of evolvability as a conservation measure says about what conservation biologists do and do not value about the particular biological systems they aim to conserve. To do this, I look at the role of evolvability preservation in traditional biodiversity-based approaches to conservation, such as species conservation, and I compare this to its role in less traditional, although increasingly more common, ecosystems-based approaches. Although these approaches arise from distinct traditions, and are often viewed as being at odds with each other, I show how thinking about the preservation of evolvability brings to bear some important similarities between them. Specifically, I highlight the dichotomy in each approach of “what is desired to persist” versus “what is allowed to change”, and I argue that such “evolvability-thinking” brings biodiversity-based approaches more in line with ecosystems-based approaches. This has a few consequences. First, it shows that the role of evolvability in conservation is much more important than first impressions suggest. Second, it motivates an understanding of evolvability as a rich biological concept that recognizes the causal significance of ecological and developmental factors in evolution. Third, it suggests how “evolvability-thinking” could potentially bridge two approaches to biological conservation---i.e., biodiversity-based approaches and ecosystems-based approaches---often viewed as disparate and incompatible.

RNA-DNA hybridization: A story of invention and vanished recognition

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What can we learn about today’s biological R&D from an account of a groundbreaking invention? In this presentation I will briefly trace the outcome of an important technique that seemingly has become marginalized; I will also examine the significance of this occurrence on today’s production of biological facts and artifacts. The invention of DNA-RNA hybridization in 1960 by Ben Hall and Sol Spiegelman had a powerful impact on the theory and discourse of molecular biology. Hybridization allowed biologists to bridge the theoretical realm and the material world of organisms. Importantly, Spiegelman and Hall correlated the hypothetical concept “information flow” with a mechanism capable of making an RNA copy of DNA, thus giving mRNA an operational meaning. Other scientists immediately recognized the power of the technique and introduced improvements. In 1965, Gillespie and Spiegelman combined several modifications and described a procedure for hybridization; their protocol immediately won immense popularity and was used to establish the basic facts of molecular biology. Since the mid-1970s, hybridization has been at the core of many DNA technologies that have revolutionized the field of molecular biology and driven biotechnology to its current position. These include the widely known techniques of polymerase chain reaction (PCR), Southern blot, DNA micro-arrays and also Crisper-cas9, in which hybridization is an essential feature of its operation (as guide-RNA). Notwithstanding its current success, the inventors' names have disappeared from the literature, and a description of the original invention is hard to find. This led me to trace the trajectories that this technology took, once it was released into the scientific domain. I will show that literary embeddedness and experimental containment, as well as several practices that have become routine in today's biological R&D can, at least partially, explain this disappearance. I will also discuss whether these practices challenge the traditional style of biological research, and what may be the implications of such practices on the study of biology and biotechnological enterprises.

Epidemiologic evidence: Use at your “own risk”?

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The use of epidemiologic evidence in clinical decision-making is now commonplace. It is exemplified by decision aids that represent the results of a clinical trial, showing how many individuals suffered the bad outcome with and without the intervention. It is here that the problem of the meaning of population evidence for the individual rears its thorny head: what meaning or relevance does this evidence have for clinical decision-making when it is an individual patient rather than a population who must decide whether to use the intervention? The language of risk has become the new language of diagnosis and prevention in medicine. Medical treatments are often said to benefit individuals by reducing their individual risk of the outcome. The problem of the meaning of population evidence thus involves the challenge of understanding this idea of the patient's own individual risk. Here, I argue that the patient's risk is an ontic concept. In light of serious problems with the concept, I provide an epistemic reinterpretation of the evidence that epidemiology provides for patient care.

I start by arguing that the patient's risk is an ontic probability: the patient's propensity towards the bad outcome. Yet epidemiologic evidence does not primarily measure the patient's individual risk, which makes this interpretation of epidemiologic evidence misleading. Moreover, understanding epidemiologic evidence as measuring the patient's risk can promote overdiagnosis (as an individual risk is inaccurately ascribed to patients) and overtreatment (as patients are misled into adopting lifestyle changes and consuming medications to lower their own risk).

Considering these concerns, I propose an epistemic reinterpretation of epidemiologic evidence as informing a rational credence that is equal to the aggregate treatment effect. Rather than measuring risks, this interpretation sees the role of epidemiologic evidence as informing medical uncertainty, and is consistent with the idea that clinical medicine is a paradigm case of decision-making under uncertainty. I end by exploring some implications of this view for risk communication and shared decision-making.

Beyond cheating: The emotional component

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Saul Sarabia-Lopez, IIF-UNAM, Mexico
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The literature on cheating detection coming from Evolutionary Psychology is well known (Cosmides and Tooby, 1992, Spence, 2004, Ermer et al. 2006, Litoiu, 2015). According to them, cheating behavior arises when an individual infringes a social rule. Or when an individual receives the benefit of being part of a social contract but he is not willing to pay the cost of being so. This notion has a social component, viz., it always presupposes a social commitment that the cheater contravenes and someone/something paying the cost of that transgression. Evolutionary psychologists and the existence of a Darwinian module to detect cheating has been widely criticized (Buller, 2005), based on good reasons.

Our proposal wipes away Evolutionary Psychology approaches since we advance the problem differently, including further elements that the now classic Litterature did not take into consideration. We account for cheating behavior as follows. First and more importantly, we distinguish between cheating and deceiving. Secondly, we single out studies in which cheating is detected (CD) and those in which cheating is produced (CP). Third, once those distinctions take place, we expand that concept of cheating to various scenarios where subjects pay the cost of such behavior. To support our claim, we offer some experimental results where we faced subjects to stimuli containing various hypothetical conditions interchanging the person who receives the consequence of the cheating behavior. Besides measuring the ability to detect cheaters, scenarios were aimed to elicit different emotional reactions. Along these lines, we linked cheating and emotional reactions. We assert this link is the clue to elucidating and understanding cheating as a phenomenon.

Psychic disturbances at organic functions. About an anomaly in the relation between organ and function

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Since Galen, the physiology has been closely linked to anatomy in the western medicine. The physiology has been habitually a teleological explanation of the human anatomy, following the premise that every organ must fulfill a function.

However, since the investigations of Sigmund Freud, it was observed an anomaly in the relation between organ and function. In effect, during the course of the certain nervous diseases, some organic functions were disturbed without that apparently the organ suffering damage or would be affected.

The sick patients studied suffered alterations the one or more physic functions: respiration, circulation, vasomotor innervation, glandular activity, etc. However, the medical examination did not reveal any organic damage or alteration. Freud called these diseases functional neuroses, for highlight this anomalous fact.

Moreover, the comparison between organic motor paralysis and hysterical paralysis showed a singular fact. While the organic paralysis conforms to the real anatomy, the hysterical paralysis did not take into consideration the medical anatomy, but imaginary anatomy. In these cases, the organ not only does not fulfill its function but it could play a foreign role, from a biological point of view.

My first purpose in this paper is to explain the way that functional neuroses alter certain organic functions. Next, I will extract some consequences about the relation between organ and function in human biology. And, finally, I will show that physiology and anatomy are not as closely related, as the medicine will think.

Constitutive relevance discovery without interventions: Boole meets Bayes nets

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In recent years, the topic of inferring relationships of constitutive relevance has received considerable attention within the debate on mechanistic explanation. The obvious reason is that the mechanistic ideal of explanation is interesting for scientific practice to the extent that it can form the basis of a methodology with direct applications (e.g., Weber, 2018). Most accounts (for an overview, see Kästner and Andersen, 2018) currently on the market aim at identifying constitutive relationships on the basis of systematic interventions. In this paper, in contrast, we focus on methods for constitutive discovery that do not rely on interventions. Our aim is to explore the strengths and weaknesses characteristic of the Boolean (Harbecke, 2015) and the Bayes net (Gebharter, 2017) approach to constitutive inference. In the course of our investigation, we shall defend the following main claims:

1. Each of the two approaches faces certain limitations in its applicability in actual research,
2. the strengths and weaknesses of the two approaches are complementary in an interesting sense, and
3. there is a way to combine and synthesize the two methods formally and heuristically.

Our investigation proceeds as follows. We first characterize the main ideas of the Boolean and the Bayes net approaches in parts 1 and 2. We then review two examples from neuroscientific research highlighting the relevance of constitutive inferences and the methodological questions behind it (part 3). The first one is the well-established case of spatial memory (Morris, Garrud, Rawlins, & O'Keefe, 1982). The second one is a more recent and more specific example on the mechanisms of prosocial behavior (Lambert, Declerck, Boone, and Parizel, 2017). Subsequently, we offer a comparative assessment of the strengths and weaknesses of the Boolean approach and the Bayes net approach (part 4), and we show how the two might be combined into a much stronger hybrid methodology that no longer bears the main weaknesses of the two approaches (part 5). Finally, we summarize our argument and point to some open questions in the context of constitutive inference (part 6).

The art of growing old: Environmental manipulations, physiological temporalities and the advent of *Microcebus murinus* as a primate model of aging

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Microcebus murinus is a small Malagasy lemur that, since the mid-1950s, has been bred and raised in metropolitan France to serve as subject for experiments. Since the establishment of the first closed colony of grey mouse lemurs at the laboratoire d'Ecologie of the French National Museum of Natural History, their uses in the laboratory have evolved from "specific studies" to "analogous studies". (Löwy I, 2000) Initially taken as sole representatives of their species, these experimental organisms have been employed since the early 1990s by research groups from several institutions in France to develop a natural primate model of aging and age-related neurodegenerative diseases, especially Alzheimer's disease.

While it now provides a biological material for the laboratory study of normal and pathological aging, the "old grey mouse lemur", identifiable by its whitened coat, shortened snout and slowed gait, has long been a curiosity. In Brunoy, it was not before the 1970s that the average life span of captive mouse lemurs, which had initially stagnated under the fateful threshold of four years, started to increase steadily. It gradually reached the current figure of approximately six years, with some individuals living close to the maximum lifespan of thirteen years. Rather than manifesting spontaneously occurring demographic trends, the increasing number of elderly primates resulted from decades-long efforts made by scientists and laboratory animal caretakers to improve colony management. Over the years, work to understand and counter erratic reproduction patterns, frequent fatalities and low life expectancy in captivity also became intertwined with more specific interventions targeting the ageing process in this species.

This paper proposes to contribute to the recent endeavor of historians and philosophers to investigate the instrumentality of the "situatedeness" of laboratory animals in certain areas of contemporary biology and biomedicine. (Ankeny R. A., Leonelli S., Nelson N. C., Ramsden E., 2014) Through the grey mouse lemur case, I intend to explore a way of obtaining laboratory organism exhibiting certain traits, here senescent traits and behavior, through intervention on their surroundings rather than on the elements of their bodies. Detailing three facets of physiological experimentation and captive breeding with this species from the mid-1950s to the present day, I will examine how the advent and maintenance of such animals in two French laboratory breeding facilities have been associated with several developments. One was the adoption of the notion of "social stress" to improve colony management and the related development of spatial arrangements and monitoring procedures to keep intraspecific relationships in check. A second was the acquisition of a relative command over the climatic factors regulating the physiological rhythms and cycles of the mouse lemur. The third was the dissociation of two ages – chronological age and cyclical age – and the efforts to accelerate aging in this species through the experimental manipulation of the annual light conditions of its physical environment. It will be argued that the "old grey mouse lemur" is, in part, the product of ecological knowledge and techniques focusing on the relationships of organisms with their environment and with each other.

Environmental ethics, meet modelling: Evaluating nature-society dualism with tools from philosophy of science

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Nature-society dualism—that is, the treatment of "nature" and "society" as non-overlapping categories—is widely criticized on environmental-ethical grounds. It is, for instance, associated with the devaluation of nature. It is also associated with environmental-ethical theories that neglect to give humans any possibility of a positive environmental role. Moreover, nature-society dualism is, one might think, incompatible with the pervasive interconnectedness of humans and their environments, especially in a highly humanized world. That being said, there are many different ways to understand nature-society dualism. On some understandings, the dualism might be susceptible to these objections, but, on other understandings, it might satisfy critics' criteria for success. By drawing on recent philosophical work on scientific modelling and the aims of science, I argue that one version of the dualism can indeed meet the specified criteria. In particular, dualism about nature and society as subsystems in models of interconnected natural and social systems is sometimes justifiable as an idealization in contemporary research on so-called "socio-ecological systems" and "coupled human and natural systems." Such research is aimed at achieving policy-relevance in a highly humanized world, and its distinctive dualism not only meets the specified criteria but also may facilitate tractable interdisciplinary research.

Is there a unique zero-force law in evolutionary biology?

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In *The Nature of Selection,* Elliott Sober (1984) defends and develops an account of evolutionary theory as a theory of forces analogous to the theory of forces used in Newtonian Mechanics. The basic idea behind Sober's account is that researchers could account for changes in evolutionary populations by citing the evolutionary forces (e.g., drift, selection, mutation, etc.) acting on the population in much the same way that one could account for the motion of objects by citing the forces acting on the object in Newtonian mechanics. In order for the "force analogy" to be effective, four "Newtonian features" must accompany the theory:

1. the forces cited must be causal;
2. there must be an account of how the forces act alone and how they act in combination;
3. there must be some zero-force law that acts as a baseline describing a state where no forces are acting on the system being studied; and
4. the net effect of all forces acting on the system must be able to be decomposed into component forces (Stephens 2004).

While the force analogy is popular among both biologists and philosophers (Stephens 2004), Sober's account is not without its critics. Some maintain, for example, that drift and selection cannot be properly called forces, arguing either that selection and drift are not causal (e.g., Matthen and Ariew 2002, 2005, 2009; Walsh et al. 2002; Walsh 2004, 2007) or that causality is necessary for something's being a force but not sufficient and thus drift cannot be counted as a force (e.g., Brandon 2006; McShea and Brandon 2010; Earnshaw 2015).

While the debate over the force-hood of selection and drift is not quite settled, another debate has arisen in the context of the evolutionary forces model. Among those who think the force model is adequate, there is some disagreement over what should count as the zero-force law of evolutionary biology. Sober (1984) suggested that the Hardy-Weinberg law should be that zero-force law (see also Barrett et al. 2012). However, others have suggested that other zero-force laws were more apt (Brandon 2006; McShea and Brandon 2010; Earnshaw 2015). These detractors argue that their candidate zero-force laws are either more conceptually plausible or better empirically supported. On the surface, it seems that what genuinely constitutes a force is central to the disagreement. However, we argue that "forcehood" is merely a distraction. Instead, we maintain that the debate is motivated by pragmatics. Taking a page from Elisabeth Lloyd (2015), we argue that the most apt "zero-force law" or baseline depends critically on the research question being pursued. We defend that claim by showing that each proposed zero-force law is empirically indistinguishable from the others, and that the conceptual differences are driven more by the question being pursued than any deeper conceptual issue about forcehood.

Cultural evolutionary theory needs an account of cultural information

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Cultural evolutionists frequently define culture in terms of information. They generally agree that culture is information transmitted through social channels, and that it plays a causal role in individuals' behaviours (e.g., Durham, 1991; Mesodui et al., 2006; Boyd & Richerson, 2005). While this "informational turn" has proved successful—especially for being able to import models from biology to cultural evolution—it is often unclear what, precisely, "information" means in this context. In fact, some authors argue that "we do not need a highly theorized account of cultural information. The notion is best understood as an open-ended heuristic prompt which encourages an examination of the ways in which bodies of behaviours, skills, beliefs, preferences, and norms reproduce from one generation to the next" (Lewens, 2015, p. 45). Contrary to this view, I argue that a positive and detailed account of cultural information is necessary for certain kind of cultural evolutionary studies. In particular, it is required for the operationalization of culture in quantitative studies, such as in empirical research on the drivers of cultural complexity (Anderson & Read, 2016). After scrutinizing the use of informational talk in cultural evolutionary theory, I argue for the insufficiency of the heuristic use of cultural information and the need for a thorough account. Particularly, I suggest that one can move beyond the mere heuristic use of information by drawing on work on biological information conducted over the last few decades by evolutionary biologists and philosophers of biology.

Historicizing the homology problem

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According to traditional evolutionary accounts, parts in different organisms are homologous when they derive from the same part in a common ancestor. Such "genealogical" accounts of homology leave important questions unanswered. What exactly does it mean for one part to be derived from another part in a common ancestor? How can these relationships of evolutionary derivation be recognized and validated? Contemporary "developmental" accounts of homology (e.g. Wagner 2014) supply promising mechanistic answers to these questions. Many philosophers have therefore worked to eliminate or adjudicate lingering tensions between contemporary genealogical and developmental perspectives. But this framing of the homology problem overlooks more than a century of post-Darwinian conceptual development. Where did the genealogical account come from in the first place? Is it really the appropriate foil to developmental genetic approaches? In this paper I argue that the genealogical perspective is not so stable as it has generally been portrayed, and that this historical variation has important philosophical consequences. I focus on two episodes in which biologists have rejected definitions of homology that appeal to common ancestry and instead championed more operational approaches. Boyden (1943, 1947) and Blackwelder (1952) defended the classical morphological criteria of "essential similarity" against the evolutionary taxonomy of Simpson (1959, 1961) and others. More recently, a minority of cladistic systematists from Patterson (1982) to Brower & de Pinna (2012) have emphasized the close (some would say synonymous) relationship between homology and synapomorphy. These episodes reveal deep connections between the fate of the homology concept and broader developments in systematics. They also suggest that theoretical definitions of homology (such as the genealogical and developmental notions considered in recent philosophical work) do not exhaust the epistemic import of the concept. Additional methods and concepts, which I refer to collectively as characterization, are required to identify, test, and revise homology judgments. These practices are but loosely coupled to theoretical perspectives on homology and further work is required to clarify the standards that govern them.

Personalized medicine: A science of the individual?

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Personalized medicine is aiming to account for specific characteristics of individual patients. It is promised to develop more precise disease predictions and targeted treatments through molecular profiling of disease risk and treatment response. Accordingly, an interesting question for philosophy of science is how the "personal" gets constituted through the new practices. How is knowledge about individual patients obtained? And to what extent does personalized medicine present a "science of the individual"? One way of approaching this question is to ask whether personalized medicine breaks with traditional approaches in medicine that rely on statistical averages and large reference classes. Our response to the question is two-fold. On the one hand, most developments within personalized medicine so far present an extension – rather than a break – with population sciences. Identification and interpretation of individual variation is done in relation to information on the many, understood as ever-growing amounts of population data. For instance, individual genomes are compared to a reference genome, and biomarkers are identified through statistical comparison of genetic variation among phenotypically defined data populations. On the other hand, some methods challenge the ways in which we typically draw inferences in the life sciences. Specifically, the use of personalized mouse models, xenografted with the tumor cells of an individual patient, have been highlighted as breaking way for a "one patient paradigm" in medicine. We explore how inferences are drawn from interventions on such “mouse avatars” and how these are translated into clinical information with implications for individual patients. We end with concluding remarks on how “the personal” is continuously shaped and negotiated in relation to larger collectives and to other species. In this discussion, we also draw attention to medically relevant aspects of the individual that cannot be represented through quantitative metrics or have to be ignored as an experimental requirement in the case of mouse avatars.

Informal models in biology

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Some abstract models in science are formally specified, while others are not. For instance, the Lotka-Volterra Model of predator-prey-interaction is formal in the sense that the mathematical equations that define it provide an explicit set of syntactical rules according to which a given manipulation of the model leads to a specific model output. By contrast, what experimental biologists often mean by “models” are accounts of molecular mechanisms that are described using natural language or represented using cartoon diagrams. These models do not seem to involve formal specifications and might therefore be called “informal models”.

There seem to be clear differences between the ways in which formal and informal model are used in scientific practice. Reasoning with an informal model is not constrained by explicitly given rules, and making sense of it requires taking into account that the model is embedded in a web of collateral information that is left implicit. However, it is not fully obvious whether the distinction between formal and informal models can be made precise, and whether informal models really are just formal models in disguise (or perhaps the other way round).

Granted that the distinction can be made, a further question that may be asked is whether informal models are models at all. As already mentioned, scientists themselves refer to them as models, and some characteristic features of modeling, such as hypothetical reasoning, abstraction and idealization, seem to be involved in their use. However, they do not mediate between theory and experiment in the same way as other models do. If we take a look at a textbook of molecular or cell biology, models appear to constitute the theory rather than acting as mediators. Furthermore, their status as autonomous objects of surrogative reasoning is less obvious because reasoning with informal often comes close to reasoning about the target system directly.

I argue that the distinction between formal and informal models is philosophically interesting and has not received sufficient attention. I discuss the two raised puzzles about informal models in biology using illustrative case studies and show that the tension with common conceptions of scientific models is not accidental, but directly related to their informal nature. I argue that, independently of whether or not in the end we decide to call them "models", they work very differently from formal models.

The many faces of the postgenomic revolution

Stephan Guttinger, London School of Economics, UK

The ongoing paradigm shifts in the postgenomic life sciences create a lot of excitement amongst researchers, both in the natural sciences and in the humanities. New findings from fields such as metagenomics, environmental epigenetics and microbiome research are transforming our picture of the human body and challenge existing notions of biological individuality and the nature of our genome(s). They also promise new avenues for medical treatments.

But the postgenomic revolution is a multifaceted phenomenon. And whilst the promises and excitement associated with it have gained significant attention from researchers, potential negative side effects of these complex paradigm shifts have been less explored. The aim of my project is to identify such negative side effects (in particular in debates about health and science policy) and to suggest solutions for how to address them.

In the context of this talk I will focus on a particular case study, namely the debate about childhood vaccination. Surveying online anti-vaccination materials I will show that postgenomics is bringing a new twist to this heated debate: as our understanding of microbes – viruses in particular – is shifting from one of necessary pathogens to one of "integrated part", anti-vaccination activists are beginning to shift their strategy accordingly. They move away from debates about the safety of specific vaccines (such as the MMR vaccine) and move towards a more general narrative of vaccines as attacking necessary components of the healthy human organism. Importantly, anti-vaccination activists are claiming that this view is not just theirs but that of mainstream science, turning a former opponent into a central ally.

The analysis will show that the paradigm shifts within biology open up a space of conceptual fluidity that can be easily twisted and potentially misused. It will also show that this new breed of anti-vaccination arguments is helped by the way in which some researchers communicate – or sell – their findings. I will conclude by reflecting on ways in which this complex development can be addressed.

"The body for family": Biopolitics of living donor liver transplantation in South Korea

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Liver transplantations from living donors (Living Donor Liver Transplantations or LDLT) are more prevalent in South Korea than any other country in the world. The high proportion of living liver donors in this area has been usually attributed to low rate of cadaveric donations resulting from religious beliefs, and endemic diseases. Drawing on field work on LDLT in South Korea, however, I attempt to show that the high rate of living donors cannot be explained away by local religion and specific medical conditions. I argue that liver transplantation as a socio-technological practice has been shaped by a biopolitical enterprise, which naturalizes both recipients' demand for transplantable organs and donors' willingness to give their organs to their loved family member. I elucidate that the biopolitics around "the body for family" has been underpinned by knowledge politics such as production of ignorance (Proctor, 2008), local institutional context and intrafamilial politics, which both contributed to making donors' suffering socially invisible. Revealing LDLT's biopolitical implications in South Korea, I propose that we need to pay attention to ethical challenges raised by the transplantation technologies and their practices.

A game-theoretic model of Richard Prum's "aesthetic selection"

Derek Halm, University of Utah, USA

Richard Prum in *The Evolution of Beauty* (2017) proposes a new selective force in evolution by natural selection: "aesthetic selection." Rather than supposing that all animals maximize fitness through mate selection, Prum argues that there are sufficient cases to suggest some animals may select for aesthetic characteristics instead of maximizing fitness. According to Prum, some female animals may select for beauty over perceived fitness in sexual partners. This theoretical departure places the evolution of a species in its own hands rather than solely in the hands of natural selection. Rather than maximizing fitness, "aesthetic selection" places individual preference as the driving force of sexual selection. Put another way, if an organism thinks a beauty signal is sufficiently sexy, they will select for it over other factors. To support this hypothesis, I explain how Prum's "aesthetic selection" arose as a reaction to Amotz Zahavi's "handicap principle" (1975) and its theoretical commitments concerning sexual selection. Following that, I construct an evolutionary game to show the long-term interaction of different players. The game compares hypothetical organisms that select for different traits and how, under certain circumstances, beauty can become a dominant strategy over selecting for fitness. While beauty may be a successful sexual strategy, the game shows that beauty is not always to a species' advantage over time: degeneracy is a possibility. While the game provides additional evidence for Prum's theory, more empirical work is necessary to determine what species can be understood via "aesthetic selection" rather than via natural selection more generally.

Is there such a thing as biological altruism?

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Biological altruism is one of the most extensively discussed topics in evolutionary biology and philosophy of biology. According to the well-accepted definition, biological altruism is a behavior where an organism increases the fitness of others at its own expense. As opposed to the psychological notion of altruism which is used to describe human behavior, the definition of biological altruism is not supposed to be based on conscious intentions. Thus, an organism is not said to behave altruistically because it wants to sacrifice its fitness for the sake of others; instead, an organism's behavior is classified as altruistic because it has the effects of increasing the fitness of others at its own expense. However, our analysis reveals that biological altruism is not a well-defined notion in biological terms, and that it does carry a vestige of the intentional concept familiar to us from the human domain. We show that there are other types of behaviors that fit the formal definition of biological altruism but are nevertheless not treated as altruistic. The most important example is parasitism: although hosts' behavior also benefits their parasites at their own expense, hosts are not seen as altruistic but rather as victims of parasitic manipulation. In order to distinguish altruism from parasitism, one must identify the donor of fitness as an "actor" rather than as a "recipient" of manipulation. But on what basis can we designate one party in an interaction among non-human organisms as active and the other as passive? We consider various possible mechanistic and evolutionary criteria, and find them insufficient. We conclude that there is no sound biological basis for telling apart biological altruism from other, seemingly unrelated behaviors.

"Playing with a dog:" Edward Stuart Russell on animal behavior

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In 1982, the University of Chicago Press reprinted Edward Stuart Russell's classic history of morphology, *Form and Function*, which was originally published in 1916. Pointing to the renaissance of interest in morphology, George Lauder commented that it was particularly appropriate to reissue Russell's "magnificent analysis of the history of thought on the relation between form and function" at this time. Russell's scientific interests were wide–ranging, however, and Form and Function was only his first book. He was an active and influential participant in the ongoing debates concerning the philosophy of biology until his death in 1954, and his later work exhibited the same scholarly depth and careful philosophical reflection as Form and Function.

Russell belonged to a distinguished intellectual community encompassing a wide range of interests. They combined outstanding experimental work in science with sensitivity to the philosophical presuppositions informing attitudes toward biological explanation. He participated in lively debates concerning the philosophical foundations of biological thought in a number of scientific and philosophical societies, developing his philosophy of biology in discussions with Alfred North Whitehead, Conway Lloyd Morgan, and John Scott Haldane, among others. His work in the twenties and thirties met with a receptive audience open to consideration of a wide range of philosophical positions.

Russell's organismal philosophy of biology represented an approach to the life sciences shared by a circle of British scientists and philosophers who raised searching questions concerning the methodology and philosophical foundations of biology. The American zoologist William Emerson Ritter had argued for an organismal conception of life, and Russell felt that Ritter's work had avoided both a reductionist mechanism and a vitalistic dualism. For Russell, the central idea of Ritter's work was that "the organism in its totality is as essential to the explanation of the elements as the elements are to an explanation of the organism. Thus, the organism, taken alive and whole, is the primary unit for biological study." In developing his own version of organismal biology as an integrative view of the organism, Russell addressed the fundamental problem of the relation of the parts to the whole. As he understood it, the organismal point of view opened the possibility of a "real and autonomous biology." This was the methodological standpoint that informed Russell's work in ethology. In practice, it translated into advocacy for the study of the intact animal in its natural environment, or as close to it as possible. This is perhaps best illustrated in his article "Playing with a Dog," published in the *Quarterly Review of Biology.*

The British organismal biologists carried on a tradition of philosophical debates concerning the nature of biological phenomena, the adequacy of mechanical explanations in biology, and the status of biology as a science. In this paper, I will explore Russell's philosophy of biology in the context of the British scientific community, investigating the importance of his professional intellectual circles for the development of his thought.

Automated judgments: Historicizing algorithms and AI in biomedicine

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I argue that the discursive relations that necessitated scientific measures for decision making spurred clinical medicine's investments and interests in algorithmic technologies for classification and diagnosis. To do so, I deploy a critical engagement with Foucault's genealogical method. I spell out the relations of discourse that connected clinical decision-making to computer sciences. Post-war medical literature identified three problematic aspects of clinical decision-making: the use of the best information at the bedside, practice variation, and providing a scientific rationale for clinical judgment. My previous research has shown how, in an effort to address these problems and improve clinical decision-making, clinical epidemiology came to reform medical education and training in order to make clinical judgment more evidence-based. Clinical epidemiology resolved underlying problematizations of clinical judgment by providing evidence about the effectiveness of treatment to determine the best course of action. What was later called evidence-based medicine (EBM), however, required accurate diagnosis in order to make the correct treatment decisions – treatments are effective only insofar as they are prescribed for the correct illnesses and conditions. The intractability of making good judgments about diagnosis in the clinic led to medicine's attempt to resolve those problems through computer technology and, later, the development of clinical algorithms, Artificial Neural Networks, and Artificial Intelligence to inform clinical decision making. My paper demonstrates the connection between EBM (the relations of discourse) and these computer science technologies through the following themes: the computer and the clinic, questioning medical authority, establishing new measurements, reforming medical education, justifying new sciences in clinical care, and linking practice with outcomes. What my analysis offers is a way to connect the discursive and social conditions that led up to the institutionalization of computer algorithms with prior forms of non-computational algorithmic thinking in EBM.

How does plant reproduction challenge sexual criteria of biological individuality?

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Debates on biological individuality have traditionally focused on vertebrate animal organisms. Authors such as Wilson (1999), Clarke (2010, 2011, 2012, 2013), Pradeu (2012), Herron et al (2013) or Godfrey-Smith (2016) have, however, broadened the issue by taking into account non-vertebrate, plants or unicellular organisms. In addition to the well-known problems of lack of strict morphological individuality, Clarke has more recently highlighted a series of difficulties that plants posed for the evolutionary and genetic conception of individuality. For my part, I would like to show more specifically here what the difficulties posed by plant reproduction are when thinking about biological individuality based on classical criteria of reproduction or sexuality. Indeed, sexual reproduction of plants is based on an alternation of generations (gametophyte, sporophyte) within complex life cycles. It is therefore not obvious, for example, that any new individual is the result of the development of a zygote, since this is not the case for the gametophyte. However, the latter is generally considered as an organism in itself. How can such paradoxes be solved? After introducing the biological elements of the problem, several epistemological approaches will be critically studied: the rejection of sexual criteria as non-universalizable, the interpretation of the entire plant life cycle as an individual; the pluralism of the criteria of individuality according to situations.

Mapping vs. representational accounts of models and simulations

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Scientific models and simulations are predominantly analysed as representational tools (Frigg and Nguyen 2017, 2016; Weisberg 2013; Giere 2010; Suárez 2010). Representational accounts expose how scientists think about models, this however does not mean that models have to be defined in terms of representation. Representationalism has recently been criticised as its ontological dimension undermines the epistemic one (de Oliveira 2018). A pragmatic approach with regard to models has been suggested.

In this paper, I argue for an alternative formal analysis of models. Contrary to the objections raised by Suárez (2003), I show that isomorphism should be used to define models. Furthermore, such definition allows to recover several aspects of representationalist analysis – the directionality and fallibility of models – by introducing an epistemic agent. Finally, mapping accounts fare better in explaining the reliability of inferences and the truth of conclusions based on models. These observations are supported by case studies (Markram et al. 2015) from the Blue Brain Project (BBP) and Human Brain Project (HBP).

1. Non-represented entities. The goal of BBP was to reconstruct the neocortical tissue of a rat with its dynamical properties. Based on simulations, it was hypothesised that the behaviour of the biological circuits depends on extracellular calcium. The justification of results relied on the assumption that the tissues were simulated correctly. However, the representation of calcium was not necessary for such simulations. This undermines the representationalist account of modelling. The mapping analysis provides a superior explanation of the success of the BBP.

2. Directionality. Even if one accepts Suárez's (2010) directionality argument against isomorphisms in the analysis of scientific representation, it does not follow that it should be applied to models. Subsequently, it is not certain that models should be understood as representational entities.

There are two different reasons to reject the directionality argument based on scientific practice. HBP has several sub-projects in which brains are either modelled or they serve as models to develop alternative computer architectures. If these techniques should succeed, the model relation should support the switch in directionality. The second observation comes from the building of computer systems that are intended to perform simulations of brains (BBP). In the construction phase, biological tissues serve as models for the construction of these systems. In the exploration phase, the relation is inverted. A notion of model based on isomorphism supports well this possibility. The directionality of perspective can be recovered when an epistemic agent is considered.

3. Epistemic justification and fallibility. There is a strong contrast between justification provided by representation and by isomorphism. Without qualification, anything can represent anything else. If model relations are analysed in terms of representation, the justification they provide is low. On the other hand, if an isomorphism holds between a source and a target, reliable inferences about the target can be drawn. The fallibility of modelling can be explained, as required by representationalists, by false beliefs of agents about the source-target relations. Such an explanation is compatible with mapping definition of models.

Wallace's 1858 essay on natural selection: Immediate and remote contexts

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There are few clues from the 1850s indicating why Wallace wrote what he did in his 1858 essay on natural selection. So historians have had to relate it to his formative years in the 1830s and 40s, and to his later autobiographical memories. The need to do this is much reduced once we recognize that the 1858 essay was written as an amplified and transformed revision of a conjectured canine varieties scenario (CVS) drafted around 1855 in Wallace's Notebook 4 (MSS pp 39–40). Like the essay this CVS was a direct countering of Lyell's view that species are limited in their variation. Wallace imagines that all the dog varieties except one become extinct, and that the surviving one increases in numbers and range and, becoming in effect a replacement species, gives rise to multiple new varieties. All of these varieties except one then become extinct, and this surviving variety again spreads in range and population, and so on.With this sequential process endlessly reiterated an indefinite departure from the character of the original species results ; and, Wallace says, all the facts can be accounted for.

The transformation of the CVS in 1858 brought two new contrasts to it:

i. the contrast between lax, effete domesticated animal living and rugged, vigorous wild animal lives ; and
ii. the contrast between the actual checked (by limited food especially) constancy and the potential unchecked exponential increasing of wild animal population numbers.

The essay's view of wild animal life was not a projection on to nature of Wallace's broadly socialist view of human society. On the contrary that view of human society is tacitly supported in the essay through an implicit third contrast

iii. between the individual self-helping struggling for existence of wild animal life and social and sympathetic human life.

This implicit animal and human life contrast (soon to be explicit in Wallace's own writings) probably drew on Spencer's *Social Statics* read by Wallace around 1853. The checked and unchecked population contrast (ii) probably drew on the Malthusian vindication of Lyell's view of species extinctions in Darwin's 1845 edition of his *Journal of Researches* which Wallace had access to in Malaya. The domestic and wild animal life contrast (i) was likely a novel reweaving of natural history commonplaces. Contrary to many writers on Wallace and Darwin, Wallace's 1858 theory is just as individualistic and non-group-selectionist as Darwin's; and was moreover entirely compatible with Darwin's analogy between natural and artificial selection, an analogy very probably embraced by Wallace as soon as he met it on reading Darwin's writings in 1859 and 60. The two men were quite right in thinking that they had converged independently on the same theory, and that the theory was not identical with this analogy but could be supported by it.

Justifying the use of temporal idealizations in biological modeling

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Discussions of idealization in philosophy of science tend to focus idealizations that simplify across spatial scales in order to understand large-scale autonomous features of complex systems. In focusing on cases of large-scale patterns that emerge across spatial scales, however, these discussions largely ignore the possibility that such patterns may emerge across temporal scales as well. In this paper I first demonstrate how the reductionism debate has set up discussions of idealization to examine only the ways in which idealizations may simplify across spatial scales. I then argue that similar large-scale patterns may emerge across temporal scales. Because certain patterns at larger scales are independent of the features of the system at smaller scales, we can justifiably use idealized models that distort features at smaller scales yet display the larger scale patters of interest. Just as these autonomous patterns can justify the use of idealizations that simplify spatial scales, I argue that they can also justify the use of idealizations that simplify temporal scales. In other words, I argue that the epistemic work of highly idealized models that capture large-scale temporal patterns is accomplished by idealization of features at shorter temporal scales. I use the example of biological optimality models to show how highly idealized models can capture large-scale temporal patterns and how this fact supports the long-term use of optimality models in biology. Unfortunately, because of the overwhelming focus on spatial scales, idealizations of this type have been largely missed by the existing literature on idealization, explanation, and modeling.

Investigating animal minds from the perspective of mental health

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Classically, the suffering of non-human animals has been viewed as different in kind from human suffering. Descartes famously argued that animals are incapable of experiencing pain, and merely react reflexively to bodily harm. Although this extreme view is not as prevalent as it once was, it still exists. Contemporary behaviorist J. S. Kennedy firmly held that we have no good reason to believe that animals can feel anything at all, and Peter Carruthers claims that, although animals technically have mental lives, they are not conscious, and therefore do not experience them. This kind of skepticism is made possible by the fact that it is difficult to produce any kind of evidence in favor of animal suffering (or consciousness in general). It seems as though any case of animal “pain” can be explained away with some reference to bodily instinct, which need not include any kind of experience of suffering.

The purpose of my project is to investigate animal suffering and consciousness from the perspective of mental health. In particular, I argue that at least some animals can experience Post-Traumatic Stress Disorder – a kind of suffering which is not easily explained merely with reference to stimulus response. Using specific case studies, I examine and compare the behavior of animals who have been affected by a traumatic event with the symptoms of human PTSD detailed in the Diagnostic and Statistical Manuel V. In the first study, a group of African elephants, all of whom were witness to the slaughter of their herds by poachers, killed over 100 rhinoceros – a violent act previously unheard of in elephants. Ecologists, puzzled by the non-normative behavior of the elephants, sought a psychological explanation. In the second study, a chimpanzee named

Jeannie was released from the New York Laboratory for Experimental Medicine and Surgery in Primates (LEMSIP) after exhibiting "serious emotional and behavioral problems." The symptoms of both the elephants and Jeannie, documented by conversationalists and sanctuary workers, match up exactly with those displayed in human PTSD. I argue that, by the DSM V's standards, these animals should be diagnosed with the disorder, and conclude that PTSD is the simplest and best explanation for the behavior of these particular animals. Although my research is so far confined to elephants and chimpanzees, I suspect that similar results can be found in many other species.

Traditionally, animal minds are studied through the observation and analysis of their abilities (whether they can solve a certain puzzle, for example). My project has not only moral implications, but epistemic ones as well; I propose that there is something to be gained by studying animals who are functioning abnormally. This perspective can provide us with a new avenue into the minds of animals, as well as give us important insight into our ethical obligation to protect not just the physical, but also the mental lives of these animals.

Transplantation and tomatoes: Retracing Anne McLaren's cold war search for graft hybrids

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One of the most fundamental claims of Lysenko's biology in the Soviet Union was that new plant species could be created through grafting. The ability of plants to supposedly exchange hereditable material without resorting to sexual crosses was held to undermine Mendelian and Morganist genetics. Yet outside of the Soviet Union, the vast majority of Western scientists were highly sceptical that graft hybrids even existed. One exception to this rule was Anne Laura Dorinthea McLaren (1927–2007), developmental biologist, first female Officer of the Royal Society and member of the Communist Party of Great Britain. Harnessing previously unpublished archival sources from the Anne McLaren Papers, this paper examines two of

McLaren's attempts to bring graft hybrids back into the scientific mainstream. The first of these case studies examines McLaren's behind-the-scenes efforts to promote the work of Czech biologist Milan Hašek. During the early 1950s, Hašek claimed to have overcome the immunological barriers between species using grafting. McLaren introduced Hašek to the British immunologist and 1960 Nobel Prize winner Peter Medawar, who later ensured that Hašek's results were published by the Royal Society. The second case study follows McLaren's attempts to verify the creation of graft hybrid tomatoes by Ruzicka Glavinic of the Faculty of Silviculture at Belgrade University. In 1958, McLaren travelled to Belgrade to observe grafting experiments. Upon her return, McLaren also endeavoured to grow graft hybrids at Nuffield Lodge in London. By retracing McLaren's Cold War era research and its reception by her peers, we gain fresh insights into the obstacles of conducting science across an ideologically-charged divide.

Where in the world is Aldo Leopold?: An examination of "The Land Ethic" in relation to late 20th century animal liberation ethics and environmentalism

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Mark Sagoff's "Animal Liberation and Environmental Ethics: Bad Marriage, Quick Divorce" (1984), aside from its memorable title, provides a crucial historical framing of two discourses in environmental ethics as oppositional; the "animal rights" or "animal liberation" view (Singer 1974; Regan 1983) and the "environmentalist" view. The question I raise in this paper, as a matter of examination for the History and Philosophy of Biology, is whether Sagoff's representation of the environmentalist movement accurately characterizes the figures he claims to be a part of the environmentalist "faction". I argue that Sagoff's representation of Aldo Leopold, an early 20th century American forester and conservationist, mischaracterizes his view from “The Land Ethic”(1949), and consequentially, his place as an “environmentalist under his account. The focus of this paper is then to explain why Leopold is not rightly placed as an “environmentalist” in Sagoff’s account of this “great divide” within environmental ethics.

Critical to this examination is Roberta L. Millstein’s (2015) argument that J. Baird Callicott, (Leopold’s leading philosophical proponent within environmental ethics), misinterprets Leopold’s Darwinian influence to have stemmed from the Descent of Man. She argues that the appropriate Darwinian influence is not the proto-sociobiological (ethical) view of Descent, but instead the ecological view from Darwin’s *Origin of Species.* I argue in support of Millstein’s reinterpretation, and from this reinterpretation, show that Sagoff has misplaced Leopold as an “environmentalist” in opposition to the “animal liberationist”.

There are two primary ways in which Leopold does not conform to the opposition argued for by Sagoff. Firstly, Sagoff endorses a clear division between the individualist ethical framework of the animal liberationist, and the holist ethical framework of the environmentalist. Secondly, the locus of ethical concern for the animal liberationist is set primarily on domestic animals, and conversely, the locus of ethical concern for the environmentalist is set primarily on wild animals (Newman, Varner, Linquist 2017). First, I argue that what sets Leopold apart from the debate construed by Sagoff is that Leopold conformed neither to a holist nor individualist framework alone (Millstein 2015). A further source of discordance between Leopold’s view and the environmentalists is that his view placed little to no difference in ethical weight or concern on whether an animal was classified as wild or domestic (1944; 1949). Finally, as a matter of historical import, Leopold was not an environmental ethicist, but instead a scientist – in many ways a proto-ecologist (Millstein 2017). When we move towards an ecological interpretation of Leopold’s view, as advocated by Millstein (2015), we shift from a “Land Ethic” understood as canonical to environmental ethics, rightly back to an examination which must engage the History and Philosophy of Biology.

Direct-to-consumer genetic testing’s red herring: “Genetic ancestry” and personalized medicine

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The growth in the direct-to-consumer genetic testing industry poses a number of challenges for healthcare practice, among a number of other areas of concern. Several companies providing this service send their customers reports including information variously referred to as genetic ethnicity, genetic heritage, biogeographic ancestry, and genetic ancestry. In this article, we argue that such information should not be used in healthcare consultations or to assess health risks. Far from representing a move toward personalized medicine, use of this information presents ethical problems. It poses risks both to patients as individuals (violating the ethical principle of beneficence) and to racialized ethnic groups (violating the ethical principle of justice), because of the way it misrepresents human genetic diversity.

Exploring biological possibility through synthetic biology

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This paper analyzes the notion of possibility in biology and demonstrates how synthetic biology can provide understanding on the modal dimension of biological systems. The discussion of biological modal concepts has usually focused on the contrast between evolutionary contingency and convergence, and the subsequent question on how sensitive evolutionary outcomes are to changes in their evolutionary pathways. However, biological possibility per se has received relatively little explicit treatment in contemporary philosophy of biology.

The aim of this paper is to reclaim the notion of biological possibility by showing how it provides a both philosophically and

biologically interesting category as well as introducing a new practically motivated way for its assessment. More precisely, we suggest that synthetic biology can provide tools to scientifically anchor reasoning about biological possibilities. Synthetic biology is a new multidisciplinary field of biotechnology that aims to take an engineer's viewpoint to biological systems and the construction of biotechnological innovations. The emergence of synthetic biology has made the hypothesizing on biological possibilities more relevant problem. Synthetic biologists can explore the boundaries of biological constraints and design systems that overcome some of the limitations of naturally evolved organisms.

We distinguish two different strategies how this can be brought to bear on biological possibility: the design of functionally new biological systems and the redesign of natural systems. Combining these approaches allows synthetic biologists to explore designs that are not naturally evolutionarily accessible. We argue that synthetic biology can be used to study the path-dependence and optimality of biological properties, and to understand whether their embeddedness is a consequence of adaptive necessity or generative entrenchment.

Finally, we draw a distinction between knowledge about global biological possibility and knowledge about more or less local contrafactual scenarios. To bring abstract possibilities to bear on more detailed evolutionary hypotheses, a principled way of presenting a how-plausibly story is needed to bridge the gap. We argue that synthetic biology presents one such method to explore biological possibility and assess the relative plausibility of evolutionary alternatives. Subsequently, these results in synthetic biology can also be relevant for the discussion on evolutionary contingency, providing new methods and insight to the study of path-dependence of biological traits as well as the prevalence of various biological constraints.

Mechanisms as causal pathways

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A main aim in the recent mechanistic literature has been to find a common and general notion of mechanism in the sciences that is present in many different scientific fields. Such a concept is commonly thought to have both methodological value, as well as ontological significance. So, the concept of mechanism has a double role: it can be used to understand scientific practice, but also to construct a comprehensive metaphysics of nature. The main claim of this paper is that it is not at all clear whether a notion of mechanism as a common and general notion present in the biomedical sciences can fulfil both these roles at once. I will argue that a promising candidate for the methodological role of mechanism in the biomedical sciences is a Causal account of Mechanism (CM), according to which a mechanism is a causal pathway that produces a phenomenon. But such an account is not very informative about the ontology of mechanisms: it does not incorporate a distinction between entities and activities or a distinction between causal and constitutive mechanisms.

To defend CM, I will focus on the concept of a causal pathway in molecular biology, that (I will argue) is an example of a biological mechanism. The notion of a causal pathway will be used to arrive at a general characterisation of mechanism as a sequence of causes that produces a phenomenon. I will show that CM satisfies certain criteria of adequacy for a methodologically central notion of mechanism: CM is i) practice-based, ii) common across fields, iii) topic-neutral, iv) diversifiable (thus compatible with more specific accounts) and v) non-trivial. Moreover, in contrast to prevalent general accounts of mechanism, CM is ontologically minimal. To defend this aspect of CM, I will offer two general difficulties for ontologically oriented general accounts of mechanism (OMs). First, if OMs are offered as general characterisations of mechanism, then, to the extent that CM is successful, the “ontological” excess content of OMs needs independent motivation. Second, there is a risk involved in ontologically inflating the concept of mechanism: the more one strengthens the ontological commitments of what counts as a mechanism, the more one weakens ones ability to apply a mechanistic strategy across a diverse range of scientific fields.

In sum, CM stresses the idea that causation is central in mechanisms. But CM combines agnosticism about the metaphysics of causation with taking mechanisms to be causal sequences (and thus real things in the world). At the same time, it takes the direction of causation, rather than non-causal constitutive relations, as the main structural feature of a mechanism. Thus, CM, in contrast to accounts that view mechanisms in terms of a specific (e.g. neo-Aristotelian) metaphysics, is ontologically minimal.

The naming of the Mikado pheasant: Ornithology, aviculture and zoogeography in the Age of Empires

Takashi Ito, Tokyo University of Foreign Studies, Japan

This paper discusses the significance of avian collection and aviculture from the late nineteenth to the early twentieth century, with a special focus on inland Taiwan, one of the remaining ornithological frontiers of the time. Much has been written about how the evolution of the Linnaean system as well as the discoveries of a vast number of species during the Enlightenment era contributed to expanding Europeans' knowledge of nature and laid the basis for the future development of biological sciences. By contrast, taxonomical studies and collecting activities from the mid-nineteenth century onwards have not received the attention they deserve, despite the fact that the discovery and identification of new species continued to open up a line of inquiries.

To fill the gap, this paper highlights the collecting activities of European bird collectors in Taiwan. While the island formerly called Formosa by Europeans was ceded to Japan at the conclusion of the first Sino-Japanese war of 1894–1895, it attracted the attention of European naturalists and collectors. They sought after birds and butterflies with a view to completing the geographical distribution of avian species. Many specimens were transported to the West, sometimes through the hands of Japanese brokers. Some of them were discussed at scientific meetings of zoological institutions such as the Zoological Society of London; and living birds were sent to aviaries for breeding. For these ornithologists, collectors, brokers and breeders, the identification of species was essential to their communications and operations.

The discussion takes the example of one particular pheasant species: the mikado pheasant. It explores how this species was initially identified by a British collector, and how the celebration of this ornithological "discovery" spread through to the United States. Moreover, the interactions between Western and Japanese ornithologists are considered too. For the latter, inland Taiwan provided a rich colonial field where they could put into practice the knowledge they obtained from the West, and by so doing, could build up the institutional basis for Japanese national zoology.

Complexity, flexibility, and the modular stance

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How can an egg produce complex, flexible, and diverse organisms? Developmental biologists have been fascinated by this significant question for several hundred years. For the past few decades, Evo-Devo which stands for evolutionary developmental biology has begun to unravel the mysteries of development in terms of genes' actions. Evo-Devo researchers have become to know that modules play key roles in development. This discovery, however, seems strange because it says that complex, flexible and diverse organisms can be developed by modules which are something rigid. So, this might be called a paradox, which however turns out to be apparent.

In this regard, there seems to be another similar paradox in a different domain: How massive mental modules can produce flexibility of thought? Since Fodor's publication of Modularity of Mind in 1983, there have been fierce debates concerning the architecture of mind among philosophers, evolutionary psychologists, and cognitive scientists. Fodor's perceptual modularity thesis has asserted that mind consists of modular perceptions and non-modular central cognition, because massive mental modules can't produce flexible thought such as abduction, IBE, etc. On the other hand, evolutionary psychologists have insisted that there is no such thing as a non-modular central cognition and therefore mind consists of massive modules.

In this paper, I'm going to criticize both Fodorian perceptual modularity thesis and massive modularity thesis, using Evo-Devo modularity. According to my definition of modularity, both their concepts of modules ignore the connectivity condition which plays a significant role in Evo-Devo modularity. They have rigid and qualitative concepts of modules which are different from Evo-Devo modularity. So, it seems that they can't solve the apparent paradox how massive mental modules can produce flexibility of mind.

In fact, the questions concerning modularity in Evo-Devo and Evolutionary Psychology might be sub-problems of a more generalized problem how massive modules can explain flexibility, complexity, and diversity of the system. The modularity revisited might be a potent solution of the universal problem of complex design and architecture. I insist we can take "modular stance" in front of any complex system to analyze it properly.

Human infants are born into a social womb: The biosocial philosophy of Adolf Portmann

Filip Jaroš, University of Hradec Králové, Czech Republic

The Swiss scholar Adolf Portmann (1897–1982) was an outstanding figure in the history of biology and the philosophy of the life sciences. He was the head of the Zoological Institute, University of Basel (1933–1968) and was the rector of the same University for a time (1947/48). Portmann's biological theory is primarily focused on the problem of animal form (Gestalt) and it poses a significant counterpart to neo-Darwinian theories about the explanatory primacy of a genetic level over the outer appearance of animals. Besides that, Portmann's morphological studies related to species-specific ontogeny and the influence of environmental surroundings can be classified as the antecedents of contemporary synthetic approaches such as "eco-evo-devo", extended synthesis or biosemiotics (cf. Kull 2016). The most influential of Portmann's concepts up to the present is his thesis of a social womb (soziale Mutterschos, Portmann 1941): human children are born premature in comparison with other primates, and they find a second womb in a social environment nurturing their healthy development. It is during the first year of extra-uterine life when a specific human nature is formed, characterized by the strong tie between an individual and a broader historical cultural whole. In our paper, we will closely analyze: a) the historical coordinates of Portmann's philosophy of the life sciences (e.g. the philosophical anthropology of A. Gehlen, H. Plessner, and their concept of humans as beings "open to the world"), b) the relation of Portmann's concept of the social womb to contemporary theories of infant helplessness (Trevathan and Rosenberg 2016).

Group selection does not act on "belonging to" properties of individuals

Ciprian Jeler, Alexandru Ioan Cuza University of Iasi, Romania

This paper has two main aims. First, I distinguish between two potential interpretations of what "group selection" means in multigroup scenarios in which the target of interest is the evolution of individual-level traits. The first potential interpretation consists in understanding "group selection" in such scenarios as selection on the component of fitness of individuals that is determined by these individuals' group membership; I call this the "belonging to" interpretation, because it essentially consists in assigning a relational or, more precisely, a "belonging to" property to the individuals of the case (depending on the group these individuals are part of) and of assuming that "group selection" here means selection on these "belonging to" properties of individuals. On the other hand, one can interpret "group selection" in such scenarios differently, by seeing the groups themselves (and their characters) as being subjected to selection and by understanding the fitness of a group as the average fitness of its individual members. According to this second interpretation, if the difference in a group-level trait between two groups causes differences in fitness between them (i.e. differences in average fitness between their individual members), then we may conclude that "group selection" is at work. Moreover, the individual type that is better represented in the fitter group will thus be indirectly favored by this selection process taking place at the group level.

This is why I call this second interpretation the "indirect explanatory role" interpretation: rather than claiming that selection is taking place at the individual level (i.e. that it acts on the "belonging to" properties of individuals), this "indirect explanatory role" interpretation sees selection as taking place at the group level, and it sees individuals belonging to the fitter groups not as direct targets of selection, but as indirect beneficiaries of this higher-level selection.

Both of these interpretations are compatible with the statistical method for analyzing group selection put forth by Lorraine Heisler and John Damuth in 1987 and known as "contextual analysis" in the multilevel selection literature. It is thus unsurprising that authors who endorse contextual analysis as a method for analyzing group selection in such scenarios (e.g. Heisler and Damuth themselves, Charles Goodnight, Samir Okasha) sometimes seem to oscillate between or even to confound these two interpretations. As a consequence, clearly demarcating these two interpretations seems useful.

In the second part of this paper, by analyzing a toy example – two groups repeatedly placed in the same environment, one of which happens to be more affected by forest fires than the other –, I argue that the "belonging to" interpretation is misleading because it leads to the detection of group selection in scenarios in which, intuitively, there is none. I also show that attempting to circumvent this difficulty by appealing to a restricted version of the "belonging to" interpretation actually renders this interpretation redundant. Therefore, I conclude that, for multi-group scenarios in which the target of interest is the evolution of individual-level traits, the "indirect explanatory role" interpretation of "group selection" is preferable.

Darwin and disenchantment

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Max Weber's *Weltentzauberung* ("disenchantment of the world") is one of the most representative commonplaces of contemporary historiography about the cultural impact of modern science.

Weber's diagnosis has led to the widespread presupposition that modern science, on the one hand, is neither oriented nor able to give meaning to the world and, on the other hand, does not empower a humanized perception of nature and would consequently produce an irreversible dehumanization of culture.

Darwin's Theory of Evolution is commonly considered as one of the most paradigmatic scientific theories embodying the Weberian thesis of scientific disenchantment. Its disenchanting effect became evident since the publication of Darwin's *Origin of Species* (*OS*) in 1859. One of the consequences frequently attributed to this disenchantment is precisely the loss of aesthetic sensibility to natural beauty. In fact, Darwin himself had occasionally commented on the influence of his scientific activity in his aesthetic sensibility, terms that seem to confirm the thesis of disenchantment.

I intend to show through an exhaustive critical study of Darwin's lexicon across the six editions of *OS* that the descriptive and explanatory knowledge of nature that Darwin held weakened the enchanted conception of nature in favour of a disenchanted conception in a non-pejorative sense. Whereas the Theory of Evolution certainly divests nature of its magical character in explaining the mechanics of Natural Selection, it also accords a more profound and completely new understanding of it to any reader. This premise can be confirmed by looking at the relevant lexical clues in Darwin's *OS*. The lexical material has been obtained using two main software packages for computational linguists: WordSmith Tools and CFL Lexical Feature Marker.

A consecutive computational analysis of the six editions of *OS* has proved that the knowledge of the evolutionary principles prompted Darwin to create a demystified, disenchanted worldview, yet, intellectually and aesthetically more valuable and intriguing. Disenchantment grew progressively in time through subsequent editions of the book. This fact is reflected in changes of Darwin's lexicon in *OS*.

This result demonstrates that the integration of the descriptive-explanatory knowledge of the world and its interpretation in a given worldview can be compatible with the satisfaction of human needs or existential instincts, including the aesthetic.

Forms of insanity: The development of the British psychiatric classification system 1870–1950

Kevin Matthew Jones, University of Leeds, UK

The most appropriate way of classifying mental health disorders has attracted the interest of philosophers of psychiatry since at least the 1970s, with much discussion being centred around successive incarnations of the APA's DSM, a document which overwhelmingly contributed to the standardisation of concepts of psychopathology across the world today. This paper seeks to provide an historical contribution to these debates by presenting a case study that has been overlooked by historians of psychiatry: attempts made to standardise the concepts of psychopathology that were used by British alienists during the mid-late C19th. The somatic turn in the conceptualisation of mental disorders that was seen across Europe from around the 1850s led to growing concern amongst British alienists about the worth of Pinel's symptom based classification of mental disorders. British mental scientists offered new classifications that attempted to offer aetiological and biological concepts of psychopathology informed by research undertaken in the fifty years since Pinel. This led to series of failed attempts to standardise concepts of psychopathology during the 1870s to the 1880s, and culminated in a fierce debate that took place at the turn of the 20th century about what a standardised psychiatric nomenclature for use by alienists British Isles should look like. The product of this episode came to be known as the "British classification system", and this would be used by doctors in the United Kingdom up until the 1950s, the beginning of the era of the global psychiatric nomenclature in the form of the DSM and the ICD.

Engineering regeneration in corals

Elis Jones, University of Exeter, UK

As the recent bleaching events have shown, many corals struggle to regenerate in the face of anthropogenic stressors. Efforts to conserve coral populations by encouraging their regeneration vary considerably. This paper examines one particular set of such practices – the creation of so-called supercorals. Supercorals are (roughly speaking) corals which have undergone human-assisted evolution in an attempt to increase their resilience against anthropogenic stressors (such as those associated with climate change). The hope is that these techniques will improve the prospects for regenerating and preserving corals and their associated ecosystems across the world.

I first survey processes and products that come under the rubric of supercorals. Due to the complex assemblage of organisms involved in coral reefs there are a large number of potential avenues for assisting coral survival, not all of which are purely evolutionary or genetic processes. From here I discuss the most popular practices employed and the efforts considered most feasible, desirable and successful. I examine the criteria and metrics used to judge feasibility, desirability and success and use these to highlight the conceptions of regeneration employed and the levels of organisation and analysis they invoke. I then examine the associated regeneration and conservation strategies being employed by conservationists.

I further deal with a complication for coral conservation strategies – the difficulty of preventing human influence (i.e. the absence of pristine corals), which makes non-intervention an impossibility and presents challenges to the standards used to assess regeneration and resilience. In sum, I make clear the link between coral biology, assisted evolution practices, concepts of regeneration and specific conservation strategies.

Rethinking early American genetics and its contexts: The castle-east controversy and fancy mouse vs. corn breeding

Sunguk Jung, University of Toronto, Canada

This paper examines the impact of empirical knowledge that practical breeders had on the development of genetic theory in the early twentieth century. Historians have investigated the relationship between practical breeding and genetics, but they mostly stress the importance of agricultural institutions such as the

United States Department of Agriculture (USDA) and agricultural experiment stations in the development of genetics in the United States. Some of these studies have demonstrated the complexity of the relationship between geneticists and practical breeders where not only scientific, but also social, political and economic factors involved. However, they tell us surprisingly little about how practical techniques or the empirical knowledge of actual breeders contributed to the development of genetics. This essay explores how different kinds of breeding techniques led early geneticists to develop different genetic theories.

For this purpose, I examine the scientific controversy between two leading early American geneticists, William E. Castle (1867–1962) and E. M. East (1879–1938). Although both appreciated Mendel's law, their interpretations of it sharply contrasted. Whereas Castle claimed that hereditary units (unit-characters or unit-factors) were modifiable under selection, East believed that they were immutable, and selection was powerless to create new varieties. I show that their contrasting views of the nature of hereditary units and the role of selection in evolution derived from different kinds of breeding practice. While Castle closely engaged with the practice of mouse fanciers who created various color varieties using mass selection, East's genetic research was based on the corn breeding practice wherein pedigree selection, instead of mass selection, was used to sort out, not create, superior varieties that already existed. This paper explains how fancy mouse and corn breeding led Castle and East to interpret Mendelian inheritance in quite different ways.

A novel account of activities

Kalewold Hailu Kalewold, University of Maryland, USA

This paper defends a novel account of activities and how to identify them. Machamer, Darden, and Craver's [MDC] (2000) influential account of mechanisms as "entities and activities organized such that they are productive of regular changes from start or set up to finish or termination conditions" launched a bourgeoning literature on mechanistic explanation (MDC 2000, 1). These New Mechanists characterized an account of explanation that is ubiquitous in at least sciences such as molecular biology and neuroscience. Although this approach has become prominent in philosophy of science, a central component of the account has received relatively little philosophical attention, namely activities.

Machamer (2004) and Bogen (2008) defend an activities view of causation influenced by Anscombe's (1971) version of causal pluralism. However, their account of activities explicitly eschews giving the identifying conditions that apply to all and only activities. This opens the activities view of causation to criticism from Franklin-Hall (2016) that the activities view fails to distinguish between causal production and mere happenings that are irrelevant to production.

Recently, Glennan (2017) has adopted activities as part of his account of a "minimal mechanism" where "a mechanism for a phenomenon consists of entities (or part) whose activities and interactions are organized so as to be responsible for the phenomenon" (Glennan 2017, 17). However, unlike MDC (2000), Machamer (2004), and Bogen (2008), Glennan (2017) still relies on mechanism and not activity as his primary account of causation.

I defend an account in which causally productive activities are what make a difference to changes between stages of a mechanism. That is, activities are causally productive of changes because they are difference makers. These activities are not one off, occurring once and never happening again. Rather, I defend an account of activities that provides a philosophical characterization of the types of activities biologists typically study. For instance, depolarization, binding, transduction, and so on are the kinds of activities neuroscientists study, while transcription, translation, phosphorylation, protein folding are the types of activities molecular biologists study. These activities are recurrent and produce the types of changes that are essential to the mechanisms biologists investigate. The account of activities as difference makers I propose is graded, allowing for a distinction between causally productive activities and (difference making) background conditions. My account of activities has two explanatory virtues that previous activities views lack; it: i) distinguishes between causally productive activities and irrelevant casual influences and ii) justifies why mechanisms are at the size and organizational level that they are in biology and not at some lower, more fundamental level.

“But is it cognition?” Interpreting claims about cognition in bacteria, plants and tissues

Fred Keijzer, University of Groningen, Netherlands

It is increasingly normal to encounter claims in the scientific and philosophical literature that cognitive processes occur in a broad variety of organisms and even in bodily tissues. Examples include the behavior of invertebrate animals, plants, slime molds and bacteria, but also the development and regeneration of animal bodies are discussed in cognitive terms. These claims concerning “basal cognition” build on the presence of features like perception, memory, decision-making and valuing. However, such claims remain controversial given long-standing common-sense judgments that limit cognition to human-level cognitive tasks. In this view, the examples just mentioned cannot be accepted as cases of cognitive phenomena unless they fulfil various stringent requirements. Here, I challenge such human-oriented exclusion of a wider interpretation of cognitive phenomena. Earlier work in the autopoietic, enactive and autonomy traditions already formulated interpretations of cognition that connect mind and life at a conceptual level. The various reports of basal cognition make an even stronger case as they provide empirical confirmation that basically all life-forms use very ingenious organizations and behaviors for dealing with their environments in ways that remained unknown or underappreciated until recently. They also show deep connections between ordinary bodily processes and the operation of nervous systems, providing new insights concerning the latter. Whether or not these cases of basal cognition fit human-based criteria for cognition is not very relevant. They simply provide a new range of empirical phenomena that should be taken seriously when it comes to the study of cognition.

Nested agency

David Kelley, University of Auckland, New Zealand

In their account of group agency, Christian List and Philip Pettit lay out criteria for what they call “minimal agency”. While we might think of humans as paradigm agents, minimal agency is extremely permissive: a minimal agent has representational states, motivational states, and the capacity to interact with the environment according to those states. With intentional states understood properly in a functional framework, this broader class of agents will include things like simple robots and single-celled organisms.

However, when considering problems within the philosophy of biology regarding groups and individuals, it becomes clear that certain assumptions underlying this account of agency need to be argued for, and not merely presupposed.

If cells and multicellular organisms (or individuals and integrated societies) count as agents, then we can observe many instances of “nested agency” in nature – interactions of agents at different “levels” analogous to List and Pettit’s account of humans and the group agents they comprise. Specifically, List and Pettit’s claims that group agents are real, non-redundant, and not readily reducible to the actions of the individuals that comprise it, are ripe for comparisons with the decision making of honeybees and the marvels of termite mound construction. Of relevance to the group agency literature will be the kinds of individual level biological organization that facilitate the emergence of a higher-level entity – in some cases, one with interests at odds to those of its component agents. Interestingly, similarities between kinds of agents may crosscut hierarchical levels in terms of organization and function (i.e. individuals of one type may resemble groups of a second type, but not individuals of the second type).

Yet, the concept of nested agency, as brought into focus via the concept of minimal agency, rests on assumptions about individuals and groups, and in particular, groups-qua-individuals. In the area of biology, agency and individuality may be understood in quite different ways. When viewed through a biological lens, differentiating between “individual agents” versus “group agents” could be pointing merely to a relative level of analysis, rather than picking out distinct types of agents. I will critically evaluate List and Pettit’s account in light of the conceptual tools offered by philosophers of biology, exposing the underlying need for a better understanding of nested agency, and more generally, individuals-qua-groups.

Cell culture and the (re-)articulation of biological time

Rosine Judith Kelz, Institute for Advanced Sustainability Science, Germany

Cell cultures are fundamental tools of contemporary biological and biomedical research. Cultured cells provide much of the biomass, or living material base, for the contemporary life sciences, as they produce enzymes, anti-bodies, RNA, DNA and viruses that are used in laboratories today. However, cells are not only “producers”, new culturing techniques have also enabled many biomedical breakthroughs of the past decades, from IVF, over induced stem cells, to the productions of “organoids”. In this paper, I return to the beginning of the development of cell culture techniques to argue that some of the core theoretical concerns prevalent in the beginning of the 20th century are still relevant for thinking about the societal and medical questions raised by cell culture techniques today. At that time theoretical biologists and philosophers were deeply concerned with questions about time and temporality – or the way living beings experience their existence in time. This also became one of the guiding questions of early cell culturists, in particular Alexis Carrel. He argued that biological time was a function of the interactions between a living organism and its milieu –isolating small pieces of tissue, Carrel argued, would allow the scientist not only to control and study these interactions, but ultimately to control time. Here the “flow” of temporal existence is not taken as a constant, but as a product of processes that take place within cells, and between cells and their milieu, that are open to intervention. Concentrating on temporality as a core organizing factor in cell research has helped bringing about an understanding of living matter as plastic and malleable, and thus as potentially "productive" in a biotechnological sense. After discussing how Carrel's concerns with time fit in with broader societal concerns and philosophical debates about temporality, I will end this paper by providing a brief outline of how these previous debates might be re-approached in light of contemporary debates about stem cell research.

Evolution of music and language

Anton Killin, Australian National University, Australia

Much of the philosophical and scientific debate surrounding the evolution of music concerns its status as an adaptation, by-product, exaptation, or cultural technology. Yet despite a proliferation of hypotheses concerning its evolutionary status, little effort has been spent on constructing an evolutionary model that tracks between series of phenotypes—explicating what we know about the evolution of hominin cognition and sociality—for the purpose of constructing a phylogenetically plausible narrative of the evolution of music compatible with contemporary interpretations of the biological, palaeoanthropological, and archaeological evidence at hand. Such a model is what I will outline in this talk. I will offer a model that emphasises the incremental evolution of music from musicality, vocal communication, and increased sociality. Connections will be drawn between the evolution of music and the evolution of language. Some theorists have posited that music is a direct evolutionary precursor to language. Charles Darwin, famously, advocated this kind of view in The Descent of Man (specifically, that music's origins are in sexual selection and that language emerged from a musical predecessor), contra Herbert Spencer's view that music is a by-product of the prosodic/emotional elements of vocal language. Neither account is satisfactory, in my view. I favour accounts of language evolution that emphasize the communicative role of manual (and facial) gestures. However, the sticking point of such accounts is the need to explain how human language shifted to a largely oral/aural medium from a largely visual one. In this talk I suggest that musicality played a role in the shift to vocal dominance in language—that the foundations of an evolving musicality (i.e., evolving largely independently of gestural communication) provided the means and medium for an incremental transition. In other words, I suggest that an evolving musicality prepared ancient hominins, morphologically and cognitively, for intentional articulate vocal production, enable the evolution of speech.

Carrier screening in Israel: Tay Sachs and other genetic disorders

Nurit Kirsh, The Open University of Israel, Israel

Over the last two decades, the high rates of genetic screening and testing in Israel have drawn great attention from social scientists (Hashilon-Dolev, Raz, Prainsack, Siegal). I claim that sociological explanations given for this phenomenon are insufficient; it is vital to know the historical events and context in order to fully understand the extensive use of genetic services by Israeli citizens. I will suggest that screening for Tay-Sachs constituted the turning point that made prenatal diagnosis so popular in Israel.

Research in Israel on the genetic characteristics of human populations began during the 1950s, shortly after the state of Israel was established in 1948. Israeli geneticists and physicians used their findings in the field of human population genetics as a foundation for and confirmation of national Jewish identity. They studied inherited polymorphic characters, such as blood groups, taste sensitivity to PTC and color blindness, as well as various clinical disorders, such as thalassemia (a hemolytic anemia), familial mediterranean fever, and deficiencies of the enzyme G6PD that cause severe allergy to broad beans. Yet Tay Sachs, a fatal inherited disorder that was very common among Ashkenazi Jews (1 out of 27 is a carrier of a mutant gene), was not studied by geneticists and physicians in Israel during the 1950s and 1960s.

In 1969, O'Brien and Okada, two biochemists from the University of California, San Diego, revealed that the cause of Tay Sachs was an absence of the Hex A enzyme. Their discovery enabled the development of an accurate and reliable biochemical test that could identify healthy carriers of Tay Sachs. While large-scale voluntary screenings for Tay Sachs were organized in Jewish communities around the world, only a limited number of Jews in Israel chose to participate.

That inclination to not test for Tay Sachs likely stemmed from an Israeli law that did not allow for an abortion based on the fetus's medical condition. In 1977, the law was changed to permit termination if the fetus was found to be at risk, either physically or mentally. This change led, rather quickly, to a wider screening for carriers of Tay-Sachs as well as the termination of fetuses. Israel's screening program for Tay-Sachs resulted in zero births of children suffering from that disease.

In 1980, the Ministry of Health established an Israeli National Program for the Detection and Prevention of Birth Defects. Today, Israel's national carrier screening program is among the most comprehensive in the world. Other countries have been slower to incorporate carrier screening because of technical and ethical concerns. I argue that the ability to prevent the births of children with Tay Sachs disease persuaded the Israeli public that using bio-medical knowledge could impact their offspring's medical future. Since Tay Sachs is undeniably horrific, its eradication did not stimulate ethical dilemmas; that attitude toward Tay Sachs screening facilitated the adoption of screening for less severe genetic disorders.

Life, death, and a puzzle of continuity

Gal Kober, Bridgewater State University, USA

This paper raises questions regarding personal identity, critical interests, and psychological continuity in a particular context of advance directives, with special focus on the effect of end of life decisions on patient interests. I discuss cases where a patient, having chosen voluntarily to stop eating and drinking in order to hasten death (VSED), asks to be fed after the point of losing mental competence due to the lack of hydration and nutrition. In such cases, a conflict arises with regard to respecting patient autonomy, since the requests articulated and recorded when the patient was fully competent contradict present wishes. This conflict highlights longstanding concerns about advance directives and the ethical status of precedent autonomy. In this paper, I discuss what constitutes continuous identity, and whether a patient in this situation could plausibly be regarded as maintaining the same identity and critical interests as were held before the process of VSED began. I draw the implications of such a conflict on personal continuity; examine epistemic questions regarding disagreement with oneself over time, and the status of the patient's privileged point of view; and consider several scenarios and their effects on the patient's critical and experiential interests. These lead me to argue that a patient articulating such a request should indeed be fed. I support this conclusion using two different arguments; the first, based on prudence and the minimization of harm; and the second, showing that precedent autonomy does not hold in such cases, due to the transformative effect that going through this process has on the patient's point of view and preferences, and the capacity to make advance decisions rationally.

Biological individuality and the new natural kinds philosophy

Robert Kok, University of Utah, USA

In this paper, I compare a recent body of work in philosophy of biology, which I'll call the "New Natural Kinds Philosophy," and which includes contributions from Slater, Magnus, Franklin-Hall, Khalidi, Jantzen, and Godman. These new approaches to natural kinds agree on a rejection of biological essentialism and on a reconciliation between species categories with fundamental concepts in contemporary evolutionary biology, namely the Ghiselin-Hull individuality thesis. Using Haber's notion of "a natural kinds inconsistent triad," I first develop a taxonomy of these new anti-essentialist accounts that treat biological species as paradigmatic natural kinds. Next, I show that the new natural kinds philosophers do not see themselves as a continuing lineage of thought from Aristotle to Kripke. Rather, these philosophers recognize their work as continuing a tradition running from Mill to Goodman to Boyd. This is evidenced by these philosophers' emphasis on scientific practice, the importance of projectability, and on successful inductive generalizations that serve to constrain our ontological categories rather than on referring to intrinsic essences. And finally, I explore whether the new natural kinds philosophy adequately deals with challenges posed by the individuality thesis and its proponents more effectively than traditional biological essentialism. This is done by considering two distinct yet related questions:

1. Do the new natural kinds accounts effectively address the criticisms faced by traditional essentialist accounts of biological taxa, and
2. Do the new natural kinds accounts offer advantages over individualist accounts of species?

I argue, that though it does address these challenges more adequately than essentialist accounts, it does so in uninteresting ways—and in more important ways, it does not.

Humans, animals, and robots: An evolutionary perspective to moral agency and responsibility

Tomi Kokkonen, University of Helsinki, Finland

Robots and artificial intelligence systems are far from being moral agents, but they are making quasi-independent choices. This has raised three philosophical questions:

1. What are the moral rules these choices should reflect?
2. How can these rules be implemented?
3. Who is responsible of the choices made?

Philosophical debates have concentrated on the questions one and three, but the question number two is not merely an engineering problem, either, and it is directly connected to the other two. Furthermore, if robots become more and more generalized and in control of more and more choices, we want them to at least simulate similar decision processes that humans are making in situations with moral relevance. Growing complexity of situations and possible choices, and the growing role of learning, necessitate a more robust system to deal with moral relevance than pre-programmed behavioral responses to a limited number of environmental triggers. It is also unlikely that a "moral system" could simply be added when needed – the morally relevant categorizations and responses need to be integrated deeper into the decision-making architecture. And this is how moral decision-making works in human psychology, too: deliberation and conscious moral judgment have their role in acquiring new ethical principles and solving new problems, but most of our moral choices are automatized.

The evolution of human moral agency gives one (and the only known) pathway to the right kind of moral agency. Furthermore, given the path-dependency of technological development and how further developmental possibilities are entrenched in the more basic architecture, we should be mindful about these issues early on. I propose that the analysis of the "building blocks" of morality and their (non-moral) function in non-human animals, as well as understanding of how the blocks "click together" to form moral agency inhumans, can (and should) guide developing artificial intelligence systems and the kind of functions their choice making should include, if we want them to simulate moral behavior, or, ideally, eventually be autonomous, morally responsible agents. I will give a brief discussion on the key points of some recent work on the natural history of human moral agency and how it is related to the evolution of agency in general. After this, I will argue that the primitive elements of weak moral agency (i.e. behavior is in accordance with what we judge to be moral) should be implemented early on, and the protomoral capacities of some social animals is a guide to this. Finally, I will outline what it would take for a robot to have strong moral agency (i.e. choices are guided by moral judgment and they are morally responsible of them) – and why, given the difference between the evolution of human morality and the design context of robotics, this is not likely to be the case.

From gut to glass: Microbial cultures and biological ontologies

Charles A. Kollmer, Princeton University, USA

There are innumerable ways to carve the world at its joints. This philosophical problem, most famously articulated by Plato in *the Phaedrus,* quietly haunts the natural sciences, and several historians and philosophers of science have commented insightfully on how the working practices of scientists, tacitly or explicitly, shape ontological categories crucial to our understanding of nature. In my talk, I will contribute to this ongoing discussion with an analysis of several episodes culled from the history of microbiology. Together, they illustrate how experimental methods and techniques, wittingly or not, imposed boundaries on microorganisms qua objects of study, carving the living world into biological individuals.

During the first half of the twentieth century, microbiologists were fascinated by a dizzying range of biological phenomena, including (but by no means limited to) nutrient cycling, enzymatic adaptation, growth, parasitism, and vitamin biosynthesis. To make these phenomena tractable within the confines of their laboratories, they availed themselves of a crucial tool of their trade: pure cultures. Though originally developed as within medical bacteriology, pure cultures later proved useful in new investigative contexts. By presenting microbiologists with an unparalleled degree of control over the chemical composition of microbial cells' environment, pure cultures made it possible to analyze biological phenomena in terms of metabolic pathways. In so doing, microbiologists helped bring a new ontology of life into view, one in which biological individuals were composed of modular molecular building blocks (i.e. enzymes, their substrates, and accompanying metabolites) and a common, evolutionarily conserved set of mechanisms transforming these structures.

My talk will reconstruct in brief several of the unexpected and largely forgotten ways in which microbiologists deployed pure cultures in their experimental systems, and the consequences this had for their conceptions of the natural world. It will make a case for a relationship between microbiologists' chemical ordering of nature and the political-economic order in which their research unfolded, an order which rendered human cultures as networks of market agents connected by the flowing exchange of commodities. The talk will conclude by reflecting on recent developments in the emergent field of metagenomics and how they challenge us to consider the plausibility of alternative biological ontologies.

Biological argumentation in early Norwegian salmon farming legislation

Widar Aalrust Kristoffersen, NTNU, Norway

The aim of this paper is to examine how biological aspects of the Norwegian salmon farming sector shaped legal and regulatory processes in its formative years. The cultivation of Atlantic salmon (*Salmo salar*) began in Norway in the 1970s, with rapid commercial success. Although initially unregulated, the fish farming sector soon drew the attention of political actors, leading to a legislative process, the so-called Lysø commission, which was intended to establish basic regulations. The most contentious issue in this process was assigning responsibility for the sector to the proper department. This dispute was due to the unique biology of the fish, which is anadromous, living in both fresh and salt water. While wild salmon, primarily of commercial importance in rivers, had long been the responsibility of the Agricultural Department, the fish farming industry depended on access to salt water. Within the context of regulating the new sector, the salmon thus became a disputed political object.

While the legislative process has been examined, the salmon has never been recognized as its most important component. However, both the dispute and all the arguments used in it stemmed ultimately from the nature of this fish. How did various actors marshal the biological facts, and what agendas was the salmon able to serve? What parts of the salmon biology could be made into political arguments, and which were of greatest importance? How did fish farmers, scientists and politicians argue about salmon, using salmon?

Using document analysis, the paper will examine the work of the Lysø commission, and the legislative process that it led up to, ending with the first permanent law in 1981. This process was ongoing through the founding years of the industry and involved the full range of concerned parties in the hearing process, showcasing a wide and diverse range of arguments. Previous historical research has examined the legal, political and social backgrounds for these arguments. However, the legislative process spanned nearly a decade, during which the sector changed in significant ways in all of these aspects. Meanwhile, the realities of the salmon biology have received little attention, in spite of remaining comparatively constant. In keeping with actor-network theory (ANT), the paper therefore proposes to regard the regulatory process from the perspective of the salmon, which framed and supported the argumentation of various actors through changing conditions, while also imposing limits on the process as a whole. This approach will shed new light on the arguments and views of the human actors during this formative period, as well as on the process by which the salmon, in its new, politicized role as a domestic animal helped to establish its regulatory and legal identity.

Extended genotypes? The consequences of adopting non-genetic inheritance to a classical framework

Ulrich Krohs, University of Münster, Germany

Epigenetic inheritance and niche-construction, among other phenomena, are often presented as necessitating an extended evolutionary synthesis. However, proponents of the framework of the modern synthesis claim that such phenomena can easily be accounted for within their more classical approach. The arguments that such integration is possible and even matches Darwin's own picture of evolution are convincing. However, integration would not come for nothing. My talk discusses the price that the modern synthesis would have to pay.

With respect to epigenetic inheritance, modern synthesis and extended synthesis need not differ in the description of its mechanisms. Nevertheless, the representation of epigenetic mechanisms in the genotype-phenotype map would differ. While the extended synthesis gives room for external, i.e. environmental, influences on the mapping, the modern synthesis would have to integrate the epigenome into the genotype-side of the map. The epigenome can then be considered to co-determine the phenotype. Insofar as it is inheritable it becomes conceptually part of the genome.

A similar move allows the modern synthesis to account for niche construction: The re-constructed environment can be conceptualized as part of the extended phenotype and thus as depending on the genotype. This works well for those environmental changes that are brought about by individuals or groups. It becomes trickier as soon as we take into account that the environmental change affects not only the constructing individuals, but also their offspring. To use a standard example: The beaver dam and the resulting water retention are inherited by future generations of beavers, which also contribute to the maintenance of the modifications of the environment. The extended phenotype thus constitutes a pathway of environmental inheritance. The way to adopt this into the framework of the modern synthesis would be to classify the dam and the environmental changes as the extended phenotype of a whole population, or of the lineage of a group. However, we are then talking about group genomes rather than about genomes of individuals.

Both examples show that the modern synthesis needs to widen its concept of a genome and of a genotype in order to accommodate the new pathways of inheritance. In epigenetic inheritance, the epigenome becomes part of the genotype. In niche construction, the genotype-phenotype map links the group genome to its extended phenotype. The modern synthesis is therefore committed to the notion of an extended genotype when integrating non-genetic inheritance into its framework.

This extended genotype, however, is context dependent in a way which does not hold for the classical genometype. I therefore argue that the changes in the modern synthesis upon adoption of the phenomena of non-genetic inheritance are as severe as the move from the modern to the extended synthesis would be.

Norm psychology, normative stress, and polarization

Ehud Lamm, Tel Aviv University, Israel

Norm psychology refers to the psychological underpinning of the human capacity to acquire and deploy social norms. Norm psychology must be clearly distinguished from any particular set of social norms to enable a full understanding of the potentially different processes through which social norms and norm psychology evolve. A key issue that will be clarified in this talk is whether people's norm psychology transcends the different normative systems they encounter. In particular, what are the different possible explanations, open to different accounts of social norms, for how someone may be highly normative with respect to one normative and social context while being less so in another socially relevant context. This requires carefully distinguishing variation in norm psychology from social and normative causes of differential adherence to norms. Understanding and measuring population variation in norm psychology and the ways in which normative systems interact are important for understanding the evolution of norm psychology and of social complexity.

Further, we will propose a notion of normative stress, a distinct type of social stress, and contrast it with the already well recognized problem of socioeconomic stress. We will ground this notion with preliminary data from studies we conducted in Israel. Israeli society is comprised of several large and often fairly self-contained yet still mutually interacting social groups. Normative stress results when people interact with others who have other social norms. Repeated, ongoing, interactions, as routinely happen in multi-cultural societies, lead to high degree of normative stress. Normative stress provides an alternative explanation of cross-cultural differences in attitudes to social norms to those found in the literature.

Multi-cultural societies are natural experiments for studying the distinction between social norms and the norm psychology of individuals. In complex, multi-cultural societies, multiple normative systems interact. Agents move between contexts in which one normative system dominates (e.g., the home) and contexts where others dominate (e.g., work), in addition to interacting with other agents driven by disparate normative systems. We will discuss how the major theoretical and empirical approaches to norm psychology can address these phenomena and evaluate which approach is most promising.

Beyond the relevance of the proposed analysis for understanding the biological and cultural evolution of norm psychology, the conceptual clarification presented and the notion of normative stress that we develop are also critical for attempts to instill new social norms (e.g., those related to climate change) and to eradicate harmful norms (e.g., female genital mutilation) in complex contemporary societies. Normative stress is also a potential factor in social and political polarization.

Are conservatism and genetic determinism the same thing?

Jonathan Latham, The Bioscience Resource Project, USA

One of the longstanding goals of political science is the development of a theory of what constitutes conservative thought. This presentation contends that conservative thought equates precisely to genetic determinism. Defining conservatism with reference to the writings of Edmund Burke I propose that his thought divides primarily into defences of patriarchy, monarchism and Christian religion. Patriarchy is a genetic determinist proposition. It posits human differences which are assigned at birth. Monarchy and its associated social order (until recently composed typically of a nobility and some variant of serfdom) are also genetic in the same sense. Going beyond Burke, who had little to say about nation and race because they were largely uncontested concepts in his day, I suggest that defences of these concepts also represent core elements of conservatism. While race is indisputably a genetic concept, nation and nationality (as the etymology implies) should also be seen primarily as such. These genetically determinist components of conservatism are perhaps most clearly revealed through the lens of the various social movements that have opposed it. Environmentalism, feminism, civil rights movements, socialism, the food movement, and gay rights, all draw their inspiration from non-genetic determinist interpretations of human nature and/or of the natural world. Finally, this assessment of the central role of genetic determinism in conservatism places it equally at the centre of politics more generally and even at the centre of Western thought itself.

Sérgio Henrique Ferreira's investigation on Bothrops jararaca and its repercussion (1965–1971)

Matheus Abude Wehbe Paes Leme, University of São Paulo, Brazil
Lilian Al-Chueyr Perreira Martins, University of São Paulo, Brazil

In the 1960s and 1970s, investigation on *Ophidia* was active in Brazil, mainly in the Butantan Insitute. Situated in São Paulo City, it provided not only the supply but also the exchange of experimental material among researchers from Brazil and abroad.

The aim of this communication is to discuss the contribution of Sérgio Henrique Ferreira (1934–2016), and the impact it had on the researches that were in progress at that time. A physician from Ribeirão Preto Medical School, University of São Paulo, Ferreira worked with Bothrops jararaca.

Ferreira's research was related to the investigation of his PhD supervisor, Prof. Maurício Rocha e Silva (1910–1983). Rocha e Silva had been working with jararaca venom and identified bradykinin as a endogenous hypotensive hormone in 1949. Later, in 1965, Ferreira detected some biological proprieties of jararaca venom, which interfered with the blood pressure system, specially potentiating bradykinin.

After describing such effects, Ferreira was able to pinpoint the most active peptide responsible for the potentiation. Further work was carried out in collaboration with research teams abroad, namely the Brookhaven National Laboratories Department of Biology and the University of Colorado School of Medicine Department of Biochemistry. The result was synthesis of the said peptide, named Bradykinin Potentiating Factor (BPF). This led to a better understanding of the role of angiotensin-converting enzyme in the destruction of bradykinin. Nevertheless, such results were only published in 1971.

In 1977, departing from Ferreira's results on the subject and work done by peers, which were part of the public domain, a research team from the Squibb Institute for Medical Research (United States) conceived a synthetic hypotensive drug, Captopril, which inhibited the agiotensin-converting enzyme.

In spite of Ferreira's achievement, whose work contributed to the development of a new class of anti-hypertensive drugs, the ACE inhibitors, remodelling the guidelines for treating hypertension, the Brazilian institutions that supported and funded his research received no royalties.

The analysis of this historical episode corroborates the view that scientific endeavor results from a collective work and points out the complexity of social, political and legal aspects related to the scientific production.

The generalized selected effects theory of function: A critical analysis

Yajuan Li, University of Sydney, Australia & Beijing Normal University, China

Justin Garson (2011, 2012, 2016, 2017) proposed that the selected effects theory of function (SE) is legitimate to explicate novel brain functions in neuroscience by appealing to his generalized selected effects theory of function (GSE). Accordingly, SE is not restricted to evolutionary biology or experimental biology (i.e. neuroscience, immunology etc.) which involves evolutionary issues. Rather, SE can also be applied to experimental biology. In this article, I intend to evaluate GSE by appealing to two criteria of function, which include the explanatory dimension of function (what a trait's function is normally) and the normative dimension of function (what a trait's dysfunction is normally). In general, these two dimensions can determine whether a theory of function is rationale. To achieve this goal, GSE is supposed to be clarified firstly. In Garson's view, GSE emphasizes that "the function of a trait consists in the activity that contributed to its bearer's differential reproduction, or differential retention, within a population" (Garson 2017, P523). Here, differential reproduction displays GSE's inheritance of SE and it allows SE and GSE to explain the occurrence of historical functions by appealing to natural selection over a phylogenic time scale. While differential retention (or differential persistence) represents GSE's extension of SE and it allows GSE to explain the appearance of novel brain functions by virtue of neural selection over an ontogenic time scale. According to Garson, neural selection is one member of his generalizing selection processes and its property lies in that it can bring about differential persistence of some entities within a population ontogenically. The problem is that, unlike other generalizations of selection processes, Garson rejected to discuss the nature of selection process. As a result, differential persistence in GSE and then GSE itself is quite vague. To clarify differential persistence in GSE, I am going to compare Justine Kingsbury's rock case and Frédéric Bouchard's quaking aspen case. As we shall see, variants within a population, then their differential fitness and then the continuing reinforcement of their differential fitness are significant elements for achieving differential persistence ontogenically. Here, I alter the expression mode of differential persistence in GSE. Though I admit that differential persistence in GSE belongs to the retained entities, I insist that this kind of differential persistence should be sustained ontogenically. And the way is that these retained entities form a functional region. In this sense, as long as the conditions permit, both the retained entities and their containing functional region are persisting ontogenically. Accordingly, the functions of the retained entities are their activities and their dysfunctions occur when there is an internal damage in their containing functional region. So, by altering the bearer of differential persistence in GSE slightly, GSE satisfies two criteria of function properly.

A unifying account of function

Ying Liu, University of Sydney, Australia

The major theories on the definition of function are the etiological account and the causal role account. The former generally defines the notion of function in terms of a trait's effect from natural selection history. The latter refers the definition of function to the current causal contributions of a systemic component to the capacity of its containing system. These two accounts are regarded as two independent accounts because the corresponding biological theories each of them bases on differ in their approaches to research problems. The etiological account of function is generated merely from evolutionary theory, while the causal role account of function comes from disciplines like molecular biology and physiology. As Mayr once put, evolutionary theory focuses on "why" questions and investigates "proximate" causes which acting on the past, while disciplines like physiology aim at "how" questions and examine "ultimate" causes which acting on the present. These two accounts of function based on these biological theories suffer from serious problems respectively and are far from giving a satisfactory explanation of function.

Yet, an emerging and promising biological field that combines evolutionary theory with molecular biology may shed new light on the debate of function. This new field is characterized by combining evolutionary and phylogenetic analysis with molecular biology, physiology, and biochemistry techniques, which provides possibilities to solve some long-standing questions surrounding function. For instance, this new approach is able to give empirical evidence of how genetic change has produced adaptive phenotypes in the evolving mechanisms. This bridges the existing gap between the macroevolution on general adaptive phenotypes and the microevolution on specific molecular changes.

Therefore, I'm motivated to generate a new philosophical unifying account of function, which reflects the latest scientific progress and has meaningful implications for other discussions. The apparent advantages of this synthetic account are that

1. it solves the main problem of causal role account — lack of norms and that
2. it addresses the core problem of etiological account — lack of empirical evidence.

Interdisciplinarity and the role of differing conceptual contexts in research programs

Katherine Liu, University of Minnesota, USA

In biological research, it is well known that context matters. This usually refers to the role of the environment. Even if environmental variables are not individually or purposely manipulated within an experiment, what can seem to be benign differences between similar experiments can lead to differing results. However, the conceptual contexts in which research programs operate are also important and worthy of attention. Different disciplines carve out boundaries in different ways, leading to different conceptual framings. This affects how and which questions are asked and answered. Here I use results from a set of experiments with yeast (Saccharomyces cerevisiae) as a case study to analyze how the conception, execution, and interpretation of a project changes under the different conceptual framings of yeast biologists versus evolutionary biologists. This additionally allows me to discuss some aspects of interdisciplinarity more broadly, such as how interdisciplinary projects can lead to broader audiences but come with difficulties when those disciplines minimally overlap in motivations and standards of evidence.

Explanations in classical genetics: A model-theoretic account

Pablo Lorenzano, Nationa University of Quilmes & CONICET, Argentina

The aim of this communication is to analyze the kind of explanations usually given in Classical Genetics (see, e.g., Sinnott & Dunn 1925). Explanations in biology have intriguing aspects to both biologists and philosophers (see, e.g., Braillard & Malaterre 2015).

First, we summarize two main aspects discussed in the literature with regard the peculiarities, or even oddities, of biological explanations in general and of Classical Genetics in particular, namely, (1) whether biological laws exist, and (2) whether causation plays a specific explanatory role in biology.

Next, paradigmatic examples of explanations in Classical Genetics will be presented in the traditional format of explanations as summarized by arguments (Hempel & Oppenheim 1948).

Later on, the nature of these explanations will be discussed by using explanations in another area of science, namely, Classical Mechanics.

To clarify the situation, and to carry out an analysis of explanations in Classical Genetics, we introduce some meta-theoretical tools provided by Sneedian structuralism (Balzer, Moulines & Sneed 1987), in particular those of theory-net, fundamental law or guiding principle, specialization, and special laws. We then applied these tools to Classical Genetics. In this application, Classical Genetics' fundamental law/guiding principle will be made explicit.

In order to to make more transparent the ontological commitments of Classical Genetics (some of which would play a causal role; see, e.g., Waters 2007, Woodward 2010), paradigmatic explanations in Classical Genetics will then be presented in a model-theoretic, structuralist format as ampliative embeddings into nomic patterns within theory-nets (Bartelborth 1996, Díez 2014, Forge 2002).

Finally, we conclude with a discussion of the presented analysis showing how it sheds light to the aforementioned intriguing aspects of biological and genetic explanations.

A new foundation for the force interpretation of evolutionary theory

Victor J. Luque, University of Valencia and UNED, Spain

This paper analyses the view of evolutionary theory as a theory of forces. The force interpretation was originally developed by Elliott Sober, where evolutionary theory would be structured by a zero-force law (what happens to a system when no forces act on it), consequence laws (which describe how forces, once they exist, produce changes in the system), and source laws (which describe the circumstances that produce forces). The force interpretation has been challenged in the last years by several authors, formulating five major critiques:

1. The action of evolutionary forces cannot be decomposed;
2. Fitness components cannot be decomposed and be added;
3. There is no common currency in which to compare the contributions of different evolutionary forces;
4. There are no source laws in evolutionary theory; and
5. The Hardy-Weinberg law is not a true zero-force law.

I argue that these critiques are not counterexamples to the force interpretation itself, but only to the original formulation elaborated by Elliott Sober. I then propose a new formalization for the force interpretation based on the Price equation that avoids these critiques. This new formalization establishes a new zero-force law (what I call The Principle of Stasis), and a single consequence law for all evolutionary systems: the Price equation. Thus, the Price equation provides a way to decompose fitness components and different evolutionary forces; gives us a common currency; helps to develop (ecological) source laws; and stablishes what happens when there are no forces acting upon an evolutionary system. In addition, this new formalization has the benefit of being more closely allied with contemporary practice in evolutionary biology than the traditional force interpretation.

A farewell to unity: The case for context in host-microbiota research

Joseph Daniel Madison, Mayo Clinic Microbiome Program, USA

Scientific research is often conducted under varying conceptual frameworks which can alter experimental interpretations, method choice, and the direction of research agendas. These conceptual frameworks are often varied within the same research program causing contradictions and conflict among scientists, institutions, and funding sources. Such contradiction and conflict often impedes research efficiency and interdisciplinary collaborations. However, these conflicts and the resulting sterilization of scientific creativity can be avoided through a context based pluralist framework for concept choice. The resulting context based choices are often characterized by risk assessment both inductive and otherwise. Such a framework is imperative for creativity, novelty, and functional social interactions within research programs. The need for context-dependent conceptual frameworks can be exemplified in the biological sciences by examining the important and rapidly expanding field of host-microbiota research. Conceptual frameworks of study for host-microbiota are varied in the unit of study ranging from organismal to functional with subtle but important conceptual differences causing such contradictions and conflict. This paper will first aim to delineate the conceptual frameworks involved in host-microbiota research. Secondly, this work will examine the importance of utilizing these multiple and often contradictory conceptual frameworks based on context and risk assessment. An argument for the application of context based conceptual frameworks for both theoretical and experimental research in host-microbiota research through pertinent examples will also be made. Lastly, the broader implications of such a framework as it applies to general philosophy of science vis-a-vis epistemology, method, and the current debates surrounding epistemic contextualism will be presented.

Reproducibility in machine learning: The case of AlphaFold

Dijana Magđinski, University of Bielefeld, Germany
Nino Tolić, independent researcher

In recent years, some areas of the social and life sciences were portrayed as facing the so-called reproducibility crisis. Increased worry that many of the scientific claims are questionable since they were not verified by replication is also present in the machine learning field of study. Researches are struggling to reproduce key findings as they usually do not have access to the source code or training conditions of the software in question. The first steps in overcoming this issue include creating open online repositories of algorithms and training data.

In this paper, we will examine the issue of reproducibility on the case study of the protein folding problem. The problem is often regarded as a big biochemistry challenge which, if solved, would contribute significantly to the advancement of life sciences in general and have a major impact on humanity.

In December 2018, a private company DeepMind Technologies significantly outperformed other teams in the Critical Assessment of Structure Prediction (CASP) protein-folding competition. Its system AlphaFold, a state-of-the-art achievement in the machine learning field of study, is being presented as a system that has enormous potential in dealing with the real-world problems, such as diagnostic and treatment of diseases caused by misfolded proteins and management of the environmental pollution problems. Naturally, DeepMind has no intentions to make their source code and training conditions publically available. Therefore, the problem of reproducibility arises.

This case presents us with a dilemma: it offers a revolutionary potential for advancement of humanity but at the same time it seems to expect that we abandon some established scientific norms. We will argue that this is a false dilemma. We will attempt to show that the validity of machine learning systems does not lie in their reproducibility, but rather in the accuracy of their predictions.

Major evolutionary transitions, human evolution and transnaturalization

Siobhan Guerrero Mc Manus, National Autonomous University of Mexico, Mexico

Major Evolutionary Transitions (MET) have given rise to new levels of organization, new dynamics within living systems and new capacities that have reshaped the face of Earth. Particularly regarding Human Evolution (HE) these transitions have inaugurated new symbolic domains and forms of socialization of a global dimension never seen in the history of the planet. The aim of this talk is to claim that a new metaphysics emerged as a consequence of this last MET and, although its particular details are contested, it is usually described as a metaphysic of the social with different strands of philosophy characterizing it in terms of social contracts, collective intentionalities, power relations, constitutive rules, etcetera. Be that as it may, if this claim is correct, we are facing a major breakthrough that poses a challenge to biological explanations, even those that are non reductive in nature, because the rise of a new metaphysics might imply that we are dealing with non homologous explananda whose explanations might fall outside the store of explanations of biological theories, even those such as Niche Construction Theory (NCT) and the Expanded Synthesis (ES). Mexican-Ecuadorian philosopher Bolivar Echeverría famously described this transition as the transnaturalization of humans. A basic tenet of his position is that it is an error to flatten out ontologies, specially human ontologies, by ignoring how previous natural traits are deeply transformed by the rise of norms and normativity among other phenomena. Explanations regarding human nature, human evolution and anthropogenesis should be sensitive to this and aim not only to explain human evolutionary novelties but to incorporate assets from human and social sciences as parts of their explanantia.

Organisms and Darwinian individuals: A metaphysical perspective

Johannes Martens, Université Catholique de Louvain, Belgium
Alexandre Guay, Université Catholique de Louvain, Belgium

What counts as a biological individual? This question, which have been heavily debated among philosophers of biology, has crucial implications for our ontology of biology. Currently, the dominant view about this problem relies on two fundamental claims: (i) the category of biological individuals is more inclusive than the category of traditional organisms; (ii) biological individuals are evolutionary individuals. Taken together, these (logically independent) claims provide a unified framework for thinking about a variety of biological individuals in the living world. Yet, some philosophers have recently defended an alternative picture (Pradeu 2010, 2016; Godfrey-Smith 2013) in which the notion of an organism and the notion of an evolutionary unit refer to two distinct—though partially overlapping—categories within the broader class of biological individuals.

In this paper, I will propose a critical analysis of this ontological representation, and assess the different metaphysical interpretations that can be given to it. To this end, I will start by distinguishing two possible interpretations that can be given to the properties “being an organism” and “being an evolutionary unit”—each can be understood as referring either to a substantial property (a “natural kind”) or to a mere, accidental property of an already individuated object (Lowe 2009). Then, I will address four (exclusive) metaphysical interpretations that can be given to this alternative picture, namely: (1) both the categories of organisms and evolutionary units are natural kinds, (2) both correspond to mere accidental properties of biological individuals (this presupposes that the domain of quantification is already given, i.e. that one knows what a biological individual is independently of the notions of organism and of evolutionary unit), and (3–4) only one of the two corresponds to a natural kind but not the other. I will show, however, that none of these four interpretations turns out to be consistent from a metaphysical perspective.

The contributions of George Newport (1803–1854) to the studies on animal reproduction and possibilities for science teaching

Natália Abdalla Martins, University of São Paulo, Brazil
Maria Elice de Brzezinski Prestes, University of São Paulo, Brazil

The nature of eggs and spermatozoa and the role they play in reproduction may seem commonplace nowadays. However, these questions were part of a great debate between the 17th and 19th centuries. In the beginning, the discussion focused on whether a new being was preformed in the female egg (ovism), preformed in the animalcules (spermatozoa) in the male semen (animalculism) or formed by the mixture of the semen and the egg (epigenism). In the 19th century, the epigenism got stronger, and the investigations focused on whether it was the animalcules or the liquid part of the semen that fertilized the egg. Many scientists performed experiments to answer this question, but none of them were considered, individually, conclusive. George Newport (1803–1854), a well-known English scientist at the time that also studied the fecundation in animals, believed that there was still lacking what he called a “proof” that the spermatozoa were the part of male semen that fecundated the eggs. Thus, Newport conducted several studies, notably replicating experiments of his main predecessors, such as Lazzaro Spallanzani (1729–1799), Pierre Prévost (1751–1839) and Jean-Baptiste Dumas (1800–1884), and published three papers on the subject between 1851 and 1854. Newport corroborated Prévost and Dumas’ conclusions that the spermatozoa are the only part of the male semen that fecundates the egg and showed that it happens by the penetration of the spermatozoon in it. Considering the relevance of these investigations in the history of biology and of the subject – animal reproduction – in science education, this communication has two goals. The first, is to present a recontextualized analysis of George Newport’s studies in an Inquiry-Guided Teaching Learning Sequence for 13-year-old students in science classes of public schools in Brazil. The second goal is to show the use of the historical episode to make explicit and reflective discussions about aspects of the nature of science, such as on the difference between inferences, observations and experiments, and the role of theories in scientific investigations, dealing with questions of objectivity and subjectivity in science.

The failure of research guidelines and the CRISPR babies: An historical review and analysis of key human embryo policy guidelines and why they can be ineffective

Kirstin R. W. Matthews, Rice University, USA

In November 2018, a Chinese scientist, He Jiankui, announced the birth of two girls who had their genome modified as embryos, through a molecular biology tool (CRISPR-Cas9), in an effort to prevent HIV/AIDS. The research was broadly criticized in the public as well as within the scientific community, for numerous questionable scientific and ethical practices. Furthermore, it brought forward concerns about who should be developing research guidelines and regulations as well as what those rules should look like for controversial areas including human embryo research, especially genetically modified embryo research. This presentation will address the scientific, ethical and policy challenges associated with regulating human embryo research, including heritable genome modifications, by reviewing historical policy reports aiming to regulate the field. The discussion will summarize the experiments and ethical concerns about the Chinese CRISPR embryo experiments as well as other recent experiments challenging traditional norms of human embryo research; this will include the development of synthetic embryos (also known as embryoids) and the in vitro culturing of human embryos to 14-days post fertilization. The talk will also review the 2017 US National Academies of Science, Engineering and Medicine (NASEM) policy report on genetic modification of humans, which created guidelines for this research, but ultimately was not successful and failed to influence He's experiments.

While the NASEM report originated in the United States, members of the committee were from around the world and the recommendations were intended to have global impact. The review will focus on how the report was developed; recommendations made by the report; and the impact of those recommendations on policy and scientific research. The presentation will also highlight ways in which it ultimately failed by comparing it to previous guidelines for human embryo research that had more success, including the UK Warnock report on in vitro fertilization (IVF) and human embryo research, which led to the UK Human Fertilisation and Embryology Act of 1990. This report laid out philosophical arguments for human embryo research, guidelines for this research, and policies that should be enacted and was able to influence research abroad. Ultimately, the presentation will show how diverse committees that were scientifically well-informed and that engaged the public, stakeholders, and religious leaders but did not always drive for a consensus had an influence on developing lasting policy with impact.

Partial proper functions

John Matthewson, Massey University, New Zealand

Natural selection comes in degrees. Some biological traits are selected more forcefully than others, some traits are on the increase while others decline, and some groups can only undergo an attenuated kind of selective process. This has downstream consequences for notions that are standardly treated as binary but depend on natural selection. For example, a biological proper function of a structure can be defined as what caused that (type of) structure to be selected in ancestral populations. However, we standardly consider proper functions to be categorical. Transporting oxygen IS a proper function of haemoglobin, while giving red blood cells their colour IS NOT. If natural selection comes in degrees, and proper functions arise through natural selection, then it seems either we require an account of how this graded process generates a binary output, or we require an account of proper functions that allows them to also come in degrees. I argue that the first of these options faces some very tough problems, especially if we wish to claim that proper functions have an objective biological basis, rather than merely reflect our particular interests. I therefore go on to outline what a graded view of proper functions might look like, and what it might entail. Although such an account appears to be the most consistent and well-motivated approach to this problem, the downstream effects will be extensive. This is particularly apparent when we consider that proper functions can underwrite a number of other key concepts, such as dysfunction, disease, and teleosemantic content.

Contingency as a causal force (or not)

Alison K. McConwell, Stanford University, USA

Is evolutionary contingency its own causal force or merely a statistical effect? In the past, philosophers of biology debated the causal status of natural selection (Millstein 2006, Matthen and Ariew 2002, Bouchard and Rosenberg 2004). Yet contingency's status as a force in evolution has not received that same direct attention. Evolutionary contingency is typically represented three different ways: modally, statistically, and in terms of its sources or processes that produce contingent evolutionary trajectories. First, evolutionary contingency is traditionally conceived of modally: In a famous longstanding debate over contingency's prevalence in evolution, contingency concerns unique outcomes dependent on historical trajectories against a background of alternative possibilities (Gould 2002, Beatty 2006, Desjardin 2011). Second, contingency in macroevolution has been construed as something like the statistical effect in the MBL computer simulated model tracking species sorting as a stochastic process (Turner 2015). And finally, some philosophers argue that contingency as a pattern is (1) either produced or sourced by stochastic processes like mutation, drift, and species sorting or (2) is testable by tracking the influential significance of those chance-based processes (McConwell and Currie 2017, McConwell forthcoming, Powell and Mariscal 2015, Travisano et al. 1995). To determine contingency's status as a force, I will survey the three alternative representations of contingency as they exist in the literature. In this paper I aim to develop what it means to consider contingency as a force in its own right compared to contingency as a pattern of statistical effect. I will analyze those possibilities in terms of both their epistemic value and the differences they potentially make to scientific inquiry.

How do we reason about formal models in biology?

Brian McLoone, Higher School of Economics, Russia

How do we reason about formal models in biology? Fictionalists claim that we do so, in part, by imagining the hypothetical model system that is described by a model. For instance, when we reason about the dynamics of Lotka-Volterra, we imagine populations of predators and prey growing and decreasing in size. A good deal of fictionalist work implies that the form of imagination involved here is visual; we "see in the mind's eye" the model system that is described by the formal model. For reasons discussed by Michael Weisberg, this version of fictionalism won't work, since even very basic models in biology, like Lotka-Volterra, are probably impossible to visualize. In the case of Lotka-Volterra, for instance, the number of organisms in a population is a continuous quantity, but it seems we can only visualize (many) organisms coming in discrete units—e.g., I can visualize one or two rabbits, but not 1.3456 rabbits. Elsewhere, I have argued that Weisberg's criticism doesn't spell doom for fictionalism in general, since many forms of imagination are non-visual. In particular, propositional imagination can be non-visual and can allow one to reason about the strange quantities found in the models that motivate Weisberg's critique. In that earlier work, however, I only gestured at how this form of reasoning works. Here, I try to develop this account more fully, drawing on some work in impossible world semantics. And, along the way, I consider various alternative, far more deflationary accounts of what is involved when we "reason" (note the scare quotes) about such models.

How does competitive research funding affect science? Insights from interviews with scientists

Stephanie Meirmans, University of Amsterdam, Netherlands

Competitive research funding likely has a large effect on science. But what exactly is this effect, and in which ways is it positive or negative? What could be improved? In my current project, we have asked these questions to active scientists across three different scientific domains (humanities, natural sciences and medical sciences), different academic seniorities (permanent and non-permanent staff) and two countries (Netherlands and Switzerland). We found that, indeed, competitive research funding does have a large effect on science, that this effect is not necessarily positive, and that many of the active scientists had ideas for how to improve matters. In this talk, I will present the results of our interviews and extract possible ways for a better organization of funding.

An explanatory role for brute facts in biology

Constantinos Mekios, Stonehill College, USA

In recent philosophical discourse, the term “brute facts” has been used to denote facts about the world that have no explanation (Fahrbach 2005). Given the broadness of this definition, phenomena, events, laws, or properties may be called brute either because their explanation remains merely unavailable to us, or because no further explanation for them exists. To resolve this ambiguity, Barnes (1994) distinguishes between those facts that fall under the former category and are, therefore, epistemically brute, and those fundamental facts about reality that are ontologically brute. Whether the existence of biological facts that are ontologically brute can be legitimately defended is a question open to philosophical debate, but addressing it does not constitute the primary focus of this paper. What I propose to examine instead is the potential significance of the notion of bruteness for explanation in biology and, correlatively, its implications for biological methodology and research.

In the philosophy of biology, considerations about brute facts are intertwined with discussions about emergence. Despite the lack of consensus on how emergence ought to be properly defined, the claim that properties count as emergent if they cannot be explained reductively in terms of the physical substrate from which they emerge has been identified as a basic thesis of the doctrine (Vintiadis 2018). Correspondingly, although the mere lack of a reductive explanation does not suffice to declare a fact brute, some emergent properties may qualify as such, provided they turn out to be altogether devoid of explanations. In this essay, a brief discussion of the problematic relationship between emergence and bruteness is intended to serve as a prelude to its main subject: the critical analysis of the role that putatively brute facts could play in accounting for properties of complex biological systems that have yet to be explained reductively. More specifically, after briefly citing some reasons for treating emergent properties, at best, as merely epistemically brute, I concentrate on the example of mathematical formalisms such as design principles, which are instrumental for some non-reductive approaches in contemporary biology. I argue that the explanatory value of these formal principles depends on their own status as brute facts about high-level constraints on biological function and structure; constraints that may be regarded as brute in so far as they are in place simply because of the way the universe is.

Questioning our evolutionary loneliness: Archaic hominin admixture through a philosophical lens

Andra Meneganzin, University of Padua, Italy
Telmo Pievani, University of Padua, Italy

Thanks to considerable advancements in ancient DNA (aDNA) extraction and analysis, human palaeogenomic research has experienced a revolution in the last decade, enabling the researchers to address, with a new line of evidence, the long-standing interest in whether anatomically modern humans and archaic human ancestors interbred.

The publication of the first draft sequence of genome of the closest evolutionary relative of present-day humans (Green et al 2010) has revealed that between 1 and 2 % of the genomes of present-day non-Africans could be of Neanderthal origin. The researchers suggested that the gene flow occurred between Neanderthals and early modern humans in the Middle East (and then elsewhere), before the latter expanded in Eurasia and diverged in different populations. Evidence for archaic admixture accumulated in the following years, involving also other hominin forms such as Denisova man. In 2018 the discovery of a first-generation hybrid, half Neanderthal, half Denisovan, has aroused enthusiasm among the scientific community (Slon et al 2018), suggesting that admixture could not be rare in hominin evolutionary past.

The body of evidence for interbreeding is ground-breaking with respect to previous models of human origins, which demands an updated theoretical perspective. We are at the frontiers of a both scientific and epistemological problem, which is rephrasing important questions in paleoanthropological research, and is re-orienting longstanding debates on patterns of replacement and migration.

First, the idea of pure groups with clearly identifiable origins and distinct evolutionary trajectories has been reconsidered. We are beginning to reshape standard tree-like models of human evolution with ones in which internal branches can episodically mix. Our evolutionary solitude is proving to be a recent event in natural history, raising questions about our evolutionary identity in light of the coexistence of multiple hominin forms until recent times. This also evokes counterfactual scenarios of our path to becoming a global species: had hybridization not occurred (and subsequent cultural interactions and exchanges), would *Homo sapiens* have been the flourishing and adaptable species we see today?

Second, interbreeding data need to be considered in order to integrate or update existing models of human origins. The old multiregional evolution (*H. sapiens* evolved from local ancestors across the Old World) is generally regarded as falsified, but the strictest version of recent African origin *(Homo sapiens* originated in a single region in Africa and dispersed from there, without any interbreeding with other lineages) has to be reconsidered. In our proposal for the conference, we will argue that human evolutionary models can increase their stability by drawing more extensively, and in a programmatic way, on different epistemic sources, adopting a consilience-based approach.

Third, the threshold of extinction of all other human forms (50 to 40 kya) raises new scientific and philosophical questions about the reasons why *Homo sapiens* has recently remained the only surviving human species. In this regard, we will propose and discuss a model based on the hypothesis of a late migration out of Africa of modern human populations (carrying symbolic behaviors) that replaced the other human forms (the Final Wave Model).

Practices of comparison in early molecular genetics

Rebecca Mertens, Bielefeld University, Germany

My talk deals with comparative practices in the development of early molecular genetics between the 1950s and 70s. I will address the question of how the use of comparison affected the ways in which novel methodological and experimental approaches, techniques, and model organisms were introduced and incorporated within existing and new scientific communities in the fields of genetics, micro biology, and molecular biology.

I will argue that practices of comparison served to localize and articulate methodological and conceptual problems in the emerging field of molecular genetics, especially with respect to the practicability, significance, and explanatory power of particular model organisms (See Ankeny 2001 for the epistemic and political implications of model organisms). I will exemplify my argument on the grounds of a case study on the re-interpretation of viruses as “genetic elements“ (Jacob/Wollman 1961). This debate influenced the development of molecular genetics in many crucial ways, most importantly with respect to the concept of genetic recombination, blurring boundaries between the phenomena of heredity, mutation, and infection, and the generalizibility of experimental systems. As will be shown, comparing viruses with other micro-organisms, like e.g. bacteria, and with higher-level organisms with respect to processes of recombination, mutation and growth as well as the structural and functional comparison between DNA and RNA on the level of macromolecular interactions helped to establish grounds of comparison (tertia comparationis) which, in turn, served as a conceptual basis for the new genetics.

How the choice of model phenomenon matters. Exploring an understudied topic in the history and philosophy of the life sciences

Robert Meunier, University of Kassel, Germany
Saliha Bayir, University of Kassel, Germany

The paper addresses model phenomena as a central aspect of research in the life sciences. “Model phenomena” is used to refer to those entities, properties or processes that become recognized as subject of investigation and are taken to represent a broader class of phenomena. An example would be the development of one organ which is studied as a model for organogenesis in general. A more complex example would be the formation of pigmentation patterns as a model for pattern formation in general, including gross morphological patterns.

While the term is not an actor’s term, the category is clearly recognized by researchers. A term often used in this context is “model system”. However, since the latter term is used for many aspects of research, including model organisms, it seems useful to introduce a specific term. To sharpen the concept, it is necessary to distinguish model phenomena from other aspects of research and see how they relate to each other. Points of comparison are, first, examples, which often have a rhetoric or pedagogical function; second, experimental paradigms, which serve as models for a kind of approach, which might then be applied to other phenomena; third, experimental operationalizations of a phenomenon. Further questions are how the choice of model organisms and model phenomena influence each other, and how the representational features and uses of model phenomena interfere with those of model organisms.

The question of model phenomena – like that of model organisms – lends itself to integrating philosophical, historical and sociological approaches:

Philosophical issues: In some cases, causal analogies will be the basis for representation, whereas in other cases internal homologies might be assumed. Sometimes general explanatory models will be suggested, while at other times, findings will be extrapolated to learn about specific phenomena other than the one studied.

Historical issues: How are model phenomena chosen? Some phenomena are initially studied because they are medically or agriculturally relevant. Once procedures and knowledge accumulate, they might become models for other phenomena. Model phenomena might also be established because they are suitable for experimental approaches in some way, or for entirely contingent reasons. Furthermore, the choice will establish possibilities and constraints for research and thus shape the history of concepts and fields.

Social issues: It can be observed that communities form around model phenomena which often cut across model organism communities. While the former are much less structured around shared infrastructures than the latter, there is still exchange of concepts, study designs and materials, and standardization of terminology or procedures often takes place.

While the importance of what is here called “model phenomena” has not gone unnoticed in the literature, there is surprisingly little systematic study of this central aspect of research in the life sciences. The paper will address the above issues by drawing on examples from the history of genetics in the 20th century, to establish an agenda for further study.

A Darwinian account of war literature

Andrew Moffatt, Florida State University, USA

It has been a century, almost to the day, since the firing of shots ceased on the Western Front in France, yet it is beyond cliché to say that the war to end all wars did nothing of the sort. But what this war did put an end to was the childlike fantasy of war that dominated the Western cultures who stumbled into it four years prior during the heady days of August. This paper investigates why such a fantasy of war so dominated the minds of the people of that era and why the First World War in particular irrevocably changed this. Specifically, this paper offers a Darwinian account of the phenomenon, closely related to William James' Darwinian account of great men and great ideas. I will argue for the conclusion that a key difference between prior wars and the Great War was the character of the literature they produced, which shaped the popular conception of not only the specific war in question, but of war more generally. In essence, I hypothesize that three factors can largely explain the difference in tenor of the accounts. The first is the pattern with which the war was fought. The more modern the war, the more constant it is. In antiquity, the actual fighting in a war may last no more than a day or two in a year, with the campaigns of Alexander, Hannibal, and even to some extent Napoleon representing clear cases, whereas in modern war it is incessant, a fact much remarked on by the soldiers in the trenches. The second factor is survivorship, an explicitly Darwinian characteristic. As war becomes more modern, a greater and greater portion of the wounded are able to recover due to advances in medicine and infrastructure. The tales these men tell will surely be different from those left physically unscarred. And finally, the dissemination of writing and opening of the press to the lower classes took the pen away from the general and placed it in the hands of the private, whose account of the war cannot help but differ in significant ways from his commander. These three factors combine to affect the tenor of the literature produced in a Darwinian fashion, replacing the glorification of war with horror. The Darwinian nature arises from the focus on the patterns of descent in a population (war writers) and provides mechanistic explanations for the patterns of evolution this population exhibits over time.

From biological traces to forensic evidence: A comparative study

Barton Moffatt, Mississippi State University, USA

The forensics science community in the United States has begun to grapple with an odd dichotomy. On one hand, new advances in DNA technology and genealogy have made great strides in bringing justice to the victims of long forgotten crimes. On the other, a massive ongoing series of faulty forensic science scandals have undermined confidence in the endeavor. For example, fields like bite-mark analysis and blood spatter interpretation lack a scientific basis for their core assumptions. The forensic science community is aware that there are problems in their practices and for the need of reform (Committee on Identifying the Needs of the Forensic Sciences Community 2009). Despite this awareness, the pace of reform progress is slow.

This paper seeks to understand the differences between faulty and successful forensic sciences by comparing two forensic technologies and the bodies of literature that support them. Specifically, I will compare the recent attempt to harness the microbiome as a forensic tool (Burcham et al 2016) and the longstanding but now suspect field of blood spatter analysis. I will look to the work of Helen Longino (1990, 2002) on scientific objectivity for insight into why one is trustworthy and the other not, despite both being supported by a peer-reviewed literature. Biological traces only become forensic evidence in the context of the right kind of scientific community.

Materially-continuous genidentity: A synthesis of substance and process ontology

Daniel Molter, University of Utah, USA

Biological individuals are said to be either *things*, as in Aristotle's primary and secondary substances, or processes, as John Dupré and many others have recently argued. This paper synthesizes substance and process ontology into a single ontology of materially-continuous genidentity (McG). Following Molter (2017), I argue that all biological individuals – from chromosomes, to species, to holobionts – are genidenticals (spatiotemporally-continuous series of causes and effects whose proximate stages share overlapping material parts). The leading edge of a biological genidentical always occupies a region of space-time that is simultaneously occupied by some quantity of matter, and it is this matter which makes a biological individual a substance. The material in a biological individual is not static, but moves in patterns that are characteristic of its kind, where "kind" is understood in terms of inherited dynamic morphology. It is the motion of its matter which makes a biological individual a process.

Just as a wave is composed of different water molecules as it propagates down a beach, the dynamic form of a biological individual propagates through new matter with each breath and each meal, such that complete replacement of material parts is possible over time, but, like the wave, proximate stages of a biological genidentical always share some material parts, as this is necessary for the continuity of causal interactions between material parts which maintain the biological individual's dynamic form. Material overlap between the proximate stages of a biological individual grounds its persistent identity as a substance, despite constantly shifting material composition, while regular patterns of causal interactions between the material parts grounds its identity as a process. Because McGs are both processes and substances, recognizing that biological individuals are McGs dissolves tension between process and substance ontology in philosophy of biology.

From underdetermination to explanation in biology and climate science

David Montminy, University of Montreal, Canada

In her 2016 book on data and biology, Sabina Leonelli refers to Chang (2004) and says that "... underdetermination is the epistemological motor of data-centric research and grounds the contemporary emphasis on both 'big' and 'open' data." Moreover, she claims, following Dewey (1938) and Longino (2006), that in order to fully appreciate the evidential value of a given dataset, one must take into account the context in which these data are produced, shared and re-used. This investigative strategy, called embodied epistemology, echoes Winter (2015) description of the pragmatic structure of scientific theories in its three core pillars: it sees "[...] knowledge as processual, purposive, pluralist, and context dependent, and on the social and cognitive structure of scientific inquiry"; it "[...] expands the notion of theory to include nonformal aspect"; and it "[...] make[s] explicit nonformal internal components of theory structure". Taking her work as a backdrop, we will start by giving details how, in biology and climate science, contextual elements, i.e. meta and non-scientific considerations, are used to frame scientific knowledge claims. We will then show how Leonelli's epistemological analysis of data management practices in biology can be use to make explicit four interpretative layers (theoretical, axiological, ideological, political) used to interpret data and produce knowledge claims in climate science. Once this is done, we will highlight the crucial role of metadata as both provider of interpretative insights and as key factors to epistemic opacity (Humphreys 2004). In short, they give guidelines for interpretation in providing details about the production techniques used to generate data, yet they make data more blunt by forcing them into standardized data-sharing platforms that precludes certain specifics that could contribute to the evidential value of given datasets. Being thus stripped of potentially relevant information, these datasets can hardly be used to confirm climate models. However, doing away with confirmation might not be as bad as it seems. To illustrate this, we will show how Katsav's (2013, 2014) possibilist conception of models is well suited to export Leonelli's (2016) embodied epistemology, initially developed to account for data management practices in biology, into climate science. Thus going from underdetermination to explanation in biology and climate science.

The Florida Everglades: An essay in ecology

Taylor Rae Morgan, Florida State University, USA

The Florida Everglades spans central and southern Florida, comprises 1.5 million acres of wetlands, and is contained within man made borders designated by the US National Park service. The Everglades is home to many species, both indigenous and introduced, and most famously houses the North American crocodiles (there are alligators too, but they are much more common in the US), along with the Florida panther, as well as the (introduced) Burmese python. The creation and founding of the Everglades National Park was both influenced by conservatism and environmentalism. The Everglades has historically and deeply been threatened by human encroachment as well as rising sea levels due to global warming. However, there has been controversy over the correct approach to the handling and policies of the Everglades, as so often in a deeply conservative Christian state such as Florida, environmentalism and ecological ideas about nature run opposite to conservative ideas about individual property rights and the role of the state. Through technology-oriented projects, economic, social and environmental issues have furthered the gulf between those who would take a scientific, naturalist approach to these problems and those who are more inclined towards an evangelical, literalist perspective. Conservative attitudes towards nature brings about interest in tourism, aesthetics (the beaches, "exotic" diversity, and beauty) and state values, and has been a motivating factor in many of Florida's previous policies, such as the "Swamplands Act of 1850" and the currently implemented "Comprehensive Everglades Restoration Plan:" a forty year, $17 billion dollar Conservative effort towards maintenance, protection, and preservation of the ever threatened ecological ground. Based on pertinent background studies and an extensive trip to the Park, this paper considers the crucial issues and conflicting positions when discussing the Everglades, and offers some proposals for moving forward.

Prospects for philosophy of virology

Gregory J. Morgan, Stevens Institute of Technology, USA

This talk will consider the range of topics that could be considered part of a future philosophy of virology, conceived of as a subfield of philosophy of biology. I will suggest that philosophical analysis of virology can provide insight into the nature of life, of species, of the tree of life, and also provide insight into more general topics in the philosophy of biology such as the nature/nurture debate. Relatedly, I suggest that an increased understanding of the ecology, diversity, and evolution of viruses had the potential to transform our understanding of many of central concepts of biology. More specifically, our conceptions of biological species, the tree of life, biodiversity, disease, evolution, and even life itself can be transformed when examined from the point of view of virology. Life is found to be a more complex concept and the sharp distinction between living and nonliving less important to the development of biology as a discipline. Species are not required for, nor a necessary consequence of, viral evolution. Furthermore, the genetic and phenotypic mosaicism found in viruses and their hosts, a consequence of viral evolution, demonstrates how traditional species concepts are simplifications and can obscure important parts of the history of life. The germ theory of disease, as an account of external agents that cause disease, also requires updating as endogenous viruses fuse with their hosts, can offer protection from other infections, and accelerate evolution. The “human” genome contains roughly 8 % viral genomes and some of these “viral” genes play vital roles in human development. The traditional tree of life, a structured series of bifurcations, has to be augmented with, or replaced by, a more complicated structure that contains reticulations caused by the virus-driven horizontal transfer of genes among distant branches.

A critical analysis of process ontology

William Morgan, The University of Sheffield, UK

Recently, some philosophers have claimed that an ontology of things, or objects, at least for the biological world, should be abandoned for an ontology of processes. According to this view, organisms are best understood not as things or objects, but as processes. Whilst some of these philosophers are only making an epistemological claim, others such as John Dupré and Daniel Nicholson are making a metaphysical claim– it is not merely useful to think about organisms as processes. Rather, organisms are processes. This view is considered to involve an ontological shift in how we understand the biological world, although one that is supported by empirical and philosophical consideration about the dynamic character of organisms. Process ontology is becoming increasingly influential in metaphysics and the philosophy of biology, and substance ontology is increasingly thought to be scientifically uninformed. In this talk, I will two do things. Firstly, I will consider whether processes ontology, at least as presented by some philosophers of biology, really is proposing a radical ontological shift for the biological world, and perhaps beyond. This will be done by considering the main claims that process ontologists are making and how they differ from the claims made by substance ontologists (supporters of an ontology of things). It will be argued that whilst the claims made by process ontologists about the nature of organisms and the biological world are plausible, they are claims that most substance ontologists will accept, given a plausible understanding of "thing" or "object". Furthermore, it is unclear how process ontology differs from a very influential and established metaphysical view about things, namely, four-dimensionalism. I am therefore unconvinced that substance ontology is proposing a radical ontological revision. Secondly, I will consider what process ontologists take to be some of the shortcomings of substance ontology, firstly, that it is unable to account for facts about the dynamic character of organisms, and secondly, that it fits badly with recent developments in quantum physics. It will be argued that whilst substance ontology can plausibly answer both of these worries, the second objection does perhaps present some difficulties for an ontology of things. It is at least not entirely obvious that matter at the fundamental level can be parcelled up into things or processes.

Be fruitful and multiply: Fitness and health in evolutionary mismatch and clinical research

Rick Morris, University of California, USA

I defend the clinical relevance of evolutionary mismatch against a common criticism. Evolutionary mismatch is, roughly, poor fit between an organism and its environment. Researchers in evolutionary medicine have proposed mismatch as a possible cause for morbidity and mortality in contemporary *Homo sapiens* populations.

Mismatch hypotheses are often taken to provide an evolutionary explanation for the health outcome in question, while simultaneously offering possible interventions for researchers and clinicians to pursue. A problem: fitness outcomes and health outcomes are distinct. Natural selection operates on fitness, not on health per se. There are cases where increased health may not contribute to fitness in the modern environment. For example: Type II diabetes after the conclusion of the reproductive career might well have relatively little fitness effect, but the health consequences can still be profound. Given that so-called "diseases of affluence" like diabetes are often treated as paradigm cases of mismatch in humans, use of the evolutionary framework may seem inappropriate.

I propose an approach for using evolutionary mismatch in clinical research which sidesteps these problems. The gist of the proposal: given causal analogies between environmental causes of morbidity and environmental causes of fitness reductions, evolutionary mismatch can be used as a heuristic to generate clinical (rather than evolutionary) hypotheses, irrespective of the fitness effects of the environmental change at issue. Even absent knowledge of fitness effects, researchers may reasonably use the mismatch heuristic to identify specific possible clinical and public health interventions. Even if there is no poor fit to environment in a straightforward evolutionary, fitness-grounded sense, the mismatch framework can be fruitful. Clinical fruitfulness, I argue, is enough to justify the clinical use of evolutionary mismatch.

Engineering the environment: Plants, phytotrons, and climate control in the cold war

David P. D. Munns, The City University of New York, USA

The pursuit of technological control over organisms and experiments has been and remains a fundamental agent of change for biology in the twentieth century. To explain how scientist's think about the world and how they create knowledge, historians have long followed and observed what technologies they have built and used, notably those famed biological technologies like electron microscopes, ultracentrifuges, and radioisotopes that have shaped biologists' ability to see and trace molecular processes. In my talk I want to outline a story runs parallel to the technologies that have helped reveal genes have been equally important technologies that have revealed the biological environment, notably phytotrons.

With a name that resounded with all the promise of the dawning atomic age, phytotrons were facilities consisting of any number of rooms or smaller cabinets, in each of which any desired set of environmental conditions could be produced and monitored by new computers. My paper argues that the construction of technologies to control the biological environment had three immense consequences. Firstly, control enabled the "environment" to be defined as a part of an experimental science of life. Secondly, phytotrons saw some biologists become technologists in their pursuit of biological knowledge. Thirdly, the construction of new laboratories with elaborate technological systems to control and regulate elements of any climate saw feedback emerge as a powerful challenge to reductionism, both because the technological control of one climatic variable destabilized another but also because it revealed organisms as complex products of genes and environments. In sum, the study of life became an exercise in the technological control over both genes and environments and so the knowledge of the machine equaled knowledge of the plant.

Some considerations about the fallacious defense of genetically modified organisms in Mexico

Julio Munoz-Rubio, Universidad Nacional Autónoma de Mexico, Mexico

In November 2017 the book entitled *Transgenic Food, Great Benefits, Abscense of Damages, Myths* was presented to the Mexican and international scientific communities as well as to he public opinion. This book constitutes the main effort so far in Mexico and probably in all Latin America to make a vehement defence of genetically modified organisms (GMO's) for human consumption. It was coordinated by Dr. Francisco Bolívar-Zapata, one of the most laureated Ibero American scientists.

The main charactersitic of this book is the use of a fallacious language as well as the comission of severe basic conceptual mistakes. Given the impossibility of describing here all of them. I will center, on one side, in showing what in Bolivar-Zapata constitutes a clear ignorance of basic concepts of the Darwinist theory.

On the other side, I center my interest in criticizing Bolivar-Zapata's concept of Horizontal Gene Transfer (HGT). In his words, this phenomenon is mistakingly and fallaciously treated. His argument proceeds as follows: HTG is a constant phenomenom along the history of Life on the Earth. It has lead, among other things, to the formation of eukariotic cells by means of endosimbiotic processes, and has produced no damage to Nature. Then, given that the industrial methods of manufacture of GMO's are based on that same basic phenomemon, these organisms will nor cause damage.

I refute this argument. The conclusión of the reasoning cannot be inferred form the premises. The Serial Endosymbiotic Theory refers to a phenomenon that lasted hundreds, if not thousands of million years of evolution. Throughout this period, the involved organisms progressively established interrelations comprising a series of slow, non-linear and most probably non-universally succesful processes. So, the apropriate condictions leading to the eucariotic cells were created by themselves thanks to a close interpenetration with the environment. In other words the organisms constituted themselves as objets and subjetcts of their own evolution. This is qualitatively different to a sudden and impositive artificial hibdirization of nucleic acids, coming, besides, from phylogenetically non-related species, which is the characteristic of the GMO's manufacture. The unpredictability of the results of this human process is very high.

From a sociological point of view, it draws attention the fact that a text that has been presented as a Supreme work to justify the comercial use of genetically modified food, despite containing these and many other crass errors and fallacies, has been edited and endorsed by the three most important Mexican institutions of higher education and scientific research: the National Autonomous University of

México, the Mexican Academy of Science and the National College. This indicates that there is an official policy of the mexican State of support the marketing of genetically modified food. All these pro-transgenic policies are carried out with disregard for the slightest scientific rigor.

A novel explanatory strategy in structural biology: Ensemble explanations of protein function

Jacob P. Neal, University of Pittsburgh, USA

Although philosophers largely acknowledge that explanations of biological phenomena can be pitched at different levels, they dispute their explanatory merits. Some have defended the position that lower-level, reductionist explanations are superior to abstract or emergent explanations that are pitched at higher levels (Kaplan and Craver 2011), whilst others have argued the exact opposite (Putnam 1975). This debate between explanatory reduction and emergence is relatively entrenched in the literature. In this paper, I look at recent theoretical and experimental advances in structural biology to argue that an increasingly common class of explanations—what I call "ensemble explanations"—fails to fit neatly into this philosophical framework. My goals in this paper are two-fold. First, I present an account of ensemble explanations, showing how they differ from other types of explanation common in structural biology. Second, I plan to argue that, although they have some resemblance to both reductive and emergent explanations, ensemble explanations of allostery resist classification as either reductive or emergent.

Ensemble explanations have been developed by protein scientists to capture the intrinsic dynamic properties of proteins (Motlagh et al. 2014). These explanations represent any protein as an ensemble of structurally distinct microstate conformations with varying stabilities. The energetically weighted ensemble captures the fact that proteins in vivo will conduct a biased random walk through conformation space, sampling lower energy microstate conformations more frequently than higher energy ones. Protein functions, such as allosteric inhibition, are then explained by reference to the state of the ensemble before and after perturbations, rather than the structural or conformational details of a single protein at a given time. In this way, ensemble explanations capture both the enthalpic properties of protein conformations as well as the entropic properties that arise from their intrinsic dynamics. Because of this feature, ensemble explanations can explain anomalous protein behaviors that resist mechanistic explanations that rely only on static 3D structures of proteins.

These ensemble explanations, I argue, are neither reductive nor emergent. They are part-whole relations with two levels: the lower-level, consisting of the structural details of individual protein conformations, and the higher-level, consisting of the ensemble-level properties that arise from the weighted contribution of all the microstates at the lower-level. However, these explanations fail to be reductive, since they do not privilege the lower-level structural and mechanistic details as accounts of reductive explanation require. Moreover, they use a property of the whole—viz., the mathematical features of the ensemble—to explain the observed protein behavior. But, ensemble explanations of protein behavior also fail to match the characterization of emergent behavior arising from self-organization described in recent philosophical accounts (Mitchell 2009, 2012; Wimsatt 2007). Ensemble explanations thus fail to fit the established frameworks in philosophy of biology for thinking about explanation. I suggest that the current debate between reductionists and anti-reductionists offers us a false choice and obscures a class of explanations that falls between these two extremes. Considering ensemble explanations, which are becoming increasingly common in protein science, forces us to rethink this seemingly intractable debate.

The evolution of multicellularity and lineage pluralism

Celso Neto, University of Calgary, Canada
Makmiller Pedroso, Towson University, USA

The evolution of multicellularity is considered a major event in the history of life, but it is still poorly understood (Maynard-Smith &

Szathmáry 1995; Michod 1999; Ratcliff et al. 2012). In this paper, we critically examine Peter Godfrey-Smith's framework for that event (2009; 2011). We show that his framework is limited because it relies on a single notion of individuality, namely Darwinian Individuals. We argue that an adequate framework also has to allow for non-Darwinian individuals (Libby and Rainey 2013). Then, we explore a consequence of this argument, namely lineage pluralism. This is the thesis that there are different kinds of biological lineages in evolution.

The evolution of multicellularity occurs when independent cells become interdependent, stick together, and then form a single collective entity. Peter Godfrey-Smith frames this event as a transition from marginal to paradigmatic Darwinian Individuals (2009). Initially, the group of independent cells is only a marginal individual because it cannot enter into selective processes as a single entity. Selection occurs at the level of individual cells rather than the cell group. To be able to enter into selection processes, the cell group has to gradually evolve higher degrees of bottleneck, germ-soma separation, and integration. As these degrees increase, the cooperation and interdependence among cells increase until they form a paradigmatic Darwinian individual (2009, 122). This individual has the highest degree of bottleneck, germ-soma separation, and integration.

Godfrey-Smith's account of the evolution of multicellularity relies on the notion of Darwinian individuals and its underlying features of bottleneck, germ-soma separation, and integration. This framework is useful to understand the properties of newly formed multicellular individuals, such as their capacity to enter into selection processes. Nonetheless, this framework is insufficient to explain the intermediary stages in the transition from unicellular to multicellular individuals. The reason is that the framework characterizes these stages only negatively. Intermediary stages are occupied by individuals that do not have a high degree of bottleneck, germ-soma separation, and integration. Still, biological literature suggests that individuals at intermediary stages have distinctive features that help to explain the evolution of multicellularity (Libby and Rainey 2013, Monte and Rainey 2014). These individuals are not Darwinian ones, as they do not exhibit heritable variation in fitness.

Still, the specific features of these non-Darwinian individuals help to explain how Darwinian individuals can evolve. For example, one can explain how bottlenecks can start evolving, an explanation that Godfrey-Smith's framework cannot offer because it already assumes bottlenecks. Therefore, one can provide a better account for the evolution of multicellularity by incorporating non-Darwinian individuals into the analysis.

A consequence of our analysis is lineage pluralism. As the biological literature invokes both Darwinian and non-Darwinian individuals, it suggests two kinds of lineage operating at the evolution of multicellularity. This pluralism matters for two reasons. First, it opposes the oversimplified and traditional definition of lineages as units of evolution (Hull 1980). Second, it dissociates the notions of lineage, genealogy, and inheritance (cf. Clarke 2016).

Schrödinger's *What is life?* 75 years on

Daniel J. Nicholson, Konrad Lorenz Institute for Evolution and Cognition Research, Austria

2019 marks 75 years since Erwin Schrödinger, one of the most celebrated physicists of the twentieth century, turned his attention to biology and published a little book titled *What Is Life?*. Much has been written on the book's instrumental role in marshalling an entire generation of physicists as well as biologists to enter the new field that came to be known as "molecular biology". Indeed, many founding figures of molecular biology have acknowledged their debt to it. Scientifically, the importance of *What Is Life?* is generally taken to lie in having introduced the idea that the hereditary material (at the time it hadn't yet been conclusively identified as DNA) contains a "code-script" that specifies the information necessary for the developmental construction of an organism. Although Schrödinger ascribed too much agency to this code-script, as he assumed that it directly determines the organism's phenotype, his insight that the genetic material contains a code that specifies the primary structure of the molecules responsible for most cellular functions has proven to be essentially correct. Similarly, Schrodinger's famous account of how organisms conform to the second law of thermodynamics, by feeding on "negative entropy" at the expense of increasing the entropy of their surroundings, is also quite correct (even if this idea was already well-known at the time). Consequently, most retrospective evaluations of *What Is Life?* (including the ones which have just appeared to commemorate its 75th anniversary) converge in praising the book for having exerted a highly positive influence on the development of molecular biology. In this paper I challenge this widely accepted interpretation by carefully dissecting the argument that Schrödinger sets out in *What Is Life?,* which concerns the nature of biological order. Schrödinger clearly demarcates the kind of order found in the physical world, which is based on the statistical averaging of vast numbers of stochastically-acting molecules that collectively display regular, law-like patterns of behaviour, from the kind of order found in the living world, which has its basis in the chemical structure of a single molecule, the self-replicating chromosome, which he conceived as a solid-state "aperiodic crystal" in order to account for its remarkable stability in the face of stochastic perturbations. Schrödinger referred to the former, physical kind of order as "order-from-disorder" and the latter, biological kind of order as "order-from-order". As I will argue, this demarcation proved disastrous for molecular biology, for it granted molecular biologists the licence for over half a century to legitimately disregard the impact of stochasticity at the molecular scale (despite being inevitable from a physical point of view), encouraging them instead to develop a highly idealized, deterministic view of the molecular mechanisms underlying the cell, which are still today often misleadingly characterized as fixed, solid-state "circuits". It has taken molecular biologists a disturbingly long time to "unlearn" Schrödinger's lessons regarding biological order and to start taking seriously the role of self-organization and stochasticity (or "noise"), and this, I claim, should be considered the real scientific legacy of *What Is Life?* 75 years on.

When is a model?

Jason Oakes, University of California, Davis, USA

Scientific modeling is diverse in its objects, including mathematical structures, computer programs, machines, material models, model organisms, simulations, forecasts, and scenarios. Describing the different parts and aspects of models according to existing classifications has significant problems. Trying to answer the question "what is a model?" is too fraught with confusion to be useful. Models are diverse, and their use is not defined by their form.

I want to be able to describe models' histories, and to distinguish between related models. For instance, when did the Lotka-Volterra equations stop being two distinct modeling activities being done by two different groups of people and become one model with "the same" formalism and "the same" referent in ecology textbooks?

My answer to these difficulties has been to propose a new approach to talking about how scientists use models, and to suggest a nomenclature that works well with this new approach. Instead of asking "what is a model?" I will ask "when is a model?" When does something function as a model, in what context, under what circumstances, for whom, and to what ends? As such, I will refer to modeling situations more often than models, and I will try to describe them in detail rather than going for a definition of its action.

Following Nelson Goodman and Catherine Elgin I consider symbolization as the criteria for modeling, and following Ronald Giere, Bas van Fraassen, and recent work in modeling studies (e.g. Mary Morgan, Tarja Knuuttila) I focus on who is doing the symbolization, with what, for whom, and for what purpose.

The only real units in existence? Biological individuals and the transplantation experiments of Leo Loeb (1869–1959)

Sibylle Obrecht, University of Zurich, Switzerland

My presentation will touch on an issue which has not yet been fully considered in the current debate on biological individuality, namely on the complex intertwining between the practice of transplantation and the conceptualization of immunological individuality. I will focus on the first three decades of the 20th century: In this period, transplantation both as a reductionist therapy concept and as a technical research tool was destabilized by biological problems which had previously not been on the agenda of the doctors and researchers involved. They had anticipated that biological differences between individuals belonging to the same species did not interfere with the outcome of their interventions. When this assumption was questioned in the 1910s, the practice of tissue and organ transplantation lost most of its importance at the bedside and the laboratory bench, in the first place because the biological issues raised by the interventions were not considered to be solved in the near future. In reductionist, laboratory-oriented approaches as they were followed in transplantation research, biological differences on an individual level were largely conceptualized as coincidental and thus not worth pursuing in a systematic manner. They were perceived as "noise" and not as "signal" (Löwy, 2003).

Against this background I will concentrate on the work and life of the German / US-American pathologist Leo Loeb (1869–1959). He is not only known as the younger brother of the eminent physiologist Jacques Loeb, but also as one of the few researchers who adhered to the practice of transplantation in the 1920s and 1930s. Drawing on representations of his experimental systems as well as on his personal notebooks and correspondence, I will focus on the reasons for this permanence. Loeb used the practice of tissue transplantation throughout his career, mainly as a standard tool in tumor research. Until the late 1910s, he understood individual variation as "noise", in accordance with transplantation discourse. However he reconsidered this interpretation, starting to conceptualize biological individuality as a "signal", as a promising epistemic object for his future laboratory research. Throughout the second half of his career he applied the transplantation of tissue to outline a concept of biological individuality which was commensurable with his mechanistic approach to living systems. According to his view, individuals were "(…) the only real units in existence". He assigned them clear-cut and static boundaries – not only because he was convinced to have found their trace in his transplantation experiments, but also because he understood individuality as an important rampart against the prevailing race and eugenics discourses.

In the long term, Leo Loeb did not succeed in stabilizing his interpretation of biological individuality, not least because he had not directly related it to an immunological interpretation. However I will suggest that his understanding of biological individuality as an epistemic object as well as his experimental systems significantly influenced the next generation of fundamental researchers and thus also the nowadays so hotly debated concept of self-non-self discrimination.

Can adaptiveness and rationality part ways?

Samir Okasha, University of Bristol, UK

This paper asks whether adaptive behaviour necessarily corresponds to rational behaviour, and if not why not. "Rational behaviour" is here understood as behaviour that satisfies the norms of traditional rational choice theory, e.g. transitivity of choice, avoidance of dominated strategies, etc. (Thus non-human organisms are perfectly capable of behaving rationally, in the sense of the term used here.) "Adaptive behaviour" is understood in the usual way, as behaviour that has evolved by natural selection because of its fitness-enhancing features in a given environment.

It is natural to think to think that rational behaviour, as understood here, should go hand-in-hand with adaptive behaviour. For if an organism behaves rationally, then it follows (from well-known results in rational choice theory), that they behave as if trying to maximize a utility function. And if an organism behaves adaptively, then it follows (by definition) that they behave as if they are trying to maximize their Darwinian fitness (given the constraints that they face). Therefore, by defining utility as fitness, it seems that it should be possible to make adaptive behaviour coincide exactly with rational behaviour. This coincidence has been explicitly defended by a number of authors, including Daniel

Dennett. Moreover, the adaptiveness-rationality coincidence is implicitly assumed by evolutionists whenever they treat an organism as having a goal (such as survival) towards which its evolved behaviour conduces; and this is of course a common mode of analysis in evolutionary biology.

However, certain theoretical considerations suggest that the adaptive and the rational can sometimes "part ways" (to use Brian Skyrms' expression), that is, that fitness-maximizing behaviour and utility-maximizing behaviour may fail to coincide. Arguments to this effect have been found in the literature of philosophy of science (Sober, Skyrms), behavioural ecology (McNamara and Houston), and economic theory (Güth, Robson and Samuelson). This paper examines six such arguments and reflects on what they teach us. The arguments concern:

1. cooperative behaviour in social dilemmas;
2. strategic behaviour in ultimatum-game scenarios;
3. the "trust game";
4. choice under risk;
5. inter-temporal choice;
6. intransitive choice.

In each case, I briefly explain how the parting of ways arises, and examine possible ways of eliminating it (e.g. by re-defining the fitness measure and/or the utility function).

The overall conclusion is that, despite what has often been thought, and despite the conceptual link between fitness and utility, rational behaviour need not correspond to adaptive behaviour nor vice-versa. When "rational" is defined independently, and invested with a sufficiently precise meaning, it becomes an open theoretical question whether behaving rationally will or will not be adaptive. Thus the "utility = fitness" idea must be treated as a theoretical hypothesis, not a definitional truth. The philosophical consequences of this, and the consequences for evolutionary biological practice, are briefly explored.

The paper draws on material from my recent book, *Agents and Goals in Evolution* (OUP 2018).

What, if anything, do we know about the history of model building in ecology and population biology in the 1960s?

Steven Orzack, Fresh Pond Research Institute, USA

The history of model building in ecology and population biology in the 1960s remains poorly understood. In part this is due to the destruction, disappearance, and/or current unavailability of most or all correspondence to/from several of the individuals who actively worked in the 1960s to make model building an important aspect of these disciplines. These individuals include Crawford Holling, Richard Levins, Robert Macarthur, and Kenneth Watt. I will

1. describe recent discoveries in the scientific literature and in archival material that help shed light on the contributions of several of these individuals and others to ecological model building in the 1960s,
2. describe new material that illuminates the history of the 1966 article by Richard Levins entitled "The Strategy of Model Building in Population Biology",
3. describe new material that provides insight into the views of Robert Macarthur on model building,
4. describe new material concerning agreement and disagreement about model building among Levins, Macarthur, and Richard Lewontin, and
5. outline the important gaps in our understanding of the history of model building in ecology and population biology in the 1960s.

Medical genetics does not need a racial classification

Kamuran Osmanoglu, University of Kansas, USA

Racial categories have been used in biomedical sciences to explain causation across the entire spectrum of diseases. It may seem tempting to consider racial classifications in medical research, as this could help identify specific genes that lead to disease susceptibility for certain racial groups—and which might thus allow us to cure these diseases more efficiently (as well as to make more precise risk estimates at the individual and population levels). However, as I will try to establish in more detail, there are two problems with this sort of view.

First, it turns out that race cannot be seen to provide useful genetic information about variation in drug response, diagnosis, or causes of disease—there just do not seem to be race-specific diseases. Of course, there are genetic diseases that vary among populations. For instance, people of Jewish descent share a risk of Tay-Sachs disease; the frequency of cystic fibrosis varies within Europe; and sickle cell anemia is distributed especially widely in a region spanning sub-Saharan Africa and the Mediterranean. However, these diseases while specific to certain population groups, are not specific to races. Second, research appears to show that race has little value in predicting health outcomes without having information about an individual's socioeconomic conditions, such as level of education, type of diet, and place of residence.

Therefore, in this paper, I will argue that

1. race has very little explanatory value as a surrogate for understanding an individual's genetic background for medical purposes; and
2. scientists should collect data about the individuals' socioeconomic conditions rather than their races for medical purposes.

This paper will (1) provide researchers with a novel solution to report human genomic variation without inappropriately relying on racial categories; and (2) help medical professionals to understand that the inequities between health and disease across populations are rooted in social experience rather than genome.

Ontology and symmetry of evolutionary theories

Jun Otsuka, Kyoto University, Japan

Ontology of a scientific theory specifies what the theory is about. Newtonian physics, for example, is about particles that have a certain mass. What, then, is the basic ontological units that underlie evolutionary dynamics?

Evolutionary theory after the Modern Synthesis has seen two major, quite opposing, ontological views of evolution, namely Mayr's population thinking and Dawkins's genocentrism, which respectively take individual organisms and genes as the fundamental units of evolution and reduce everything above to them.

The first part of the talk compares these two rival theses, with the goal of demonstrating that the difference in ontological assumptions leads to different conceptions as to what count as legitimate causes of evolution and how to conduct evolutionary researches, thereby defining or supporting respective research strategies.

With this remark, the second part analyzes these onto-causal-methodological complexes from the perspective of symmetry and invariance, where the basic idea is that an ontological unit of a theory must be invariant under a group of admissible transformations (cf. Jantzen 2015, Synthese 192(11)). The question then boils down to identifying admissible transformations for each of the ontological frameworks mentioned above. I argue that while Mayr's population thinking admits just one transformation, i.e. identity transformation, the admissible transformations for Dawkins include any allele substitution at other loci. These two sets of transformations represent two extremes in the language of group theory (trivial and commutative/abelian groups), which is the standard formal apparatus to characterize transformations.

The natural next question, then, is whether there is an alternative ontological framework between these two extremes. Commutativity breaks down if there is epistasis, which "multiplies" basic units. The final part of the talk explores the possibility of expressing "modules" in evolutionary developmental biology along this line, i.e., as symmetries under a group of transformations that are neither identity or abelian.

Changing the perspective in the study of social learning: From “transmission of information” to “relational developmental process”

Murillo Pagnotta, University of St Andrews, UK

Humans and non-human animals develop new skills throughout their lifespan. In many cases, what and how individuals learn depend on their historical relations with others around them. Within contemporary behavioural sciences, this class of phenomena is called “social learning” and the behaviours which appear dependent on social learning are commonly referred to as “cultural”. The number of studies focusing on social learning and the number of species examined have increased dramatically in the past few decades. This has improved our understanding of the similarities and differences in learning and social life among species, including humans and other animals.

The suggestion that cognitive processes are fundamentally like computational processes involving mental representations still dominates the field of social learning, notwithstanding talks of the mind as embodied, extended, embedded, and enacted. Within the dominant framework, behaviour is commonly conceived of as being controlled by “information” encoded in the brain, and social learning is commonly conceived of in terms of “transmission of information” between individuals.

However, the term “information” and the transmission analogy require critical examination. Oftentimes, individuals adjust their behaviour relative to what the other is doing and this mutual sensitivity produces a history of nonlinear causal influences not captured by the transmission analogy. On the other hand, the dominant way of thinking reinforces common but problematic oppositions including nature/nurture, biology/culture, body/mind, and organism/environment. These oppositions have been under criticism for decades within the biological, cognitive, and social sciences, but these critical discussions seem to have been largely ignored by the field.

I attempt to offer a positive alternative account of social learning that does not rely on an underspecified notion of information, on the transmission analogy, or on the problematic oppositions cited above. This alternative framework integrates ideas from "developmental systems theory" in biology, "ecological-enactive" approaches in the cognitive sciences, and "relational thinking" in social anthropology. Supported by a relational-processual view of ontogeny, behaviour, and social life, I explore the notions of ecological information, abilities, affordances, and intentions to argue that cases of social learning can be conceived of as relational developmental processes rather than as transmission of information.

Are model organisms like theoretical models?

Veli-Pekka Parkkinen, University of Bergen, Norway

This presentation compares the epistemic roles of theoretical models and model organisms in science. One way to study the role of model organisms in science is to assume that model organisms and theoretical models play a broadly similar epistemic role – that of indirect representation of a target through the study of a surrogate system – and then to focus on the differences in research practice that are necessitated by the ontological status of the model (abstract object vs. concrete, living entity). Recently, Levy and Currie (2015) have challenged this approach. Levy and Currie argue that model organism research and theoretical modelling differ in the strategies researchers use to justify model-to-target inferences, such that the idea of modelling as indirect representation does not similarly apply to both.

I defend a similar conclusion, but argue that the distinction between animal models and theoretical models does not always track a difference in the strategies of justifying model-to-target inferences. Instead, Levy and Currie's point can be argued for by questioning an implicit assumption of the indirect representation view, wherein all modelling practices are taken to be forms of ampliative inference from the features of the model to features of concrete target systems. This assumption is true of animal models (and other concrete models): animal models function as surrogate sources of evidence from which results are transferred to their targets by empirical extrapolation. By contrast, in many paradigmatic cases of theoretical modelling, the interesting conclusions drawn from a model are not ampliative, but fully entailed by the modelling assumptions. Here, the (theoretical) model functions as an extension of the cognitive abilities of the modeler: by encoding assumptions about the structure of the target in a form (e.g. equations, graphs) to which transparent rules of inference can be applied, the model can be used to reach conclusions entailed by those assumptions that could not be reached by unaided cognition.

Observation and experiment in agricultural meteorology

Giuditta Parolini, Technische Universität Berlin, Germany

Observational and experimental work is at the core of scientific research in the life sciences. Both active intervention and collecting observations are crucial in the study of living phenomena, when long-term trends must be identified and explained. How do observational and experimental activities interplay, if they do at all? Do they interfere with one another? Do scientists attach a different value to experimental and observational data? And what about the data collected by lay people?

The paper will address these issues by considering a case study in agricultural meteorology, the discipline that studies how weather factors affect crop growth and livestock performance. In agricultural meteorology both observation and experiment are necessary to understand how weather conditions and agricultural output are correlated, and to single out the most relevant variables for forecasting agricultural output in relation to meteorological conditions.

The paper will examine the agricultural meteorological scheme set up by the British Ministry of Agriculture and Fisheries in the 1920s. The British agricultural and horticultural stations, which were involved in the scheme, collected meteorological, crop and phenological data and participated in experiments involving specific crops, such as wheat. The British scheme remained active for over twenty years and benefited from the contributions of scientific experts – meteorologists, agricultural scientists, statisticians – who planned experiments, directed observations and analysed the data, and lay people, who collected phenological data. It provides, therefore, a relevant example of the long-term observational and experimental initiatives undertaken within the framework of agricultural meteorology, and of the interdisciplinary collaborations that made these activities possible.

In my talk I will consider the field and laboratory experiments and statistical investigations promoted within this scheme, the scientists involved in these researches (in particular, the meteorologist William Napier Shaw and the statisticians Ronald A. Fisher and Joseph O. Irwin), the tools and practices used to collect agricultural and meteorological data, the principles that guided the experimental research, and the contrasting ambitions which supported the scientific work carried out by the British agricultural meteorological scheme. In so doing, I will be able to address the complementarity of observational and experimental work in the life sciences and the different expectations that scientific experts have towards observational and experimental data.

Shallow predictions vs. mechanistic predictions

Viorel Pâslaru, University of Dayton, USA

Prediction based on descriptions of mechanisms plays an important role in scientific practice, yet it has received virtually no attention from philosophers of mechanisms. In this paper, offer a contribution to remedy this lacuna.

The new mechanistic philosophy distanced itself from the DN model regarding the vehicle of explanation, yet it shows signs of commitment to Hempel's symmetry thesis that views explanation and prediction as the same description used relative to a past, or respectively, future event. Machamer, Darden and Craver (2000) endorse this view when they say that appropriately specified schemata can be used to make predictions. This idea can be seen assumed or asserted in various works on mechanisms, such as the consensus characterization of mechanisms by Illari and Williamson (2012), Woodward's counterfactual account of mechanisms, and in Casini et al. (2011) and Gebharter and Kaiser's (2014) modelling of mechanisms.

These assertions and assumptions of the explanation-prediction symmetry have not been followed by a demonstration that the two are indeed symmetrical, or by an examination of the differences between them. In a prima facie breach of tradition, Craver (2006) suggests that the two are different because '[e]xplanations are supposed to do more than merely predict", but he does not explore the difference.

In this paper, I show that there are several types of predictions based on descriptions of mechanisms. First, there is the class of shallow predictions. It includes predictions based on phenomenal models of mechanisms, or on how-possibly models. Predictions based on correlations are also included in this class. Models that underlies shallow predictions are phenomenally adequate for a narrow range of features of characteristics of the phenomenon under scrutiny and, as a result, allows only few predictions of its features. Second, there is the class of mechanistic predictions, which are formulated on the basis of descriptions of mechanisms of various degrees of completeness. Descriptions closer to being ideally complete offer answers to a wider range of questions about how the mechanism would behave under a variety of interventions on it or if it was situated in a variety of conditions. As a result, they offer a wide range of predictions about the features of the phenomenon produced by the mechanism, as well as about the effects of changes in the constituents of the mechanism.

Furthermore, I show that mechanistic predictions also satisfy to a large extent the demands placed upon satisfactory mechanistic explanations. Mechanistic predictions can predict various facets of a multifaceted phenomenon produced by the mechanism, both in normal as well as in precipitating, inhibiting and modulating conditions. A mechanistic prediction requires an accurate account of the components, their interactions and organization.

While the proposed account of mechanistic prediction offers support for the explanation-prediction symmetry thesis, it does not rule out cases of acceptable predictions that are not symmetric with complete descriptions of mechanisms. This is the case of novel predictions based on causal models that are not complete descriptions of mechanisms.

Catching the protean concept of fitness and its metamorphoses

Nicolas Pastor, IHPST, France

The concept of fitness shares a long history with the darwinian theory of evolution. It derives from Spencer's formula (1864) « the survival of the fittest » and we can find its first occurrence in Pearson's Grammar of Science (1900) where it appears in close relation to a constellation of characters, such as health and strength, but mainly fertility. Thus, its main features are present from the start : fitness is explanatory as it tries to encapsulate the reasons why some individuals are fitter than others and it is potentially predictive if we extrapolate from the known reproductive rates to display the future composition of a given population. Duality is at the heart of this concept as evidenced more by its pervasive and telling pairwise presentations : fitness relative (Fisher 1930) and absolute fitness, expected fitness and realized fitness (Burian 1983), vernacular and predictive fitness (Matthen and Ariew 2002), indivual and mean fitness (Orr 2009), organismic fitness and metrological role of fitness (Pence and Ramsey 2013). In this talk, we will focus mainly on two accounts of fitnesss that are intimately connected in the fundamental theorem of natural selection (Fisher 1930) and yet they can be discordant : fitness variation as an increase in the malthusian parameter (e.g. Lotka 1914, Fisher 1941) and fitness variation as an improvement of the constitution of a population or a species (e.g. Kimura 1958, Lande 1975). These accounts diverge not only in that they entail two discordant ways of calculating and normalizing fitness, but they also constrain our way of thinking about natural selection and especially how we separate the action of natural selection from that of the environment. Fitness is always context dependent (Mills and Beatty 1979), but it is also the case for the speed of mass particles measured in a particular frame of reference. This analogy should encourage us to define unequivocally what are the relevant units of selection insofar as they act like frame of reference for the evolutionary biologists. To complete this task, we will assert a profound connection between the nature of the ecological context – emphasizing on the types of competition (e.g. biotic and abiotic, intragroup and intergroup) – and these two accounts of fitness. By developping our previous analogy with physics, we will argue that the important point here is not the reduction of fitness concepts to a unique account but to find means of connecting quantitatively and conceptually the diverse versions of fitness, just like we can find rules to change the frame of reference in mechanics. This would constitute a first step in order to reconcile the many faces of fitness. In the last part of our presentation, we will discuss other avenues that we feel necessary to explore in order to catch the protean concept of fitness and its metamorphoses.

Blind cooperation: The evolution of redundancy via ignorance

Makmiller Pedroso, Towson University, USA

One curious phenomenon of several social groups is that they are "redundant" in the sense that they contain more cooperators than strictly needed to complete certain group tasks, such as foraging. Redundancy is puzzling because redundant groups are particularly susceptible to being invaded by defectors. Yet, redundancy can be found in groups formed by a wide range of organisms, including insects and microbes. Jonathan Birch (2012) has recently argued that coercive behaviors might account for redundancy using insect colonies as a case study. However, microbial examples suggest that redundancy can evolve without coercive behaviors. This paper formulates an explanation for redundancy that does not require targeted punishment of defectors; instead, it proposes that redundancy might be due to ignorance. Specifically, it is suggested that redundancy evolves as a by-product of selection when group members have to decide whether to cooperate or not without knowing the strategy of the other members. Accordingly, possessing information about the strategies of the group members might undermine rather than facilitate cooperation within groups.

Canguilhem's notion of "milieu" and its relevance for environmental epigenetics

Guillaume Pelletier, Université Laval, Canada

The rise of environmental epigenetics, which studies the impact of environmental factors (ex: nutrition or pollution) on epigenetic modification and phenotypic variations, has led to what Jörg Niewöhner has called a "molecularization" of biography and milieu (2011). From this perspective, as socio-material environments are increasingly described via the molecular effect of their active substances on human metabolism, new questions concerning biological reductionism, environmental determinism, and the possibility of shaping human environments have come to the fore. The work of French philosopher Georges Canguilhem (1904–1995) seems especially relevant to shed light on many of these issues. In Knowledge of Life, Canguilhem traces the historical evolution of the concept of "milieu", and introduces the common origin of two often opposed views: milieu understood as a mechanical and quantifiable space and as a qualitative centre of existence. Drawing on the biological work of K. Goldstein and J. von Uexküll, he seeks to recuperate the second view and argues that organisms – and in particular human organisms – actively contribute to the shaping and organisation of their own milieu. This view can be better understood by placing it in Canguilhem's "biological philosophy" and his claim that norms and values are an irreducible and essential aspect of living beings. This talk purports to show how Canguilhem's genealogy of the concept of milieu can help us understand the aforementioned issues, in a context where environments are increasingly characterized in quantifiable terms.

Between science and religion: How biology teachers teach evolution?

Gonzalo Peñaloza, Unidad de Monterrey, Mexico

Science and religion are dissimilar world-views that set up, perhaps, the two most powerful cultural and intellectual forces of contemporary society. They are frameworks within which to think, and social constructions that encompass political and cultural behaviour. Nonetheless, science and religion have a wide variety of meanings and aspects that, therefore, must be taken into account when describing, defining and relating them.

Throughout history, religion has played a key role in the development of science. In every particular case we can find examples. For instance, some Christian traditions have fostered research about the natural world under the assumption that knowing creation was a way of knowing its creator. On the other hand, for instance, some Christian traditions has been challenged by many scientific developments in fields such as the origin of human beings, genetic modification, the contingency of evolution, the mind-body relationship, among others. Either way, science and religion are world-views that, throughout human history, have been related in many ways.

The relationship between religion and science has been widely discussed from many different perspectives. One of the notable findings is that they do not share some basic ontological and epistemological assumptions. Various models have been presented to highlight and clarify how these differences effect their interaction. Although from a theoretical point of view, it is not clear if these interactions occur in everyday practice or how subjects adopt them in specific situations. Therefore, there is gap between practical life and the theoretical relationships between science and religion. For instance, it is possible for a person to agree with a certain kind of relationship in some subjects but not in others. Thus, any model of the relationship between religion and science is an abstraction and a simplification that does not necessarily have a correlate in everyday life.

On the other hand, evolution has been a point of divergence between science and religion, because it offers a view of the development of life that, in some cases, challenges some central religious dogmas. Although importance of evolution to understand the life phenomena, evolution teaching confronts several tensions, especially respect to religious teachers and students beliefs. The way in which such conceptions – of the relationship between science and religion – interact with the teaching of evolution is not clearly or deeply understood.

Paper deals with Colombian biology teacher's ideas about relationship between science and religion, and their evolution teaching practice. Base on a multiple case study and using semi-structured interviews, classroom recordings and group discussion, we used worldview theory and socio-cultural perspectives to analyse how the relationship between science and religion can explain teacher's approaches when teaching about evolution. We propose that understanding of this relation is part of a subject worldview, and this could be incompatible with evolution teaching. Paper contributes to understand implications of nature of religious beliefs to scientific education, in a context of growing cultural diversity.

Theory of mind in nonhuman primates

Alba Leticia Pérez Ruiz, CEFPSVLT, Mexico

A theory of mind is a particular cognitive ability to understand others as intentional agents. It means to attribute mental states to one-self and others. In the last decades, many studies have tried to answer the question "Do nonhuman primates have a theory of mind?"

It is known that nonhuman primates understand about the behavior of conspecifics. They recognize the members of the group and their relationships and use this information to predict behavior of others, but the question is if they have knowledge of the mind of others. That is, to interpret their minds in terms of intentional states such as beliefs and desires.

To analyze the psychological states that non human primates may understand in others is important to take in account different levels as behavior and visual perception, attention and intentions and knowledge and beliefs.

Distinct types of behavior have been considered to be representative of theory of mind in nonhuman primates: self-awareness, knowledge attribution, perspective taking and deception among others. These behaviors are related to social intelligence.

The purpose of this work is to analyze and argue about the different perspectives about theory of mind in nonhuman primates, particularly in apes.

There is evidence that chimpanzees understand the goals, intentions, perception and knowledge of others. But there is no clear evidence about their understanding of false beliefs. Mental life is complex and implicates many psychological states. It means that there are different ways in which animals might understand the psychological states of others. Our nearest primate relatives are a good subject to study this complexity and the evolution of theory of mind.

Bacterial organelles: From metaphor to conceptual change

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Bacterial microcompartments appear as polyhedral bodies in cells and are functionally analogous to eukaryotic organelles. The first type discovered, the carboxysome, was first observed in the 1950s through electron microscopy—although at the time researchers thought the micrographs represented phage-infected bacteria. In the 1970s it was shown that the carbon-fixing protein Rubisco was associated with the observed polyhedral body and so they were dubbed carboxysomes to reflect the enzymatic function. In the last two decades, we have realized that these polyhedral bodies are widespread and functionally diverse; however all share a bounding shell composed of multiple homologous proteins. Subcellular structures with these shells are collectively known as Bacterial Microcompartments (BMCs). In the last decade, the understanding of BMCs has increased significantly, both in terms of key structural and functional features shared by various types of BMCs, as well as identifying new BMCs, serving different biochemical functions in bacteria. In this talk we will show how this research has been influenced by the deployment of multiple metaphors, which structure key observations, guide hypothesis development and experimental design. One in particular provides an overall framework for research: BMC as organelle. Following Mary Hesse's (1966) analysis, the metaphor depends on a positive analogy: both eukaryotic organelles and BMCs sequester certain enzymatic functions from the cytosol, and are surrounded by a selectively permeable boundary. As Hesse would expect, researchers followed the strategy of exploring the neutral analogy (features where it is not known in advance whether or not the target of investigation is like the source concept), to learn more about BMCs. In this case, there is a further area of interest: the negative analogy, or ways in which the source concept (organelle) differs from the target of investigation (BMC). For example, eukaryotic organelles are bound by a lipid membrane while BMCs are bound by a protein shell. We will show how this negative analogy, along with the use of a metaphor source concept from biology itself, generates the possibility of conceptual change. Among biologists, there is currently a lack of consensus about whether BMCs are organelles. While the positive analogy weighs in favor of an expanded organelle concept that includes BMCs, such a metaphor-driven change suggests further conceptual revision as well, especially to the concept of subcellular membranes. The issue is not so much the question of whether a membrane is a necessary feature of an organelle, but whether protein—rather than lipid—can constitute a membrane. These semantic disconnects reflect the research experience of the researchers, producing barriers to change that are gradually displaced on the way to consensus.

Forms and limits of reductionism in stem cell research

Anja Pichl, Bielefeld University, Germany

This paper investigates forms and limits of reductionism in stem cell research. The paper starts with a short discussion of recent accounts of explanatory reduction in life science research (in recourse to Brigandt and Love 2017, Hüttemann and Love 2011, Kaiser 2015) in order

1. to achieve an adequate working definition for the exploration of stem cell research and
2. to substantiate the claim that for investigating reductionism in any field of life science research, both explanatory strategies and concepts of the object of research need to be studied as they are deeply intertwined.

Consequently, the two foci of analysis of forms and limits of reductionism in stem cell research will be on: 1. prevailing explanatory strategies such as Fagan's "joint account of mechanistic explanation" (Fagan 2013) and the question whether their ascribed ability to account for interdependencies of parts and other features makes them non-reductive. The aspired reduction of stemness to molecular properties in some research programs and the study of whole organism processes like biological development and tissue regeneration on the level of individual cells have to be taken into account as well. 2. Stem cell concepts, especially Fagans "abstract stem cell model" and the evidential constraints analysed by her (Fagan 2013) will be the second focal point. This comprises also a short recapitulation of the classic stem cell debate on whether stem cells are states or entities (Zipori 2004, Leychkiz et al. 2009, Laplane 2016) in light of the question whether, and if so, in what regard both options might be characterized as being reductive. Finally, calls for moving beyond reductionism within the stem cell and philosophy of life sciences communities (Robert et al. 2006, Lander 2009, Flake 2004) will be discussed with regard to their claims concerning limits of reductionism in stem cell research and proposals how to handle or overcome them. In conclusion, the potential contribution of the analysis of reductionism in stem cell research for the broader debate on explanatory reductionism in biology and vice versa will be reflected upon. A hypothesis for the outlook will be that the focus on biomedical application predominant in stem cell research – clinical goals have been argued to be constitutive for the field (Fagan 2013) – reinforces certain forms of reductionism as they promise to provide an otherwise hardly imaginable level of control.

“A ripple rather than a revolution”? – John Maynard Smith on Stephen J. Gould’s challenges to neo-Darwinism

Helen Piel, University of Leeds and The British Library, UK

The Darwinian theory of evolution has had to contend with questions about its validity and explanatory power since the publication of *The Origin of Species* by Charles Darwin in 1859. But new developments and discoveries usually confirm the ideas first suggested 160 years ago. In the first half of the twentieth century, neo-Darwinism combined Darwinian natural selection with Mendelian genetics, a development headed most prominently by J. B. S. Haldane, R. A. Fisher and Sewall Wright. The neo-Darwinian perspective of evolution has come to dominate evolutionary biology since, but that has not saved it from being challenged. These challenges to Darwinism in general and neo-Darwinism in particular can be external, such as, perhaps most famously, from religion in general and creationism in particular, or internal, coming from within science.

Starting in the early 1970s, the theory of punctuated equilibria (Eldredge and Gould 1972) and the so-called Spandrels paper (Gould and Lewontin 1979) questioned neo-Darwinian orthodoxy specifically. The American palaeontologist Stephen Jay Gould (1941–2002) was the leading voice among a number of palaeobiologists, palaeontologists moving into evolutionary biology. John Maynard Smith (1920–2004), called the senior statesman of British evolutionary biology, was trained by J. B. S. Haldane and continued in a strongly neo-Darwinian tradition throughout his fifty year-long career. He reacted to and responded to Gould’s and Gould-inspired challenges to neo-Darwinism.

This paper will use archival material (in particular correspondence) and published primary sources (both strictly scientific and aimed at wider audiences) to explore Maynard Smith’s interaction with and his views of Gould and his theories. It will explore in how far his views changed – he famously welcomed palaeontology to the "High Table" of evolutionary biology in 1984 – and whether Gould had any influence on Maynard Smith's own research, such as with regards to how Maynard Smith dealt with questions of development and constraints.

Life stories, life structures, and systems of equations

Jesse Powell, Florida State University, USA

This paper reexamines a conclusion drawn in Ruse (1971) and (1975) about the usefulness of narrative explanation in biology. The model of "narrative explanation" given by T. A. Goudge is described as a kind of explanation distinct from those of the covering law kind meant to render intelligible to human minds unique events in evolutionary history that cannot be subsumed in a more general kind. Narrative explanation thus set up is inevitably knocked down, and it is suggested that the uniqueness of events is not a bar to the use of laws in their explanations. Ruse claims that the epistemic goal of good scientific explanations is to identify a set of sufficient conditions for an event and that it is necessary to appeal to scientific laws in order to secure such a set, something that Goudge's model of explanation cannot do. There has been enough work done on both the nature of narratives and explanations that this debate deserves an update. By making use of recent work done on structural equation models, and recent narrative research done in philosophy, sociolinguistics and computer science, I argue that narrative explanations can both give historical explanations of unique phenomena and appeal to laws. Under my redescription of narrative explanation in biology, the utility of the paradigmatic case of narrative explanation picked out by Goudge is explicated, narrative explanations are made mathematically formalizable, and they are brought into contact with fruitful areas of research in contemporary mathematics and science. What emerges from this is a view of narrative explanation that is compatible with a structuralist philosophy of science.

The fruitful shrub: The necessity of female pubic hair in early modern Europe

Karlyn Prisco, Florida State University, USA

Historians are paying an increasing amount of attention to the differences between men and women in the Early Modern Period. The most apparent differences between the sexes are the physical, corporeal characteristics of their bodies and the means by which they are regarded. One feature of the human body that becomes an area of interest is body hair. Specifically in women, pubic hair became the main area of focus. Its presence served as a marker of being womanly in Early Modern Europe, and the various qualities of the hair were taken into account. Like a beard on the face of a man, the female pubic hair garnered attention and could mark the status of one's womanhood, as well as their overall quality as a woman. Because pubic hair was not uniform from body to body, the color, thickness, and overall qualities of the hair itself could be regarded in different manners. Women's pubic hair marked sexual maturity, implied fertility, and served as a means of concealing the mystery of the female genitals. Thus, pubic hair could become a defining factor in one's femininity because it represented the readiness for intercourse and reproduction. In addition to pubic hair connecting with sexuality, the means by which hair hid and concealed the genitals represented female modesty and the necessity for a woman to hide her sexuality. By exploring both texts in the medical genre and erotica of the Early Modern Period, an argument can be made not only for the aesthetic nature of female pubic hair, but also for the reliance upon and necessity of its presence. Therefore, female pubic hair was not simply an extension of the body, but it was symbolic for female sexuality, beauty, and modesty.

The human nature of E. O. Wilson: A critical response from dialectical neo-Lamarckism

Alí Yólotl Sánchez Ramírez, UNAM, Mexico

The study of the so-called Human Nature is the theme on E. O. Wilson's books *On Human Nature* (1979), *Genes, Mind, and Culture* (1981), *Promethean Fire* (1983) and *The Social Conquest of Earth* (2012). For Wilson, from a biological basis Human Nature has deployed culture as an element subsumed by our biology. Wilson's proposal has an explicit commitment to neo-Darwinism which considers survival and reproduction as the goal of life, and takes the fitness as the primordial element guiding the evolutionary process. This is a position of adaptationist nature that directs our way of conceiving human evolution in a very particular way.

In the present work I develop a critical position to Wilson's idea of human nature based on the works of Eva Jablonka, Marion Lamb, Richard Levins and Richard Lewontin, authors who have made extensive criticisms of reductionist, essentialist and gene-centered methods extensively developed by Wilson. I focus on the characteristics of his proposal in *The Social Conquest of Earth* in relation to human nature, which are seen in a new context of discussion by incorporating elements of epigenetics and distancing from positions as that of Richard Dawkins's *The Selfish Gene.*

From neo-Lamarckism I intend to constitute an argument against the proposal of human nature as a series of pancultural, static and invariable elements that are the product of biological evolution by natural selection. I use the concept of dialectical neo-Lamarckism as an original proposal that integrates the evolutionary vision of neo-Lamarckism and the ontology and epistemology of dialectical biology. This dialectical neo-Lamarckism can help explain the evolution of species better than neo-Darwinism, at least in relation to the active role of the organism in evolution, and that related to hereditary multidimensionality. With respect to the first, Lewontin (1985, 2000) defends this active role but without referring to the neo-lamarckist conception which is incorporated in this current paper.

With the incorporation of hereditary multidimensionality the discussion about human nature is enriched allowing the coupling of the symbolic and behavioral dimensions to be seen in an autonomous way independent from genetics. However, the interaction between these different dimensions of the inheritance is not denied, for I propose that there is a dialectical interpenetration between hereditary dimensions.

Therefore, the explanation does not remain in a separation of the parts but these are mutually determined. I believe that with an active subject in conjunction with the interpenetration between the different levels of inheritance a novel conception of human nature can be generated. Dialectical biology, thus, can be consolidated as the philosophy that most strongly opposes reductionism, essentialism and mechanism in favor of a processual and historical vision with an anti-dichotomic spirit that seeks to transcend dualistic and mutually exclusive oppositions such as nature / culture and innate / learned.

Phylogenetic competition: Defining the selective environment

Grant Ramsey, University of Leuven, Belgium
Hugh Desmond, University of Leuven, Belgium

Even though natural selection is often said to be simply a difference in fitness between individuals, this is strictly speaking inaccurate: the individuals must also share a selective environment (Brandon 1990). However, under what conditions do two individuals share a selective environment? Previous approaches have held that two individuals share a selective environment only if they are part of the same population (e.g., Millstein 2014), or if they share the same ecological conditions (Abrams 2014). However, both accounts assume that the individuals are conspecifics, and not only is it often difficult to determine whether individuals are conspecific, it is also unclear why individuals need to be in the same species in order to share a selective environment.

Our proposal is that two organisms share a selective environment if and only if they are in phylogenetic competition. Informally, phylogenetic competition occurs when two organisms compete to have their descendants represented in descendant populations. This occurs when branches from one descendant lineage displace branches from another descendant lineage. More precisely we define it as follows:

Phylogenetic competition between individuals X1 and X2 at time t occurs if and only if, their respective descendant spaces intersect (at some later time t′), and a higher fitness of X1 causes a lower expected occupation of the intersection space at t′ by descendants of X2, and vice versa.

In this paper we argue that this is what it means for two individuals to share a common selective environment. While this account abstracts from the phylogenetic relatedness of the individuals, as well as the similarity of the factors in their respective physical environments, we will also argue how more traditional measures of populational or phylogenetic relatedness, or similarity in ecological conditions can be useful empirical indicators for phylogenetic competition.

After introducing basic concepts of the environment and giving a critical overview of the two main approaches to delimiting the selective environment, we outline in detail what phylogenetic competition is and how it can be formalized. Finally, we discuss wider implications of phylogenetic competition.

Chromatin landscape, nuclear architecture, and genetic circuits: Integrating multiple perspectives of cell organization and behaviour

Andrew S. Reynolds, Cape Breton University, Canada
Brigitte Nerlich, University of Nottingham, UK

Early discussion of a genetic code inscribed in DNA suggested a close resemblance between the sequence of nucleotide triplets ("codons") arranged along the length of the DNA molecule and codes written in computer or natural languages. Human codes are typically arranged as two-dimensional scripts (read either horizontally from left to right as in English, horizontally right to left as in Arabic, and from top of page to bottom, or vertically top to bottom as in traditional Chinese and Japanese). But because the nucleotides making up the "genetic code" of DNA are normally packaged in densely coiled chromatin structures wound around histone proteins, the cell machinery responsible for "reading" (copying, transcribing, and translating) the genetic "information" does not always have direct access to the relevant nucleotide segments. Accessibility to coding segments and tagging of nucleotide sequences with epigenetic markers (e.g. methylation) have significant effects on which genes are active and when. Determining therefore how chromatin is organized, located, and modified within the environment of the cell nucleus has become a vital research topic. Since the 1980s researchers have increasingly spoken of chromatin landscape and nuclear architecture to highlight these three-dimensional topographical features of the nuclear genome. This talk will:

1. provide a preliminary history of the employment of these phrases in the literature from the 1980s to the present, detailing how an apparently implicit consensus formed around them, and
2. discuss the significance of these metaphors for scientific understanding of chromatin biology and genetics, and
3. consider how these quite distinct perspectives (the linear genetic code and the topological chromatin landscape-nuclear architecture frameworks) are integrated into a coherent account of cell structure and function.

Does every cell have a sex? Four approaches

Sarah Richardson, Harvard University, USA

"Every Cell Has a Sex" has over the past decade become the slogan of elite women's health research committed to the study of sex differences in biology. Fulfilling the cause of women's health, these advocates claim, is not limited to research on women's reproductive organs and diseases – it extends to every organ, and every cell. The notion that sex is a ubiquitous element not localized to gross regions of sexual dimorphism is a historically new and unique understanding of sex, one prompted by the arrival of a molecular understanding of the basis of sex determination provided by genetics and endocrinology. Scientists who assert that "every cell has a sex" have usually implied an essentialist, binary conception of sex as an omnipresent trait at every level of biological organization. According to this essentialist account of sex, maleness and femaleness have an "essence" represented by a set of biochemical factors causally linked to sex. Any biological object of analysis, whether a whole organism or a single cell, that contains those factors is male or female. But there is a different way of understanding the omnipresentist claim – one that is non-essentialist, non-binary, and contextualist. All cells may indeed have a "sex," by virtue of the networked ecology of the body, but "sex" need not be binary. Here, "sex" is a pragmatic construct derived from the context-specific and processual history of a biological component. On this view, every cell does have a sex, but just what "sex" is becomes suddenly very plural. Sex is not just "male" or "female." This talk frames the broader stakes of claims that every level and component of biological organization has a sex, briefly outlines four stances with respect to the question of whether every cell has a sex, and argues for the merits of one of these approaches, which I call "sex contextualism."

Building the case for comparative neurobiology

Jason Scott Robert, Arizona State University, USA

Philosopher Jason Robert argued a decade ago that "Only a rigorously comparative biology and biomedicine, operating at multiple levels of organization and analysis, and grounded in both ecological context and in evolutionary considerations about relatedness and divergence, can begin to shed adequate light on life itself, and on our peculiarly human form of it" (Robert 2008, 432–433). His argument considered the diverse historical and philosophical literature on model organisms, revealing that beyond the scientific rationale for research with particular organisms, there are both historically and epistemically contingent reasons at play. Model organisms are laboratory-friendly and experimentally tractable: they yield to analysis. But model organisms are also highly derived research tools, built to make experiments work. It is becoming increasingly common to query the usefulness of particular model organisms in particular experimental contexts, but few would dispute the general usefulness of model organisms in biology. Even so, it is clear that model organisms have canalized entire research domains, with both good and bad consequences. The benefits of canalization include easy replication (or disconfirmation) of key findings and beneficial economies of scale facilitating significant growth of research opportunities. But because research is heavily dependent on particular models, the models are so entrenched that it can be difficult to work with other organisms instead.

In this paper, I attempt to build another aspect of the case for a "rigorously comparative biology and biomedicine" that is narrower than Robert's case in targeting neurobiology (rather than biology writ large).

Rodents are overrepresented in neuroscience research (Manger et al. 2008), and yet substantial variation in cortical organization (for instance) amongst rodents (for instance) is almost never acknowledged (Krubitzer et al. 2011). Krubitzer and colleagues have emphasized that rodents represent 2277 species within 34 families and five suborders. As they conclude, "the rodent model" of anything is a fiction, and likely a dangerous one in the neurosciences. But the call for a comparative approach in the neurosciences has largely fallen on indifferent ears. Why might this be the case? Krubitzer et al. (2011) propose that given available techniques and economic and ethical considerations, only mice or rats are viable experimental subjects. This is so even when the experimental question of interest makes no sense to ask of mice or rats.

A comparative neurobiology requires research with a broader swathe of animals within rodentia but also beyond this order. Of course, neuroscientists work as well with worms, fishes, flies, birds, cats, monkeys, too. Some work even with humans. Even so, comparative approaches remain exceptional rather than du jour, taking a distant second to animal-model based approaches where the experimental animal is supposed to stand-in for other animals (including humans). And even where comparative approaches are evident, too often the comparisons are superficial and designed to show similarity rather than more frank and designed to reveal what's really going on.

These are strong critical claims. In the paper, I justify them, articulate a rationale, and lay out desiderata for a genuinely comparative neurobiology.

Balancing both the philosophical and practical problems that arise from advanced pediatric medical technologies

Sarah M. Roe, Southern Connecticut State University, USA

For years, philosophers have been focused on the ethical concerns rapidly advancing medical technologies pose. Indeed, advancing technologies have long plagued philosophers who question our readiness for and deployment of new advancements. On the other hand, medical professionals who utilize advanced technologies have been more concerned with the transition of patient care from pediatric to adult practitioners. Transitioning health care from pediatric settings to adult health care settings when an adolescent with a chronic illness is progressing into young adulthood comes with many additional challenges.

By utilizing case studies regarding new robotic cardiac assist devices, this paper brings both the practical and the philosophical together. I argue for the use of a new ethical notion referred to as the disadvantaged standard. The disadvantaged standard states that when determining whether or not to move forward with a new and partially unknown medical advancement, both the medical and philosophical communities would best be served to focus on the societal position and medical plight of the least advantaged patient. By focusing on concerns regarding uncertainty and allowing for real-world input, ethicists, medical practitioners and medical researchers can learn something about rapidly advancing medical technologies and the attitude we should have toward them.

Carving brains: Are modules and mechanisms the same?

Aida Roige, University of Maryland, USA

Cognitive neuroscientists and psychologists often use the terms "modules" and "mechanisms" to refer to distinctive parts of our mental equipment that are responsible for certain mental or behavioral outcomes. In so doing, they treat them as, if not exchangeable, at least picking up extensionally the same thing. Two largely unconnected philosophical literatures have provided accounts of mechanisms (e.g. MDC 2000, Glennan 2018) and modules (e.g. Fodor 1983, Carruthers 2006) that are purportedly continuous with the scientific literature. Very roughly, mechanisms are entities and activities organized such that they are productive of a phenomenon. (Mental) modules are functionally dissociable systems, that typically exhibit a series of properties --domain specificity, dedicated neural implementation, (wide scope) information encapsulation, and so forth. Obviously, the accounts differ in the terminology and properties used to characterize their targets. But if we look past these initial divergences, and interpret the accounts realistically, would we carve the same mind/brain units? In this paper, I argue that we would not: the two accounts carry too different metaphysical commitments. Modules and mechanisms have different conditions of persistence (a mechanism is only so when is productive; modules remain even when they do not act), different conditions of individuation (modules are functionally individuated; while such thing is insufficient for mechanists such as Craver (2006)), and they fit in divergent hierarchies. I will end by exploring some interesting implications of this exercise, for both the cognitive and the life sciences.

Scientific conceptions of race and their impact on pictorial representations of Homo sapiens in Mexico

Erica Torrens Rojas, National University of Mexico, Mexico

For some years, the field of STS has focused on the need to write transnational connected narratives, based on a reciprocal treatment of global and local contexts that describe the dynamics of scientific practices to explain the role of transnational exchange networks and the circulation of scientific knowledge, people, artifacts and practices.

This talk explores on the one hand, the genesis of scientific conceptions of race in Mexico and their accompanying impact on the racialization of bodies in eighteenth century and on the representation of *Homo sapiens* in nineteenth century. Both, the racialization of bodies and the reconstruction of human ancestry produced several visual representations which circulated in both a local and a global framework. This circulation of novel representational modes strongly influenced debates on race and national identity formation, especially during the nineteenth century when the term "mestizo" powerfully appeared in the political discourse as a symbol of identity in the formation of the Mexican Nation State and as a homogenizing center of national identity.

On the other hand, I will talk about some representational practices related to the reconstruction of human ancestry in Mexican popular visual culture. Its aim is to show first, the lasting impact and power that both early and biased western visualizations of human ancestry have had in contemporary scientific education in Mexico; and second, the influence of non-Darwinian thinking of early twentieth century in Mexican representation of evolutionary theory. This in turn seeks to enlighten the global dynamics that shaped and reshaped local narratives.

Understanding cancer progression and its control: An analysis of immune contribution to metastasis causality

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Thomas Pradeu, ImmunoConcEpT laboratory, France
Nicolas Larmonier, ImmunoConcEpT laboratory, France

Ongoing progress in cancer research is improving our comprehension of the spatial and temporal complexity of tumour progression, indeed characterised by the pleiotropic involvement of the tissue environment at different stages of the illness (Plutynski 2018). While supplementing our thorough appreciation of the cell-intrinsic properties of transformation, these advances still face serious difficulties, such as those linked to tumour recurrence and systemic spread.

Metastasis is currently the leading cause of cancer mortality, correlating with disease severity and resistance to conventional therapy.

Beyond its accepted description as a multistep process resulting in the development of secondary tumours at distant sites, certain observations remain partly unexplained and conceptually challenging. For instance the report of organ specificity for secondary growth, describing the apparent tropism of primary tumour cells for particular metastatic tissues, complicates the understood causality of cancer cell dissemination and subsequent implantation.

The “seed and soil” theory of metastasis, initially coined by Paget (1889), stipulates that such patterns can be explained by favourable interactions between circulating tumour cells (the “seed”) and specific microenvironments encountered during their migration (the “soil”). While maintaining an illustrative role, its exact premises and implications may benefit from a revisited analysis in the light of recent clinical and experimental observations. In particular, the evidence of distant “pre-metastatic niche” preparation, involving both tumour-derived factors and pre-existing host components hijacked by the malignant context, could defy the explicative power of the analogy.

Triggered by these considerations is the objective to decipher the implication of the immune system in cancer progression, given the delicate balance between its protective and pro-tumoral activities. Indeed pre-metastatic processes are frequently associated with immune cell recruitment, inflammatory signalling and structural remodelling, with a direct contribution of these features to tumour development and secondary seeding. As a matter of fact, those populations of suppressive and pro-invasive immune cells may actively encourage “seed” persistence and enable distant metastasis by establishing a hospitable and/or attractive environment in future “soils”.

Hence the pressing question of determining the exact role of host immunity in metastasis causality: to what extent, and how, do the immune actors of cancer progression contribute to the preparation and specificity of secondary sites? Underlying the conceptual framework of the “seed and soil” hypothesis, would this reflection help better understand the relative contributions of pro-metastatic factors, and how may it affect practical and therapeutic considerations?

In my research, I propose to address this issue from both a conceptual and an experimental point of view, through a case study of metastatic tropism in a mouse model of breast cancer known to specifically disseminate to the lungs. The characteristics of a subset of pro-tumoral myeloid cells are monitored through the course of tumour evolution and in differential environments, in an attempt to better understand their early accumulation at pre-metastatic sites.

Organizational etiological teleology: A selected-effect approach to biological self-regulation

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Javier Gonzalez de Prado, UNED, Spain

According to selected-effects theories (for instance, Neander 1991; Griffiths 1993), selection is a source of teleology: purposes are effects preserved or promoted through a selective process. Selected-effects theories are favored by several authors who want to claim that Darwinian evolution introduces teleology in the biological world.

For the purposes of this presentation, we take selected-effects theories for granted, although we will provide some motivation for them by appeal to certain response-dependent meta-normative views about value, more specifically, views according to which value is generated by evaluative responses. While most selected-effects theories concentrate on natural selection (for an exception, see Garson 2017), our goal is to argue that there are other types of selective processes in biology and that such processes should be seen as giving rise to distinctive types of evaluative standards. More specifically, we suggest that biological self-regulation (the mechanisms by which organisms monitor and regulate their own behavior and that has been the object of careful study in the biological sciences) can be seen as a selective process.

In general, biological organisms include dedicated regulatory mechanisms that compensate for possible perturbations and keep the state of the system within certain ranges (Bich et al 2015). The pressures that such self-regulatory submechanisms exercise on the states of the organism are a form of discriminatory reinforcement, as a result of which certain tendencies are inhibited while others are promoted. It is reasonable, therefore, to characterize biological self-regulation as a selective process.

So, those who accept selected-effects theories of teleology should also grant that biological self-regulation is a source of teleology – at least to the same extent that selected-effects theories are taken to vindicate the view that biological teleology is generated by natural selection. The purposes and evaluative standards introduced by self-regulation are independent of -and arguably sometimes conflicting with- the standards associated with natural selection. Given that self-regulation is ubiquitous in the biological world, it is to be expected that the evaluative standards generated by it will play a prominent role in our explanations of biological phenomena. We think that the approach sketched in this paper offers an appealing integrative picture of the evaluative dimension of biology.

The making of the "Butterfly Kingdom": Hans Sauter (1871–1943) and the institutionalization of Japanese entomology in the early twentieth century

Ayako Sakurai, Senshu University, Japan

Hans Sauter (1871–1943), a German entomologist, field naturalist and collector, is now an obscure figure except in the history of early-twentieth-century lepidopterology. His name is now chiefly remembered for the extensive collection of Taiwanese butterflies owned by a number of European museums, such as the Senckenberg German Entomological Institute in Müncheberg. Sauter collected the specimens in a short period from 1905 to 1914 in Taiwan, which had been under Japanese rule since 1895. The butterflies, partly sold and partly donated to European museums, scholars, collectors and dealers, revealed the island's unusually rich entomological fauna, particularly the high concentration of lepidoptera species, consequently establishing the island's renown as the "Butterfly Kingdom."

The purpose of this paper is to reassess Sauter's collecting activities, setting them against

1. the island's socioeconomic and political developments in the early twentieth century and
2. the institutionalization of entomology both in Taiwan and in Japan.

It will investigate how and why Sauter was so successful in obtaining the specimens, even in the interior regions which had been inaccessible to most European travelers. The paper will argue that Sauter's success was chiefly due to his unique position allowing him access not only to European, but also to Japanese and Chinese intellectual resources and personal networks. It will also show how Sauter's findings opened up Taiwan to a number of ambitious scholars and collectors, making it into a focal point for entomological investigations. Amongst them were Japanese entomologists, such as Shonen Matsumura (1872–1960), Tokuichi Shiraki (1882–1970) and Teiso Esaki (1899–1957), who capitalized on the colonial government's attempt to turn the nascent colony into an agriculturally productive territory, and eventually succeeded in institutionalizing entomology within the Japanese academia.

Against naturalistic theories of disease

Roger Sansom, Texas A & M University, USA

Naturalistic theories of disease propose that biological facts determine that something is a disease. I criticize the motivation for naturalistic accounts of disease in favor of a normative view.

Biostatistical theories claim that diseases are impairments of normal function, understood relative to the normal survival and reproduction of a natural class. They struggle to classify conditions that are common in certain populations as disease: such as arthritis in the aged. In defending his biostatisical account, Boorse (1975) contends that such objections incorrectly equate the question: is it a disease? with the question: should it be treated? He thinks some diseases should not be treated and some conditions that are not diseased should. I bring to bear the idea that classifying a condition such as homosexuality as a disease does harm, even if you also think that it should not be treated.

Selected effect theories claim that diseases are failures to produce the selected effect that is responsible for the trait being selected in its evolutionary history. They struggle to not classify homosexuality as a disease, given the strong prima facie case that homosexuals have lower fitness than heterosexuals. In defending selected effect theories of disease, Griffiths and Matthewson (2018) adopt Carnap's (1950) view of concepts that demands that we not merely analyze, but should explicate the nature of disease. Correct explication should provide concepts that are fruitful in discovering natural laws. I argue that while "elected effect dysfunction" may be a fruitful concept in this sense, "disease" is not. A cohesive account of disease will not be naturalistic, but normative—probably a well-being account. The term "disease" is fundamentally therapeutic—one for the medical profession to use in doing good, rather than the scientific profession to use for cutting nature at its joints.

Causality and explanation in phylogenetic systematics

Marcelo Domingos de Santis, University of São Paulo, Brazil

Phylogenetic Systematics, a discipline of evolutionary biology, seeks to propose classifications (reflecting the evolutionary process) using an objective method for the elaboration of a hypothesis on the evolutionary history of the groups (ancestral-descendant relation). This is made through a differentiated analysis of the characteristics of a set of species including an ancestral (hypothetical) and all its descendant. The derived characters, apomorphy, being the evidence for common ancestry. For this, it is used, for example, the criterion of optimality of parsimony, as a result of the congruence of the characters (differentiating homoplasies of homologies).

The Systematic methodology is still highly influenced by Popper's ideas; therefore, these scientists "transformed" his ideas so that it could become testable and falsifiable accordingly. As Popper used the same deductive-nomological model of explanation by Hempel, which in his late phase disregarded any mention of causal elements, the systematists also disregarded it, and instead adhered to a hypothetical-deductive approach to cladistic analysis. One of the corollaries of this approach is the assertion of these scientists that

i. the explanatory power of a genealogy is measured by the degree to which it can avoid postulating homoplasies;
ii. the potential to maximize explanatory power is a consequence of minimizing ad hoc hypotheses of homoplay;
iii. homoplasies do not explain anything.

Thus, these scientists argue that any causal theory is unnecessary to explain the existence of actual groups or characters in the world. However, the usual deductivist interpretations of Popper (and Hempel) simply do not apply to phylogenetic inference. Hypotheses of homoplasy do not qualify as ad hoc hypotheses in the Popperian sense, since homoplasies are a result of evolution, being part of their background knowledge; thus, it can not be characterized as ad hoc hypotheses.

The "explanatory" account discussed in this essay will be different and new, being more appropriate to systematics than the nomological-deductive or falsifiability model. In this way, it will be argued that Salmon's "trace transmission" model can be used, having the resources for an understanding and application in the systematics. Adaptations will be made because the Salmon model was developed primarily for physics and processes, and considering the inclusion of methodologies of historical science, especially those formulated by Cleland. With the advent of this causal explanation thesis, scientists of this research program will be able to better understand/explain phenomena in scientific practice, resulting in a new empirical understanding. For instance, a homoplasy (a similarity that is not the result of ancestry) that one seek for an explanation of "why" it is the case, can reveal aspects of the process of evolution that resulted in diversification of organisms throughout history.

Cooperation and competition in big biology: The Human Genome Project (1990–2003)

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The Human Genome Project (ca. 1990–2003) was shaped in its very core by the co-existence of cooperation and competition. On the one hand, cooperation was necessary to reach the project's ambitious goals – on the other hand, there was substantial scientific and economic competition between the participating laboratories and nations. Existing historical and STS scholarship of the HGP has mostly examined either cooperation or competition, while competition has almost exclusively been discussed in view of the notorious rivalry between the publicly funded HGP and Craig Venter's private enterprise Celera Genomics.

This paper argues that within the HGP, cooperation and competition, as two modes of interaction, always coexisted; and that this coexistence was crucial for how the epistemic goals, practices, and norms of the participating research groups were defined. This claim will be fleshed out at the example of the HGP's pilot project: the sequencing of the roundworm's genome *(Caenorhabditis elegans)* by the UK research group headed by Sir John E. Sulston. I will argue that both cooperation and competition were considered legitimate strategies within this group, as long as they enabled the efficient and successful completion of the project. Analysing this case also sheds some light on the investigation of British genomics and science policy under the Thatcher government.

Biological functions of episodic memory

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Recent debate concerning the biological function of episodic memory faces a host of methodological problems that have not been adequately recognized. As a result, the debate has been prevented from making progress. The core obstacle, I argue, is a failure to adequately distinguish between the different questions that a functional theory of episodic memory could be intended to answer. Using Mayr's distinction between proximate/ultimate causality and Tinbergen's four questions as a framework, I distinguish the "ultimate" evolutionary question, from the "proximate" questions of survival value and causality. Although participants in the debate—philosophers, evolutionary psychologists, cognitive psychologists, and neuroscientists—purport to answer the evolutionary question, many of them, including several leading theorists, fail to provide any historical evidence, relying instead on evidence that is appropriate to answer the proximate causal question of how episodic memory works now. Progress can be made in the debate through a clearer recognition of the different theoretical frameworks for functional thinking, their different explanatory roles, and their different evidential bases. At the least, greater clarity with respect to these different conceptions of function can help debunk the assumption that episodic memory must have only one function.

Moreover, while it is interesting to develop hypotheses as to the genetic evolution of episodic memory, it is unclear whether crucial historical evidence is available. Although episodic memory is thought to be a uniquely human trait, available historical evidence at best seems to indicate operation of factual (semantic) memory, which many non-human species also exhibit. I propose that future research may make greater progress by addressing the question of episodic memory's "biological function" in Tinbergen's sense of survival value. This reorientation might allow for better-evidenced functional explanations of episodic memory, that do not require certain problematic historical assumptions.

We need to talk about Richard Owen: A contextual analysis of Owen's period in the Royal College of Surgeons (1827–1856)

Daniela Sclavo, University College of London, UK

The historiography of Richard Owen has focused on certain aspects of his character; from his difficult personality, rivalries, keenness on power, political allegiances to his museum enterprise and his standing-point on transmutation. However, an integral understanding of him still lacks in the literature. More specifically, of his years in the Royal College of Surgeons (1827–1856) – a period that remains in the shadow of Darwinism. In this work, Moral Economy is used as an analytical tool to illustrate the non-monetary resource management that Owen undertook in a specific social context in order to achieve his ambitions of institutionalising the field of Comparative Anatomy and being Britain's most eminent naturalist. Through the study of Owen's growth and expenditure of socio-political, intellectual, and emotional capital, a more humane and neutral portrayal of this much controversial figure is exposed. As a little-explored avenue, Owen's emotional capital is further developed. Indeed, Owen's historiography has focused particularly on his professional correspondence with other men. However, Owen's personal letters mainly to his wife, mother and sisters – his female world –, reveal a distinctive emotional expression than the one he exposes with his male colleagues, patrons and even friends. Thus, Owen's emotional capital touches on how his intimate relationship with his family represented an important pillar in the development of his career. Owen's emotional capital provided a space where he privately curated his other capitals and thus, that it had a direct impact on his professional development. This gives us access to Owen's more intimate thought and integrates a little-explored arena of Owen's life to his historic understanding. Together with an analysis of his socio-political and intellectual capitals, this paper brings about a synthetic and more complex approach where single behaviours are not over-interpreted, but normalised. Therefore, this work challenges the long-held vision of an overwhelmingly defensive and power-centred naturalist.

"Diversity" conflicts with "heterogeneity"

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Aaron M. Ellison, Harvard University, USA

We argue that a conceptual tension exists between "diversity" and "heterogeneity", and that glossing over their differences has non-trivial epistemic costs for biodiversity models. We briefly review how these terms are used in science; articulate a linguistic intuition regarding common parlance and test it with the Corpus of Contemporary American English (COCA). The results reveal conflicting rather than interchangeable meanings: "heterogeneity" implies a collective entity that integrates different entities, whereas a nonspecific “diversity” implies divergence, not integration. When modeling species whose distribution is especially sensitive to human presence, e.g. endangered, patchily distributed or flagship species, the impact of local knowledge and heritage is plausibly a relevant causal factor for the survival of these species. Yet it is typically not considered “knowledge” but rather “anecdotes” by ecologists and conservation biologists. We argue that if different local groups hold different descriptions of their locality; and if these different descriptions readily suggest different practices for sampling and modeling species distribution in that locality, and if some model descriptions become invisible if academics do not seek local descriptions as part of their collective description, then using a heterogeneous or diverse view of “difference” will plausibly lead to different model descriptions, causal explanations and policy recommendations for conserving that species distribution: some epistemically better than others. To conclude, given the complex eco-social dynamics of ecological systems and their biodiversity conservation models, seeking “heterogeneous” rather than “diverse” sources of information can improve biodiversity models.

The hidden mechanisms of life. The transformation of the image of biology through the contributions of Emil du Bois-Reymond

Carlos Hugo Sierra, Open and Distance National University & University of Basque Country, Spain

The main purpose of this paper is to present the main ideas about the epistemological consequences of the work of the German physician and physiologist Emil du Bois-Reymond (1818–1896), related to electrophysiology, bioelectricity and animal electricity, insofar as it contributes to develop a new explanation of living things. On the one hand and in opposition to the metaphysical teleological perspective of the organism, conceived as an entity endowed with a “vital force”, he is a firm defender of the mechanistic biology which collects and applies to the organic matter the laws of physics and chemistry. From this point of view, this new understanding of life, which takes place in the context of the intellectual atmosphere of the Anatomisches Museum in Berlin, implies the need to move away from a qualitative (or romantic) perspective of research to adopt, with mathematical precision, modern methods of experimentation (which leads him to participate in the first generation of reductionists in the field of life sciences along with Hermann von Helmholtz, Rudolf Virchow, and Ernst Haeckel).

In addition to this and beyond the aspects related to physiology, it is necessary to indicate that Bois-Reymond popularized the theory of Darwin, whom he met in 1866, among the students of Germany in the second half of the 19th century, proposing the unification of the thermodynamic principle of conservation of energy and the natural selection. In relation to natural selection, it is important to underlie that Bois-Reymond contemplates a reinterpretation of the principle of transformation of the living (which has been the germ of continuous disputes in biological thought since 1800, when the French botanist Frédéric Gérard introduced this hypothesis in his work Théorie de l'evolution des formes organiques, 1841–1849), which acts as a blind mechanism, questioning the idea of planned design coming from natural theology. All these perspectives found in the general work of Emil du Bois-Reymond *(Über die Grenzen des Naturerkennens,* 1871, *Reden,* 1886/1887, *Untersuchungen über tierische Elektrizität,* 1848 & 1884) will undoubtedly have important consequences in the historical formation of modern biology.

The Darwinian analogy between artificial and natural selection and its social dimension

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Debora Minikoski, State of Paraná, Brazil

Analogical reasonings are widely employed by scientists to explain the unknown from background knowledge. Charles Darwin, aiming to explain better natural selection, proposed an analogy between human artificial selection and natural selection; thus, the unknown – natural selection – should be, accordingly to the pattern of analogical reasoning, better understood from the artificial selection. The situation in which Darwin stood could then be described as follows:

a. there is a need to establish analogical reasoning;
b. there is a practice available that, if developed, can constitute knowledge;
c. Darwin offers this development (through his domestication of pigeons and his theoretical study on domestication);
d. finally, he sets forth the basis of the analogy with which the *Origin of Species* begins.

Our presentation does not question such a description. However, on the basis of James Secord's article "Darwin and the Breeders: A Social History" (1986), we understand that step (c) above would need to be presented in a different way, because Darwin not only had to develop and to improve the knowledge of breeders, but it also had to scientifically legitimize such knowledge, since the practice of breeders – although well established as such – was not scientifically established at the time. Darwin, therefore, in addition to developing and perfecting the knowledge already produced by the breeders, simultaneously needed to legitimize the practice of human artificial selection, for only in this way, argues Secord, could the analogy be evaluated from a scientific point of view. So, his procedure involved both scientific procedures (his domestication experiments of pigeons) and social justificatory procedures (showing a fairly detailed presentation of the community of breeders: how successful they were, how they are a subject matter in a specific literature and finally how their practice was inaccessible to the layman). Assuming Secord's interpretation, Darwin's proposition of analogy then needs to be understood both from an epistemological point of view (through the sequence (a-d) above), and from a pragmatic point of view. However, it has become common, in traditional approaches to the philosophy of science, to link such procedure to relativistic conceptions, conceptions that would obscure the achievements of scientists, making them mere reflections of social demands. In this traditional interpretation, either the scientist produces theoretical and experimental work, or he is a negotiator who neglects nature in function of his social interests. The aim fo this presentation is to show, instead, that this combination (science and social) reinforces the scientism of Darwin's procedures. In this presentation, after briefly introduce the notion of analogy and after to introduce the Secord's argument we offer, from chapter 1 of *Origin of Species,* a complement to such argument. Then, we argue, based on a sociological conception of scientific knowledge, which the social setting of Darwinian analogy proposed by Secord further strengthens Darwin's scientific procedures, because we understand that by distinguishing the two moments of Darwin's strategy for his defense of the analogy, this shows the scientist even more, say, scientific.

Configuration of hypotheses with trace observations forms paleobiology's epistemic challenge

John Alexander Sime, University of Pennsylvania, USA

The uncertain relationship between trace observations, such as fossil remains, and past biological patterns and processes due to loss of information ("incompleteness") is frequently regarded by scientists and philosophers as the primary epistemic challenge of historical science. I argue the more significant challenge for paleobiologists, with the objective of formulating correct explanations about the past, is to understand how differential ascertainment of trace evidence, owing to processes of amalgamation or attrition, shifts support among the set of plausible biological explanations. Loss of information on its own is not sufficient to judge the adequacy of the fossil record; neontologists frequently encounter similar gaps in observation due to universal constraints on sampling. Two questions in paleobiology from the last forty years illustrate this epistemic problem. First, is the pattern of morphological trait evolution in the fossil record more often punctuated or gradual? Second, is the evolution of anti-/predatory traits in marine animals driven by the process of coevolution or escalation? There is commonly more than one plausible hypothesis for any past biological phenomenon, each hypothesis specifying a different set of relevant traces.

Consequently, it is difficult to articulate an appropriate standard for choosing the best explanation among the available options. The discovery of traces that might decide between competing hypotheses (i.e. “smoking guns”) often just temporarily shifts the evidential landscape rather than finally settling the question. Paleobiologists can explore the appropriate standards of theory choice by using background theory to formulate auxiliary hypotheses about the landscape of trace evidence and its long-term stability.

Dreaming of a universal biology

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There is a long discussion about what is specifically shifting in postgenomic life sciences such as systems biology or synthetic biology. To explain the shift, a number of plausible candidates exist. For instance, one could point at a shift away from reductionism towards a form of holism. Alternatively, one could claim that different explanation strategies are followed, situated on the system instead of the molecular level. A third possibility is to stress the prominence of synthesis and simulation in the life sciences, leading to a picture where biology no longer observes, but constructs nature.

Although these accounts are insightful, they also have their problems. This paper will therefore propose to identify an additional shift that might shed a new light on these developments. Postgenomic life sciences are characterized by a different way in which they articulate biological nature. One could see a shift away from “terrestrial biology”, with all its particularities and contingencies, towards what the actors in the field call a “universal biology”: life as it could be rather than how it exists on Earth. We are thus confronted not only with a range of novel answers, but also radically different ways of posing questions. In that sense, it could be argued that the object of study has shifted away from existing biological beings towards what one could call biological possibilia.

This paper will illustrate this by the historical case study of the research in the origins of life. By contrasting early approaches, associated with authors such as Stanley Miller or J. D. Bernal, with contemporary authors such as Pier Luigi Luisi or Stephen Mann, this shift towards universal biology can be fleshed out.

Finally, and perhaps most importantly, this novel understanding can shed light on the increasing affinities of fundamental research and applications in postgenomic life sciences. In other words, it can offer an explanation of why engineering and design have become so central to these disciplines and how it became possible that the distinction between basic research and applications have been reconfigured in its contemporary form in these life sciences.

Dealing with genetic uncertainty: Risks, errors, and value

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For genetic screening to be effective, we need to know the relationship between different genetic variants and the incidence of disease. However, many genetic diseases, like BRCA1/2 forms of breast and ovarian cancer, have Variants of Uncertain Significance (VUSs). VUSs are variants whose association with disease is uncertain due to either conflicting evidence or a lack of evidence for such an association. VUSs make precise categorization of genetic variants and, thereby, prediction and prevention of disease more difficult: How confident must we be that a variant is associated with a disease before we call it pathogenic?

To help ameliorate these difficulties, several different schemes have been proposed to categorize variants. These schemes set different thresholds, but they all attempt to provide clinically useful information while simultaneous minimizing the chance of errors. Yet, these schemes fail to accommodate patients' various attitudes towards risk. Rational agents can be risk seeking, risk averse, or risk neutral. Patients with different risk profiles will approach these errors and their cost differently. By failing to accommodate the differences in risk profiles, these schemes impose certain risks on patients, risks that patients may be unwilling to bear. Therefore, we need a better way of developing these schemes, one that recognizes and accommodates the different risk profiles that patients have. The purpose of this paper is to provide a way to do exactly that. It shows how we can develop different schemes to help minimize the risk of error while accommodating patients' differing risk profiles.

Research ethical requirements and standards in the archiving of eyewitness documents

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The concept of oral history is relevant to historians, practitioners and recipients who can also move beyond traditional historical science. This approach allows one to turn to history "from below" or "from within". Research ethics issues are important in all phases of the research process – from planning to implementation to publication – and must be reflected time and time again. This is especially true of qualitative research, as it establishes a personal relationship between the researchers and the researchers (see Miethe 2010).

Research ethical principles in dealing with time-based sources were formulated in subject-specific codes of ethics; some of these principles raise specific questions. Although the high value of self-reflexivity offers fundamentally good conditions for ethically reflected research action, but it is unclear if and how this potential will be used. I would like to pick three out of the multitude of challenges that arise from the peculiarity of the archive material: the anonymization, the development and the physical decay.

So far, research-ethical questions are rarely explicitly discussed in the German-language qualitative methodology debate. There is a need for discussion, partly because certain principles are not feasible and new technologies in the age of the Internet raise new questions.

The aim of all efforts is to create the greatest possible transparency for all involved, to continuously develop the existing concepts on ethics and data protection and in this sense to contribute to the quality of qualitative research.

Science “Fiction”: The future according to the founders of modern biology

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J. B. S. Haldane’s 1924 essay “Daedalus: Or, Science and the Future” uses a fictional narrator living 100 years in the future. The essay describes different advancements in science and technology with particular attention to how developments in biology change our political and social institutions. Daedalus, along with Haldane’s other works like *The Last Judgement* are an intellectual exercise to explore the future of biology as well as potential expectations and fears that society might have. Haldane’s imaginary future is a place where science and ideology can interact without the constraints of reality and rigor. Haldane was not alone in his combined interest of biology and science fiction. Notably, we have Julian Huxley’s *The Tissue-Culture King,* Hermann Muller’s *Life Forms on Other Worlds,* J. D. Bernal *The World, the Flesh & the Devil; an Enquiry into the Future of the Three Enemies of the Rational Soul,* and George Simpson’s *The Dechronization of Sam Magruder.* The current manuscript will analyze these six works and compare their ideas of possible futures.

The analyses of these texts will be based on the key concepts of Space of Experience and Horizon of Expectation developed by historian Reinhart Koselleck in his work *Futures Past On the Semantics of Historical Time* and on the more recent ideas of Daniel Rosenberg and Susan Friend in their book *Histories of the Future.* The historiography of the future is an interesting toolkit allowing us to rethink the forms and functions that historical writing about the future has taken. As Rosenberg and Friend put it: “Exploring links between panic and nostalgia, waiting and utopia, technology and messianism, prophecy and trauma, it brings together critical meditations on the social, cultural, and intellectual forces that create narratives and practices of the future.”

The purpose of this manuscript is to obtain insight into the role of speculation, prognostication and prophesies of impending doom in the speculative fiction of the founders of modern biology. Looking at these six works, we can gain insight into the research programs of their authors as well as their ideology and speculations about the future of biology. I put forth that the suggested analysis and methodology will allow us to explore the prophesized new frontiers of biology and to boldly go into an imagined future and it risks by these influential biologists. Bernal's and Haldane's warnings of scientific advancements without an appropriate ideological, socialism. Huxley's vision of the unlimited potential that biology can bring. Muller's and Simpson's use of imagination to better understand their field. By considering these scientists' views of the future as outlined in their texts we can better understand their motivation to engage in popular and public science. The future in this text appears as a place where ideology and imagination were set loose. The analysis of this will give us a new perspective into some of the major actors within the history of biology in the twentieth century.

Cui bono? Experiments on animals in the light of the activity of ethical committees in Poland

Agata Strządała, Wroclaw Medical University, Poland

Both applicants as well as members of committees who evaluate research proposals face challenges not only of scientific nature but also legal, philosophical and ethical ones. The texts examines the most common problems, conflicts of values, and misunderstandings connected with biomedical research on animals.

Some issues derive from the juxtaposition of goals underlying the research and the wellbeing of wild animals. According to Directive 2010/66/EU article 9 tests on wild animals are banned with exception that scientific goal can not be achieved otherwise. Nonetheless, many of research purposes, for example research on parasites and infections of wild animals, as well as the research on genetics of wildlife, may contribute towards more effective protection of wild species.

In case of laboratory animals the conflict arises between value of basic research and the 3Rs rules. From a short-term perspective, reduction of pain and suffering of animals may seem more important than basic research. However, from a long-term perspective, sacrifice of laboratory animals may potentially leads to development or improvement of drugs, treatments for both humans and animals or better ways to protect species. The conflict which arises is then between the welfare of individual animals and of the species or of natural life in general.

A common problem regarding tests on farm animals is the blurry difference between the research procedure and regular veterinary procedure or typical diagnostic test (USG, blood drawing). Hence it might be unclear whether a given procedure constitutes an experiment.

Another issue concerns the retrospective assessment of research projects (Directive 2010/66/EU article 39). Negative results of tests are less likely to be published in scientific journals since their attractiveness in academic milieu is lesser comparing to positive results. This trend may lead to a situation where similar projects are repeated and animals are sacrificed in vain.

The European Convention for the Protection of Vertebrate Animals used for Experimental and other Scientific Purposes of the Council of Europe proclaimed the 3Rs rules: Replacement (animals are no longer used for the test), Reduction (fewer animals are used to achieve the defined aim of the test), Refinement (a test that causes less distress to the animals used is carried out), and as the additional the 4th rule Removal (end of unnecessary use of animals in research) as the core of ethical research on animals. While frequently the 3Rs are treated as a mere formality.

Another issue is the adoption of subject-test animals: the lack of coherent system of adoption, limited publicity on the topic and lack of assurances whether the adopted animals will be treated properly and provided with a regular veterinary checks.

In summary, ethical committees attempt to balance conflicting values (animal welfare vs. liberty of research). Special focus should be given to the practical challenge of implementing such values in a manner which curtails unnecessary bureaucracy while truly fulfilling the ideas behind the 3Rs rule.

What is “narrative possibility”?

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Many have argued that a distinctive feature of evolutionary explanations is that they come in the form of narratives (or some of them do, anyway) (Beatty 2017; Hull 195; Mayr 1983; Richards 1992). Different authors have given different characterizations of what, precisely, a narrative explanation is, but certain common features do seem to stand out in many cases. One such feature is the notion of contingency or possibility as an important feature of narratives (Beatty 2017; Gallie 1964; Gould 1989). The basic idea is that for any narrative, the way things in fact turned out is a contingent affair—some alternative set of outcomes (or histories) seems entirely possible, and narrative explanations ought to help us understand this.

Up to now, authors have attempted to make sense of narrative possibility in one of two ways. They have taken either (what I will call) the ontic approach or the epistemic approach. On an ontic approach, narrative explanations of evolutionary phenomena explain their targets by situating them within a matrix of real historical possibilities. This is to say that the ontic theorist takes it to be the case that there really are alternative possible histories for the same explanatory targets, and this is what narrative explanations are helping us to understand (Beatty 2017). Alternatively, the epistemic approach is driven primarily by considerations of evidential underdetermination (Swaim forthcoming). On this approach the reason for including “possibilities” in our account is just that many histories seem compatible with the evidence out of which we construct narratives, not because alternative histories are real.

Here I’d like to develop another approach that I call compatibilist. The compatibilist view seeks to accommodate the intuition that narrative possibility should be somehow more robust than the conceptually thin epistemic version, but also avoid committing to substantive claims about alternative histories and their ontological status. To fill out the compatibilist conception of narrative possibility, I’ll look to Darwin’s discussion of his “Principle of Divergence” (Darwin 1859, 112–115). Darwin’s fundamental claim is that organisms with greater ability to diversify (or specialize, etc.) will thereby be better able "seize upon the places in the polity of nature" (p. 112). Framing narrative possibility in terms of the Principle of Divergence allows us to cast our thinking about possibility in terms of capacities and affordances (see Pence and Swaim 2018). Narrative possibility, then, can be understood in terms of a relation between features of organisms (capacities) and features of their ecological context (affordances). Understood in this way, I argue that we can retain some conception of narrative possibility that respects a robust notion of "possibility" without appealing to alternate histories. Narrative possibilities need only facts about the actual history of evolution, not ones that might have obtained, but failed to.

An immunological view of organismal identity

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The capacity of organisms to persist across time despite changes in their material constitution has puzzled philosophers since Ancient Greece. As an upshot of these early debates, today's advocates of animalism (which is a stance in a personal identity debate) define identity as a continuity of life processes or as a persistence of characteristic inner structures. In addition, philosophers of biology developed various versions of continuism (some of them appealing to genidentity), processualism or conventionalism about diachronic identity. Following previous work on immune-based identity by authors like Tauber and Pradeu an attempt is made here to suggest that immunology offers a unique perspective on diachronic identity of organisms. In fact, being preoccupied with the problem of how the immune system manages to tolerate the same organism over time, this field promises to find observer-independent correlates of organismal persistence. Burnet, who was one of the first to address this problem explicitly, proposed that sustained immune tolerance of the organism is safeguarded by absence of reactivity of the immune system to an antigenic essence or a self of this organism. However, existence of such molecular essences has been put into question and evidence has been provided to show that the repertoire of molecules that the immune system tolerates or attacks constantly changes due to the activity of specialized cell populations like regulatory T cells and other cells. Despite this plasticity, the immune system appears to react against certain transformations in cell characteristics. These transformations, signalizing changes towards neoplastic phenotype, are markers of cell identity loss or a change for the immune system. In fact, lacking sole molecular markers of identity, somatic cells bear characteristic gene expression signatures, which define what they are, histologically, and which when altered may indicate tumorigenic change. The role of the immune system as a guardian of diachronic identity is further highlighted by the studies of complete metamorphosis, which is a process of a radical but sometimes gradual and progressive reconstitution of the body plan and inner physiology of the organism. This process, being considered by philosophers like Van Inwagen as a genuine case of identity change in animals, demands complete reorganization of the immune system, whose components unless annihilated and later rebuilt in the adult interfere with this form of transition. Overall, the immune system studies suggest that the simple view of organismal identity as a continuous process of life may be equally wrong as the one that postulates existence of immutable structures. In fact, from the point of view of the immune system function, only certain types of continuous changes in the organism ensure organismal identity and those that do not, tend to be eliminated at the cellular level by the system.

Staging of the natural sciences, or the making of young naturalists (Spain, 1960–1970s)

Carlos Tabernero, Universidad Autónoma de Barcelona, Spain

This paper will explore a cross-platform storytelling strategy concerning natural history content, produced in 1960–1970s Spain by Felix Rodríguez de la Fuente (1928–1980), a pioneering and highly influential naturalist, activist and natural history author and broadcaster in that context, the turbulent last years of Franco's regime in Spain. It will focus on how he blended the portrayal of local wildlife with the depiction of scientific and media practices, and how he played these elements together, in a very successful feedback loop across different platforms and formats, to actively engage audiences in naturalist-like (scientific, activist, media) practices in their everyday-life endeavors.

In this regard, it will pay particular attention to a collection of comics published at the turn of those decades, and which he used to further stress the nature conservation messages of his wider editorial, and TV outputs. These comics featured fiction stories where he, as a naturalist and broadcaster, was the main character, or at least one of the heroes. In addition, they were coupled with explicitly educational content, also produced as cartoons, as well as a Q&A section about animals, from pets to wildlife, plainly aimed at actively engaging young readers in developing work concerning the study and conservation of nature and the relations of human communities with it.

Upon these sources, this paper will analyze how these narratives about nature and the natural sciences were articulated alongside other widely popular comics, and also in relation to all the other media products Rodríguez de la Fuente was generating at the time. In addition, it will also examine how these narratives, altogether, worked as key constituents of intensely negotiated strategies of modernization, in this case with the natural sciences as both focal point and main source of knowledge.

Situated in the last years of Franco's regime in Spain, a noticeably changing context regarding politics, science and media, this study will allow to discuss historically the relationship between natural history media, educational content, and the development of different storytelling strategies, and will thus contribute to the understanding of key features of contemporary, media-driven science communication.

Anti-essentialist arguments and the "essentialism myth" in the context of pre-Darwinian classification and stereotyping human categories

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In my presentation I will compare the implications of the following claims:

1. psychological essentialism underlies the formation of stereotypes about human groups;
2. pre-Darwinian taxonomists held essentialist beliefs about biological species.

Pre-Darwinian essentialism is claimed to be inconsistent with evolutionary biology as empirically wrong, leading to typological thinking and clashing with gradual evolution. Essentialist stereotypes about human groups are claimed to lead to false assumptions about the homogeneity of these groups, overgeneralizations, supposed sharpness of the group boundaries and fixity of mutual power relations between these groups. I will analyse how anti-essentialist claims are approached in these two contexts by asking whether we are not dealing with something like the "essentialism myth" in both cases.

The suggestion concerning the "essentialism myth" is well known in the context of philosophy of biology. Staffan Müller-Wille and Mary Winsor have claimed that this myth has been adopted by many philosophers and that in reality, there was no such thing as pre-Darwinian essentialism. As Müller-Wille and Winsor claim, the pre-Darwinian taxonomies were formed on the basis of typical exemplars, not the essential properties of taxa. I want to claim that there is also the "essentialism myth" when it comes to the discussions about the possible cognitive models underlying the formation of stereotypes about human groups, although my reasons for making this claim are somewhat different from the arguments given by Winsor and Müller-Wille.

Firstly, it has to be noted that most anti-essentialist arguments are targeted against essentialism concerning shared-nature particular material properties; Müller-Wille's and Winsor's suggestions about the "essentialism myth" also concern this sort of essentialism. Nowadays, shared-nature particular material essentialism is quite easily demonstrated to be wrong both in the context of evolutionary biology and in the case of human groups, and when pointed out that there simply are no particular material properties that species or group members share, people are quite fine with giving up this sort of essentialism. At the same time, these people might still be holding the allegedly essentialist stereotypes about human categories. Hence my claims about the "essentialism myth" concern psychological essentialism as a cognitive model that is assumed to involve a much wider variety of reasoning patterns than the ones related to shared-nature particular material essences.

Secondly, as I will demonstrate, several reasoning patterns that are associated with psychological essentialism can actually be held even without positing essences to categories – calling these reasoning patterns all "essentialist" and contrasting them with prototype theory (the main competitor of the cognitive model of psychological essentialism) is not justified. Most empirical studies aiming to demonstrate the applicability of the cognitive model of psychological essentialism are methodologically inadequate; they merely demonstrate the presence of some phenomena that are taken as indications of essentialist representations of categories (holding theoretical assumptions about these categories, believing that these categories are "inductively rich" etc.). Inferring the presence of essentialism from the presence of these indications without sufficient warranty is one of the biggest myth-invokers about psychological essentialism and its alleged applications in different contexts.

The modern evolutionary synthesis: A radical reformulation of a structurally flawed paradigm

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More than seventy years after the Modern Evolutionary Synthesis was recognized as a Kuhnian paradigm or widely accepted theoretical framework that inspires and guides research in a particular scientific field, it seems to sink ever deeper in a quack mire of disputes and challenges. Some scholars question the utility of evolutionary master-theories, other scholars and biologists have developed radically new theories or updated, expanded or extended versions of the

Modern Synthesis. We agree with the reformists that the Modern Synthesis should be reformed. Substantive reformulations of paradigms are, as a matter of fact, an integral part of Thomas Kuhn's theory of science. Our proposed reformulation is conservative, though, in that it aims at changing the structure of the Modern Synthesis, rather than its greatly extended and substantially modified content, let alone its properly understood neo-Darwinian core. It thus wants to rectify a number of previously identified structural flaws in this theory that, in their turn, are the product of a few fundamental and specific characteristics of the field of evolutionary biology and that largely explain why it is so contentious: the Modern Evolutionary Synthesis is the product of a lopsided constriction and an unfinished synthesis, it did not bridge the gap between organism-focused and gene-focused biologists and it is also remarkably fuzzy. However, the new, Lakatosian structure that we propose for a modern version of Darwin's theory of evolution is at the same time also radically innovative as it entails a very different and more indirect kind of synthesis of evolutionary data and concepts than that which resulted in the Modern Synthesis.

"Servants of science": The lives of Rose, Farce and Tarzan, chimpanzees at the Pasteur Institute of Kindia (Guinea) during the French colonial period

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This paper tells the story of three chimpanzees (Rose, Farce and Tarzan) captured in Western Africa and subjected to biomedical and/or psychological experiments at the Pasteur Institutes in Paris and Kindia, French Guinea. My approach follows up recent studies that promote a more "animal-centered history" of medicine and the life sciences, treating animals as subjects and agents with their own histories (Cassidy, Mason Debtinger, Schoefert, Woods, Montgomery, Munz, Baratay, Herzfeld, Burkhardt). This paper shows how the life trajectories of these chimps crossed the boundaries between bacteriology and psychology, the laboratory and the field, the Metropolis and the colonies in the context of the French colonial Empire. Also, drawing on studies which call for a representation of animals that helps rethink human cultures, this paper aims to show how these three chimps were servants of Pasteurian science and thereby, "a fundamental part of the apparatus of colonial science" (Haraway, Leblan). By confronting scientific discourses with situated practices, it challenges the idea of a one-sided imposition of imperialist knowledge over native knowledge and shows how Western scientists mobilized a wide variety of sources of knowledge, including the knowledge of indigenous peoples for the capture of the animals, their maintenance in captivity, and their transfer to the Metropolis. While much has been written on the history of colonial science, often exploring the role of Western scientists in the colonies, this paper aims at making the apes more visible as actors in colonial science. On the one hand, I will show how apes played a role in the development of both bacteriology and animal psychology, as well as providing a powerful resource for colonial scientists in the establishment and presentation of their work and public persona. On the other hand, it will reconstitute the role native people played in the production of scientific knowledge about apes, and explore the different ways in which they understood and represented these animals.

Preliminary considerations for an epistemology of organoids

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Organoids can be defined as masses of cell or tissues obtained in vitro foreshadowing organs. Even if organoid research already has a long history, they have only recently been considered as a major breakthrough method in experimental biology in reference publications. Aside from being a method, they also seem to fall within the definition of "bio-objects", that is one of the many novel hybrid and/or intermediary entities produced by biotechnologies and synthetic biology. Nonetheless, because they are often described as miniaturized or simplified versions of organs, they also are in continuity with them, and therefore they mainly question our understanding of these natural functional units in the classic hierachical, integrated view of organisms. They provide new experimental tools to reevaluate the tension existing between the machine conception of organisms, here the anatomical description of metazoans in terms of finite and delimitated organs as parts, and their holistic description as non separable entities, both in developmental and functional perspectives, within the physiological organism. In addition, organoids' incompletness suggest more gradual defintions of what a functional unit means in metazoans. Organoids also question our understanding of autonomy and integrity in biological systems: they are from animal origin but they are not produced by the animals they derive from, and this creates new possibilities for transferts, exchanges, hybridizations, with possible consequences in evolutionary dynamics. Unexpectedly, this resonates with some properties of natural "rogue units" of the animal phylum: transmissible tumors. As a result, new expressions of what animal life is may come to actual existence, raising major societal and ethical issues, along with the fundamental epistemic ones.

Susanne K. Langer's process philosophy of biology

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In her later work, Susanne K. Langer (1895–1985) developed a process-oriented philosophy of biology that anticipates some of the themes of recent and current process philosophy of biology. Langer had studied with Alfred North Whitehead when she was a student at Radcliffe in the 1920s. During the 1940s and 1950s, she became known primarily for her work in the philosophy of art. She was also a leading exponent, in North America, of Ernst Cassirer's neo-Kantian philosophy of symbolic forms. But Whitehead's work exerted a lasting influence on her thinking. In the late 1950s and early 1960s, after taking her first permanent academic position at what was then Connecticut College for Women, Langer turned to philosophy of biology and psychology to help support her theory of art as the symbolic representation of human emotional life. In this later phase of her career, she returned in some ways to her Whiteheadian roots. In her last major philosophical work, *Mind: An Essay on Human Feeling* (1967; 1972), Langer argues that the most fundamental components of living systems are not things but acts, or temporally drawn out living processes. She offers a detailed analysis of biological acts (or we might say, processes) in terms of their temporal structure. She treats acts as ontologically basic, arguing that "an organism is built up by its own acts" (1967, p. 371). I argue that Langer's process-oriented approach presages more recent developments in process philosophy of biology. She was writing at a time when philosophy of biology was beginning to take shape as a subfield of philosophy of science, and her work got little attention from philosophers of science at the time. But it is worth revisiting today, in part because her theoretical interest in the arts, especially music, distinguishes her version of process philosophy from other approaches. Impressed by what she called "the kinship between organic and artistic forms," she offers an account of biological acts that, I suggest, treats the basic components of living systems as having dynamic temporal structure reminiscent of musical phrases (1967, p. 199). In this paper, I briefly sketch Langer's theory of biological acts, place it in the context of the rest of her philosophical work, and point to some insights that are relevant to contemporary work on biological processes.

Interactionism through and interlevel relational perspective

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In this proposal we address several epistemological issues regarding the nature-nurture dichotomy and the alleged conceptual limitations of the presumed (and canonical) interactive solution.

As Evelyn F. Keller has pointed recently, one of the most remarkable features of the nature-nurture debate is how often it drives us into two apparently contradictory results: on the one, the repeated announcement that the debate has been solved, through the general acquiescence that the answer requires simultaneously both aspects, and, on the other, the persistence of the discussion (Keller 2010, 1).

Since Oyama (1985) (continued in other works as, v.g., Oyama 2001 or several of those collected in Oyama 2000) and even earlier with Lewontin (v.g., 1982, 1983 or also 2000 and Lewontin et al. 1984) –just to mention two basic references without presuming the relevance of others– it is being noticed the difficulty to get beyond the mere statements, more or less rhetoric, asserting, for instance, that development is the result of the "interaction" between genes and environment. There is a certain "interactionist consensus" that almost no one defies but which often is poorly understood.

Other authors have also confronted this paradoxical situation of the (dis)solution of a problem that comes back continually and have been forced to make an effort of clarification in order to show that, though they propose to overcome the debate along these lines, the mere appeal to interaction, just a plain "both are necessary", without any further development or precision, doesn't only leave the problem unresolved but it even contributes to its perpetuation (Umerez 2009). Let's call it the problem of the putative solution.

A common ground of the research programs carried out by those authors sharing the views represented here by Oyama (developmental systems theory, DST) and Lewontin (dialectical biology) is a criticism of our alleged current understanding of genetic causation. Some critics of this reaction defend, though, that the issue is not as much a problem with our way to understand genetic causation in an standard interactionist sense but with some particular interpretations, simplifications or renderings of that view that may lead us to unwanted consequences as, for instance, genetic determinism, separation and independence of causes, disassociation of internal and external factors, etc. (Kitcher 2001, Schaffner 2016).

The general problem then is yet how to improve that putative solution in order to arrive at a substantive formulation of interactionism, that is, one that goes beyond the truism of appealing to the necessity of taking into account diverse factors when trying to identify and understand biological phenomena. Additionally, we think it will be illuminating to link that analysis with the effort to understand biological organization from an explicitly hierarchical perspective in terms of levels of organization and the action of material constraints that instantiate their relation.

Thus, we will start by drawing a map of those interactionist but critical approaches more directly relevant to biological issues and try to define their scope and limitations. This review is complemented with Pattee’s complementary approach to biological organization, which is not couched in the usual terms of interactionism but can be fruitfully interpreted in this sense (Umerez 2001). Finally, we will inscribe this account within an organizational perspective, explicitly hierarchical, developed around the concept of constraint (Umerez 1994, Umerez 2016) as the tool to instantiate materially the connections assumed.

Art’s take on CRISPR: An argument for artistic complications to the metaphors of genome editing

Nora S. Vaage, Maastricht University, Netherlands

An increasing number of artists are currently engaging with biology hands-on, creating living artworks using the tools of biotechnology. The proposed paper will address how such artworks complicate the metaphors commonly used in advanced biotechnology, focusing on the metaphors of CRISPR: a technology of power and control, used to “cut-and-paste” using “genetic scissors” or even “scalpels”. Although a versatile tool applied in a number of biological sciences, CRISPR seems increasingly to be associated with the engineering vision of synthetic biology. CRISPR’s advertised property of precise, quick and easy genetic engineering fits well with synthetic biology’s aim of creating standardized “biological machines”.

My approach is inspired by Lakoff and Johnson’s (1980) argument that such language mechanisms shape how we understand life itself, as well as ensuing scholars’ work on metaphors within the life sciences, from Evelyn Fox Keller to Brigitte Nerlich. I emphasize the continuity from mechanistic perceptions of life stretching back to the ancient Greeks, but in this paper focus primarily on the present-day, starting from the existing "master metaphors" of "life as machines", "the book of life", and "ecological systems". I argue that, with the public discourse on CRISPR as a technology of precision and control, artworks provide an interesting counter-image to the dominant metaphors. Paying attention to how artists collaborate with philosophers, biologists and engineers (amongst others), I discuss the artworks *The Origin of Species* (Marta de Menezes and María Antonia González Valerio), *Make Do and Mend* (Anna Dumitriu) and Common Flowers/WhiteOut (BCL). I stress how these artworks in different ways challenge assumptions about CRISPR's role in biology and in society, through emphasizing cultural contexts and the wondrous strangeness and messiness of life.

Is a broken clock only right twice a day? Strategies in the calibration and synchronization of biological clocks

Katherine Valde, Boston University, USA
Alisa Bokulich, Boston University, USA

Biologists rely on indirect measures, such as the accumulations of genetic mutations (the "molecular clock") or fossil locations in layers of sediment (the "biostratigraphic clock"), to infer temporal information about events in the deep past. Unfortunately, each of these biological clocks can only provide partial and imperfect information. For example, the fossil record is known to be incomplete and biased in various respects; and while statistically speaking neutral mutations can accumulate in DNA sequences at predictable rates, understanding neutral mutations or how often they occur in actual populations poses substantial difficulty. A key question then is how do we calibrate and synchronize such clocks when we know that neither of them is fully accurate?

This talk investigates the methodological challenges and strategies involved in calibrating and synchronizing the molecular and biostratigraphic clocks. Comparisons of these clocks reveal that each has different strengths and weaknesses. Dates obtained using biostratigraphic clocks tend to be biased towards being too young, and dates obtained using molecular clocks tend to be biased towards being too old. Notably, they fail to agree for some key events such as dating the divergences of avian birds, vascular plants, and placental mammals. Understanding the reasons for these disagreements allows scientists to identify assumptions that go into the reading of these molecular and biostratigraphic clocks. This process of trying to synchronize and recalibrate allows scientists to generate improved systems of time telling. Although these "broken" clocks might never have read time correctly, through iterative recalibration scientists are able to improve these biological clocks, even in the absence of a reliable independent standard.

Is it ever morally permissible to select for deafness in one's child?

Jacqueline Mae Wallis, University of Bristol, UK

As reproductive genetic technologies advance, families have more options to choose what sort of child they want to have. Using preimplantation genetic diagnosis (PGD), for example, allows parents to evaluate several existing embryos before selecting which to implant via IVF. One of the traits PGD can identify is genetic deafness, and hearing embryos are now preferentially selected around the globe using this method. Importantly, some Deaf families desire a deaf child, and PGD-IVF is also an option for them.

Selection for genetic deafness, however, encounters widespread disapproval in the hearing community, including mainstream philosophy and bioethics. In this paper I first address the proposed moral harm(s) of selecting for deafness, which I collect into three main categories:

1. harming the child,
2. restricting the child's future life plans, and
3. introducing a harmful state of affairs.

All the supposed moral harms of selecting for deafness, I attempt to show, rely on assumptions about the inherent "badness" of being deaf (or its consequences). The source of these assumptions is often a medicalized model of disability (and deafness) as bad-difference, as a condition that makes an overall negative impact on one's well-being. To evaluate the moral permissibility of selecting for deafness, we must therefore discern the relevant impact of deafness on a future child's overall well-being. To avoid begging the question in this case, I propose we challenge the bad-difference view of disability.

Towards this goal, I next apply Elizabeth Barnes' (2009, 2016) value-neutral model of disability as mere-difference to the case of selecting for deafness. Under this model, to be deaf is to have a "minority body," and deafness is neutral with respect to overall well-being. Testimonies of disabled people are vital for dismantling societal stigma about disability; in bad-difference views such testimonies are too often subject to epistemic injustice. I draw on evidence from Deaf Studies and Disability Studies to build a better understanding of deafness, the Deaf community, and the circumstances relevant to reproductive selection that may obtain for some Deaf families. Selection for deafness, understood as biological mere-difference and valued for its cultural identity, need not necessitate any impermissible moral harms. I thus advocate that it is sometimes morally permissible to select for deafness in one's child.

Bridging between biology and law: European GMO law as a case for applied &HPS

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Laws regulating the permissibility of producing and releasing genetically modified organisms (GMOs) into the environment address a multitude of normatively loaded issues and frequently lead to heated public debate. Drafting new legislature as well as interpreting and operationalizing current GMO law draws on knowledge from both (applied) biology and the study of law.

In a case study, I show how &HPS can contribute to an applied and socially relevant context by clarifying concepts and by reflecting on (implicit and value-laden) ontological choices:

The European GMO Directive regulates the deliberate release of GMOs, such as genetically modified crops in agriculture. Its legal definition of GMO depends on the interpretation of the vaguely formulated phrase “altered in a way that does not occur naturally” (Art. 2(2) 2001/18/EC). However, this phrase decides which organisms do or do not fall under the regulatory obligations of European GMO law, with far reaching implications for what is planted on our fields and served on our plates.

I provide a framework for interpreting the European GMO definition, by identifying two main issues that challenge its straightforward application to organisms bread by new breeding techniques:

1. Three contradicting concepts of naturalness can be distinguished (Siipi, 2008; Siipi & Ahteensuu, 2016).
2. In an outcome-based approach, concepts of biological modalities are required for the operationalization of natural possibilities (cf. Huber, 2017). Given knowledge on mutation rates, an organism would have to be “reasonably probable to occur naturally” (Huang et al., 2016).

The truth-values of scientific statements regarding the legal status of GMOs depend then on deciding between the above (1) different concepts of naturalness and (2) different biological modalities. An unambiguous operationalization of the GMO definition for regulatory practice is thus necessarily based on ontological choices. Following Ludwig (2016), ontological choices are – at least in part – dependent on non-epistemic values.

For clarification of scientific issues, Lawyers call on experts from biology and biotechnology to draw on empirical evidence and scientific ontologies. The above considerations on value laden ontological choices beg for reflection about the role of scientific expert opinions delivered for law.

However, it seems that relevant ontological choices can be made explicit and &HPS can take on the role of go-to-discipline for the clarification of conceptual issues in such interdisciplinary normative contexts.

Comprehension as compression: Understanding understanding

John S. Wilkins, University of Melbourne, Australia

All nervous systems by nature desire to process information. Consequently, entities with nervous systems tend to find information everywhere, and on the principle that if some is good a lot is better, we have come up with "Big Data", which is often suggested as the solution to the problems of one science or another, although it is unclear exactly what counts as big data and how it is supposed to do this. In this paper I will argue (i) that understanding does not and cannot come from larger and higher dimensionality data sets, but from structure in the data that can be literally comprehended; and (ii) that big data multiplies uncertainties unless it can be summarized. In short, data is not knowledge; knowledge is not comprehension; comprehension is not wisdom.

Sources of evolutionary contingency and entropy: Chance variation and genetic drift

T. Y. William Wong, University of Cambridge, UK

Although there is no current consensus as to what the evolutionary contingency thesis amounts to, contingency-theorists have gestured to a series of phenomena ranging from processes central to modern evolutionary theory like natural selection or random mutations to rare Armageddon-like events as what accounts for evolutionary contingency. These phenomena constitute a class which may be aptly called the "sources of contingency". The idea is that these phenomena lead to evolutionarily contingent outcomes in virtue of some inherent chanciness.

The modern synthesis prescribes, at least, two candidates for this class of phenomena: the so-called "chance variation" (e.g. random mutations, recombination) and genetic drift, which shall be the focus of the paper.

Biologists and philosophers of biology have historically taken these two evolutionary factors to be "chancy" in a number of different ways. However, as we shall see, not all of these ways are sufficient to account for evolutionary contingency. Some senses of chance are simply irrelevant to the evolutionary contingency thesis whereas other senses of chance, although relevant, are met with great resistance from the empirical data. Although the current evidence is ultimately inconclusive regarding whether chance variations and genetic drift are chancy in some senses, there is sufficient evidence to believe that chance variation and genetic drift can be non-chancy (and hence, directional) in, at least, two other senses – one of which directly opposes the evolutionary contingency thesis. That is – contra the gesturing of contingency-theorists, chance variation and genetic drift are not always paradigmatic sources of contingency.

Additionally, the evolutionary contingency thesis is taken to be spectral. That is – contingency theses can differ in the amount of contingency they assert for evolutionary outcomes. Accordingly, sources of contingency ought to be able to varyingly account for instances of evolutionary contingency that differ in degree. To this end, I introduce the idea of a "possible outcome array" and import Shannon's informational entropy as a statistical measure to allow contingency-theorists to quantitatively assess the strength of a source of contingency. In brief, if the process of mutagenesis, recombination, or drift leads to an array of possible outcomes that are equiprobable (i.e. the probability distribution is uniform), then entropy is maximised, and the source of contingency is said to be absolutely strong. However, as the possible outcomes diverge from equiprobability, entropy minimizes, and the source is said to be weaker. This is significant because molecular, mutational, and replicative studies in biology are often informative of the possible outcome array of certain biological processes. Even if not, it is feasible to experimentally obtain probability distribution tables – the case is especially clear in mutagenesis. Insofar as entropies can be calculated, contingency-theorists can empirically determine the strengths of various sources of contingency.

Extracting morality from evolution: What a strong evolutionary moral realism means for moral facts

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Arguably, the most pervasive opinion regarding the upshot of evolutionary explanations of morality is that they're deflationary of moral realism. However, the encampment of evolutionary moral realists is not small. I explore this debate by examining one particular evolutionary account of morality – Street's "adaptive-link account", which claims that our moral beliefs are largely the result of natural selection for beliefs that encourage adaptive behaviours – and the putative dilemma it poses to moral realists who accept it or something like it. These moral realists must either deny or affirm the "tracking thesis", Street argues, which states that our moral beliefs track the moral facts. If they deny it, moral realists must accept that our moral beliefs, as adaptive links, are very likely to be mistaken. On the other hand, accepting the tracking thesis leaves moral realists with the burden of accounting for this tracking – Street argues they can do this only by claiming that having moral beliefs that grasp the moral facts is adaptive. However, this conflicts with the more scientifically plausible adaptive-link account. Thus, moral realists face a "Darwinian Dilemma".

I explore one apparent solution to this dilemma, which rests in accepting that our moral beliefs were at least partially selected for their benefit as adaptive links, but positing further that moral beliefs that form adaptive links are likely to track the truth. This solution, while less parsimonious than the adaptive-link account in itself, is of particular interest because it is open to both the naturalist and non-naturalist moral realist, and places illuminating demands on how moral facts must be conceived. I argue that naturalist moral realists are committed to one of several conceptions of moral facts as a special set of prudential facts. Thus, naturalists who accept an evolutionary explanation of morality sacrifice understanding moral facts as having a distinct normative compulsion, and this compulsion is precisely what we want from moral realism. Non-naturalists avoid this problem, but face a distinct challenge that also threatens the distinct normative compulsion we want from morality. I conclude that accepting an evolutionary account of our moral beliefs and maintaining that they track moral facts necessarily leads to a conception of moral facts that is unsatisfactory.

A Complementary Grounding for Contrasting Topological Explanation with Mechanistic Explanation

Zhang Xin, Peking University, China

Topological explanation has always been put in contrast with mechanistic explanation. The main reason is that while the former explains a system feature by citing topological or graph-theoretical properties of the system (e.g. scale-freeness, small-worldness), the later explains by listing a sequence of activities performed by entities within the system. However, one one hand, by examining three paradigm topological explanations (i.e. the ecological case from Huneman 2010, the immunological case from Jones 2014 and the epidemiological case from Watts & Strogatz 1998), I contend that all these three cases contain mechanistic ingredients. On the other hand, topological or graph-theoretical properties are organizational properties and it is widely agreed that mechanistic explanations contain organizational properties of the systems under focus. Therefore, both kinds of explanations contain both organizational and mechanistic ingredients and this indicates that aforementioned reason cannot support the contrasting relation between these two kinds of explanation. In face of this, I raise a new argument for why these two kinds of explanations shall be put in contrast. The crux of this argument is twofold. First, although mechanistic explanation contains organizational ingredients, it is the mechanistic ingredients (i.e. sequences of activities) that answer scientists' curiously. Second, although certain topological explanations contain mechanistic ingredients, it is the organizational ingredients in these explanations that answer scientists' curiosity. Based on this distinction, I content that these two kinds of explanation are in contrast.

Theory construction by exploration: From the PaJaMo experiment to the synthesis of protein

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This paper aims to explore how exploratory experiments lead to the construction of new theories. I argue that the PaJaMo experiment (Pardee, Jacob, and Monod 1959) is exploratory and plays a crucial role in the construction of the protein-synthesis theory. Philosophers have argued that the PaJaMo experiment plays an important role in deducing hypotheses (Schaffner 1974), discovering mechanisms (Darden and Craver 2002), and solving problems (Weber 2005). However, they understand the PaJaMo experiment as a means for testing hypotheses, models, or theories. This paper will argue that the essential character of the PaJaMo experiment is both testing and exploring. It is used to test an "exploratory model" (the induction model), help develop a new model (the repressor model), and finally construct a new theory (the protein synthesis). According to literature, exploratory experiments are "driven by the elementary desire to obtain empirical regularities and to find proper concepts" (Steinle 1997: S70). The aims of typical exploratory experiments include identifying regularities and developing new concepts, isolating or manipulating particular entities or phenomena, developing experimental techniques, instrumentation, or simulations, and resolving anomalies (Elliot 2007:324). In exploring exploratory experimentation, philosophers seem to make a basic distinction between theory-driven experimentation and exploratory experimentation. I will argue that the basic dichotomy is not suitable for the PaJaMo experiment. Although the PaJaMo experiment is exploratory, it was guided by an exploratory model, say, the induction model. An exploratory model is tentative, being used to explore and discover novel phenomena. In this paper, I will explore the combination of exploratory models and exploratory experiments.

Correcting life in the postgenomic era? The rise of genome editing in South Korea

Doogab Yi, Seoul National University, South Korea

This paper examines a scientific career of one of the most prominent genetic engineering scientists in South Korea, Dr. Jin-soo Kim. As he often introduces himself, he is "an entrepreneur and chemist-turned-biologist." He is quite renowned for his work on genome editing at Seoul National University, and for his founding of ToolGen, one of the largest gene editing companies in South Korea. I will follow his career within the context of the rise of biotechnology in the postgenomic era in South Korea. I will first examine his early career from a research scientist at a private research institute to a founder of a postgenomic biotech company within the rise of the venture capital industry in South Korea. The Korean government, faced with an economic crisis, tried to promote post-genomics in order to capitalize on the data and knowledge gained through the Human Genome Project. Then I will analyze his return to an academic post at Seoul National University in the early 2000s, at a time when the university tried to institutionalize academic capitalism in the field of post-genomics. In many ways, his return came to be regarded as an attempt to correct academic life toward economic development. By 2014, he has emerged as one of the most prominent entrepreneurial scientists at Seoul National University, directing cutting-edge research teams both at the Institute for Basic Science and ToolGen. By reflecting on his boundary crossing between the academy and industry, this paper ends with a brief discussion on a recent controversy over the ownership of the CRISPR patents development at Seoul National University.

Epistemic values, trade-offs, and multiple-models juxtaposition

Yoshinari Yoshida, University of Minnesota, USA

The formulation of scientific models is often under the constraint of trade-offs among different epistemic values. This paper characterizes multiple-models juxtaposition (MMJ), a strategy for dealing with such trade-offs. MMJ displays models of similar but distinct phenomena together and fulfills epistemic values both in the individual models and through a comparison of those models. It enables the fulfillment of several epistemic values that a single model cannot exhibit simultaneously because of trade-offs among them. To show how MMJ functions in scientific research, I focus on a concrete case from the investigation of branching morphogenesis in developmental biology. This case study illustrates how MMJ coordinates the values of wide scope and detail simultaneously. Models of distinct morphogenetic mechanisms are often displayed together in this area of inquiry, which provides a generalization about common features between those mechanisms while maintaining non-negligible detail in the individual models. I also contrast MMJ with multiple-models idealization (MMI), which is another strategy for dealing with trade-offs among epistemic values and has received substantial philosophical scrutiny. Although MMI and MMJ both utilize multiple models to simultaneously fulfill epistemic values that are in trade-off relationships, they exhibit several contrasting features: they differ in kinds of phenomena they deal with, similarity of the models involved in them, what roles are played by the comparison of models, and whether they are based on particular ways of presenting models. I point out that comparing MMJ and MMI helps us better understand the scientific practice of MMJ, as well as MMI, and suggests that further inquiry is needed to understand the diverse ways that scientists fulfill a variety of epistemic values.

The case of mechanistic explanation in molecular biology: Abstraction or idealization?

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The philosophical debates over the last several decades have made abundantly clear that much of scientific practice relies on models that, in some sense, are simplified versions of their target systems.

In this paper I argue for two things. First, the popular and widely used notions of abstraction and idealization face numerous issues with regard to their characterization. I provide a survey of the literature (e.g., Godfrey-Smith ([2009]), Frigg an Hartmann ([2012]), Levy and Bechtel ([2013]) etc.) to show that, few notable exceptions notwithstanding, there currently exists a “standard view” according to which, roughly speaking, an idealization concerns a distortion of a feature in a model, and as such it introduces a falsehood into the model, whereas an abstraction concerns an omission of an (irrelevant) feature. Second, the lack of conceptual clarity with respect to these notions poisons various other debates including the one on mechanistic explanation.

Regarding the first problem, I argue that the standard view fails to provide an adequate characterization of either of the notions. Here, I list only some of the issues. For instance, not every distortion counts as an idealization, nor does just any falsehood (see Levy ([2018]) for a related idea). Abstraction, understood as a procedure by which one subtracts individual features from the target system, is akin to rational reconstruction rather than a description of the model-building process. This is because scientists often do not know what features the target system has, and the point of modeling is to find out precisely that (Portides [2018]). It also proves rather difficult to apply the standard view to actual scientific cases. Hence, in practice the distinction is often blurred. All this shows that the standard view is based on a confusion, and more importantly, it introduces additional confusion into other debates in which the notions of abstraction and idealization play key roles (see below).

The second problem concerns the implications the conceptual confusion of the standard view has for various other debates. Here, I argue that some of the recent attempts to challenge the framework of the new mechanistic account of explanation is wrong-headed precisely because it relies on the standard view. In a recent paper, Love and Nathan ([2015]) argue that the mechanistic account of explanation cannot account for idealizations that scientists often employ. They discuss the case of modeling gene transcription and argue that scientists commonly introduce three misrepresentations into their models (i.e. treating molecular complexes as if they were single molecules, disregarding the fuzzy nature of the process in which various molecules constantly bind and detach, and omitting the role of concentrations). Love and Nathan take these assumptions to be idealizations, using the standard view characterization. However, they define abstraction as “the intentional omission of detail” (p. 763), yet they claim that when “known difference makers are intentionally omitted from the representation” (p. 767) we are to understand it as an act of idealization. Thus, they seem to conflate abstraction with idealization.

Importantly, the approach and analysis of Love and Nathan has explicitly been embraced by several authors in the debate on mechanisms (e.g. van Eck and Mennes ([2016]); Rice ([2017]); Halina ([2018])). This introduces a dangerous precedent, one that could spark a long-lasting debate without realizing that it builds on a wrong footing.

From infusions to onions: Goethe's theory-building practice

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Goethe's morphology had an impact on major research traditions in biology and physics, linking Charles Darwin and D'Arcy Thompson, and leading up to Heisenberg. Tracing Goethe's concept-use and interest in specific types of model-organisms helps one to reconstruct his complex theory-building practice.

So far comparatively little research has targeted Goethe's research practice (Amrine 1996): the note-books, manuscript drafts that preceded his scientific publications, and his drawings, diagrams, "paper tools". The paper reconstructs the terminological and diagrammatic development in Goethe's notes before 1790, spanning from his early work on Infusoria to his experiments with germination, and his notes to the Metamorphosis of Plants. Some parallels will be drawn with early osteological and mature morphological works.

The paper has three parts, first Goethe's model organisms are investigated, where observations could lead to the furthering of the conceptual framework for the study. These include Tremella, studies of germinating beans, and specific groups, either taxonomic (cacti, onions) or developmental (perfoliate flowers). Specific forms facilitated the model-building, and these included individuals, like teratological (monstrous) examples.

Second Goethe's theory-building practice is outlined. Goethe repeatedly uses polarities as explanatory crutches, and locates advancing/progressive series (Zammito 2018, Zemplén 2017). Most of the explanatory terms create geometrical or intermodal spaces. In the early work on plants "expansion-contraction", in later botanical texts "vertical" and "spiral" tendencies.

Third the stages of the development of the conceptual framework is discussed, from the early use of ontologically flexible "points" (Goldstein, 2011) to the proliferation of technical vocabulary in the notes. The early notes show the interest in a modular conception of life and development, in composites that are asymmetrical, and in the scalability of living forms. In his work on cotyledons the transition between distinct organs and features is investigated. As Goethe's views developed, he refined his attitude towards Linné and his systematic biology, and made interesting critical remarks. The analysis suggests that Goethe's concept of morphology does not fundamentally rely on a "species" concept. Also, in some contrast to mainstream approaches linked to medical faculties and physiology (Haller, Blumenbach, and later Kielmeyer) Goethe's focus on botany resulted in an approach sensitive to the problem of "artificial systems", and the mereological questions of life (sexual and asexual reproduction in plants, pluripotency). In conclusion some changes in the usage of key terms, the node, and the leaf, and the move from a supra-individual ideal-type to an infraindividual one will be highlighted.

Two senses of relative importance and the testability of empirical adaptationism

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At the very end of the introduction in the sixth (and also final) edition of *The Origin of Species,* Darwin (1872, p. 4) wrote that, "I am convinced that Natural Selection has been the most important, but not the exclusive, means of modification." Although it is not clear what exactly Darwin means by this claim, his idea that natural selection plays a somewhat more important role than other factors in evolution has been maintained in quite a few biologists' understanding of evolution (e.g., Losos, 2014; Mayer, 2014). Some biologists and philosophers of biology, such as Orzack and Sober (1994), Godfrey-Smith (2001), and Lewens (2009), have attempted to articulate this idea and formulate it as a claim about nature under the name of empirical adaptationism. What is common among these formulations is that they all involve the causal power and scope of natural selection.

In this paper, I will raise some issues about the testability of empirical adaptationism. I argue that empirical adaptationism involves two senses of relative importance – one based on relative causal power and the other based on relative frequency. Based on this observation, I further argue that empirical adaptationism is scientifically untestable unless several issues concerning these two senses of relative importance can be resolved.

According to the first sense of relative importance, a causal factor is more important than any other if it has greater causal efficacy in the production of a phenomenon. For example, the gravity of the moon is a more important cause of the tides on Earth than the gravity of the sun because the moon has a bigger influence on tidal height. One issue of using this sense of relative importance in empirical adaptationism is that it is not always clear how to measure the relative causal importance of natural selection and other evolutionary factors. For example, suppose that the evolution of a trait is influenced first by genetic drift and then by natural selection. Since the working of natural selection is based on the consequence of genetic drift, it does not make sense to compare the relative causal importance of natural selection and genetic drift in cases like this.

According to the second sense of relative importance, a factor is more important than any other if the proportion of phenomena in a domain explained or caused by this factor is greater than that explained or caused by any other factor. For example, driver negligence can be thought of as the most important cause of automobile accidents in a region if most automobile accidents occurring in this region are caused by driver negligence. One issue of using this sense of relative importance in empirical adaptationism is that it is not clear how to decide the universal set of all extant traits in nature. If the test of empirical adaptationism is based only on the traits that have already been studied, there is no way to guarantee that the conclusion based on these traits is applicable to what happened to all traits in nature.

Who should not be harmed: Human and non-human in the animal experimentation debate

Yunjie Zhang, Glasgow University, UK

In animal ethics, when ethicists discuss whether a practical matter is morally wrong, they often apply utilitarianism view and moral rights view (hereafter MRV) to explore. For example, both of two theories argue against animal performance, against animal hunting, and against the animal factory, etc. Although they are argued from different moral perspectives, both theories can reach agreements and yield the same conclusions on the above cases. However, on the issue of animal experimentations, these two theories seem to be unable to reach an agreement. Whether non-human animals should be used in scientific experiments is a point of serious contention between utilitarianism and MRV. The former is supportive provided, the results of the experiments can bring more benefits. The latter is totally opposed because regardless of benefit animal experiments violate the right of animals not to be harmed. In short, unlike other cases, the issue of animal experimentation seems to be the biggest conflict between these two main theories of animal ethics.

Accordingly, some animal ethicists think it is necessary to find an application to reconcile in MRV and utilitarianism on the issue of animal experimentation. Gary Varner is one of them, he argues that the MRV is much more complicated, especially when rights are in conflicts, and the problem of animal experimentation is such a case. Therefore, the issue of animal rights cannot be simply considered in the case of animal experimentations. He also suggests using the “worse-off principle” to deal with this problem, and that its application seems likely to reconcile in utilitarianism and the MRV. The worse-off principle, simply says is, if the harm faced by a few individuals makes them worse-off than anyone, then this principle allows the rights of majority to be overridden rather than those few individuals. Alan C. Clune, however, emphasizes Regan's view of the "worse-off principle"; it only applies to special circumstances rather than generally, such as routine, or institutional cases of conflict. Animal testing is both routine and institutional, so Varner's prospect of applying the principle to animal testing for convergence fails. Also, Clune argues that the "worse-off principle" presents a form of perfectionism which is morally pernicious. From my point of view, I agree with Clune, but I think it is noteworthy that the "worse-off principle" itself is in a way inconsistent with Regan's normative MRV view for animals; thus, the "worse-off principle" has no possibility of rapprochement from the MRV view, of reconciling with utilitarianism.

In this essay, I will mainly divide into four main parts.

1. I will first provide a brief background of the debate; explaining the MRV and utilitarianism's different views on animal experimentation.
2. I will introduce Varner's proposal of the "worse-off principle" and how this deals with the conflict.
3. I will point out Clune's rebuttals that the "worse-off principle" may fail.
4. My worries and arguments about the worse-off principle is that this principle violates the core idea of inherent value that the MRV relies on and therefore the principle cannot be derived from the MRV. Because of this, I doubt this principle can solve convergence issues between MRV and utilitarianism.

Element analyses or rats' tail-raising: Total synthesis and determination of insulin in China, 1958–1972

Jing Zhu, East China Normal University, China

In 1965, Chinese scientists announced that they had synthesized biologically active bovine insulin in crystalline form and thus achieved the first successful protein synthesis in the world. Total synthesis of bovine insulin, a major scientific project in Mao's China, was seen as a testament to socialist China's scientific capabilities and a significant achievement in fundamental biochemistry in Chinese history. Previous studies (Xiong and Wang, 2005) have provided a detailed account of this historic research and analyzed a specific Mao-era style of scientific research, which was of a military favor and emphasized collaboration, secrecy, and extensive mobilization of human resources. However, they overlooked the debate about whether bovine insulin was successfully synthesized, how to identify the artificially synthesized bovine insulin, and the relative scientific contribution between the researchers from different fields and institutions involved in this project. The debate began in 1964 and continued even when China made the announcement of the successful synthesis of bovine insulin in 1965. What was the inherent purpose of the project, and what external functions did it serve? How did Chinese scientists in different research fields identity and guard their intellectual status and judgments under the influence of regularization/mobilization-oriented science policies? Who made the judgement of the results and by what criteria? And finally did the debate manifest itself differently when one moves to the world of national science and pure science?

From the perspective of Hasok Chang's (2014) activity-based analysis of systems of scientific practice, this article examines the debate concerning the project of total synthesis and crystal structure determination of insulin in China in terms of aims, science policy context, epistemic activities, research resources and scientific evaluations. This article finds that what caused the debate between Chinese organic chemists and biochemists are their different epistemic criteria of the determination and synthesis of biomolecules, and their different understandings of life. Scientists' appealing to national prestige and writings of Friedrich Engels, a co-founder of Marxism, intensified the debate, especially with respect to how to understand the relationship between insulin and living life, and what contributions the work on the synthesis of insulin made to international scientific research. What ended the controversy was the following crystal structure determination of insulin, in which Chinese scientists obtained the three-dimensional crystal structure of insulin with X-ray diffraction method and got recognition through international scientific communication. This episode shows the complexity of scientific evaluation as a scientific activity and how this activity was shaped by intellectual interactions among scientists and science policies.

Animals, pleasure, and animal pleasures

Jason Zinser, University of Wisconsin, USA

There have been considerable empirical and philosophical explorations of nonhuman animal pain, and for good reasons. There are puzzles about the nature of pain, its evolutionary function, and our ability to identify which animals experience phenomenological pain. However, there has been proportionally little exploring animal pleasure. First, I will explore various questions surrounding animal pleasure, such as: What are the dimensions of pleasure that nonhuman animals can experience? What is the function of pleasure? And which animals can feel pleasure (and how can we tell)? I will explore the empirical and conceptual work on pleasure and use the existing work on pain as a model for how to explore pleasure, while being mindful of salient differences that might arise between treatments of pleasure and pain.

Secondly, I will briefly explore the ethical dimensions of animal pleasure. For example, one argument for "humane" meat is that it would actually increase overall pleasure by allowing animals, which experience a variety of pleasures throughout their life, to exist. Thus, understanding and accounting for animal pleasure may be used to respond to some arguments prohibiting the use of any animals. It may be such that the consumption of "happy meat" should be promoted, once animal pleasure is accounted for. A second ethical question that an exploration of pleasure might contribute to is whether factory farming is merely repugnant (in Parfitian terms) or worse? Do factory farmed animals have a minimum amount of pleasure which outweighs the pain they endure or is their life, on balance, one of negative utility. Finally, I will explore whether an understanding of animal pleasure holds any novel implications for the treatment of wildlife.

Mixed media and poster presentations

Epidemiology at the interface of environment and health: Three strategies for evidential claims on the exposome

Stefano Canali, Leibniz Universität Hannover, Germany

Philosophy and Epidemiology. Most of the philosophical scholarship on epidemiology has focused on causality, by looking at causal explanations and interpretations of epidemiological results in terms of causal claims. In this poster, I take a different approach and present an account of contemporary epidemiology based on the notion of evidential claims. Building on philosophical analyses of data practices in biology and evidential reasoning in archaeology, I argue that focusing on the dynamics of evidential claims enables to identify distinct approaches, methods, and types of evidential reasoning at work in epidemiology.

Focus and Methodology. I use a philosophy-of-science-in-practice approach and take a close look at ongoing environmental epidemiology that applies the “exposome approach” and investigates the totality of exposures faced by individuals. I ground my analysis on qualitative interviews, participatory observation and discussions with researchers in the EXPOsOMICS project.

Evidential Claims on the Exposome: Three Strategies. My account based on evidential claims enables to identify three main strategies employed to generate evidential claims. Each strategy encompasses a distinct approach to the phenomena under study; a distinct kind of work that researchers carry out; and a distinct type of evidential claims.

These three strategies are:

1. The macro strategy, which generates scoping claims that restrict the sample and provides an initial understanding of the phenomena under study; it can be seen in the initial selection of data from cohort studies.

2. The micro strategy, which is applied at various steps of research (omics analysis, geographical information systems and experimental studies) to collect data of significantly different types and generate evidential claims on structures at the microscopic level of investigation.
3. The association strategy, that uses evidence from the macro and micro strategies to generate evidential claims at the statistical level of associations between environmental exposures and outcomes of interest.

Discussion. I argue that distinguishing strategies for evidential claims yields significant insights. It enables to unpack the epistemic issues and challenges that concern each strategy and, in turn, influence research done at a different stage. It gives a characterisation of the context of data practices in terms of evidential claims, which shows how much epidemiological research is not necessarily about causal claims, but neither is to be overlooked as producing 'raw data'. In this way, it provides a new philosophical perspective on the epistemology and practice of epidemiological research at the interface of environment and health.

Monster mash: History and practice of creature design

Kristine Grønning Ericson, Yale University, USA

The practice of designing animals, monsters, and other creatures for the film and video game industries has roots in scientific illustration, as well as the history of reconstructing and imagining extinct or theoretical creatures--dinosaurs, mammoths, mermaids, monsters.

In film and video games, these creatures' visual appearances must satisfy the logic of a story's environment and its real or invented natural history. The artists who develop and visualize these characters call themselves creature designers, and they often have training in scientific illustration or paleontological reconstruction. Creature designers may recreate existing animals through close anatomical study or invent new, hypothetical creatures with features based on those of known animals. When inventing a creature, some designers imagine an evolutionary path whereby a creature's form corresponds to factors including the story's hypothetical environment. The design of a creature will often proceed in tandem with the design of the environment, ensuring a logical evolutionary history. Whether a creature has two, four, or eight legs may satisfy narrative requirements but also imply the creature's predator-prey relationships and imagined evolutionary development in a swamp, desert, forest, or other environment.

Through a historical study of scientific illustration and reconstruction as well as interviews with currently practicing creature designers, I will investigate the links between contemporary creature design and past forms of creature imagination and visualization. The work of creature designers demonstrates the potential to creatively imagine possible futures that are grounded in scientific knowledge and practices. With this research, I am proposing to create a hybrid presentation of a paper accompanied by my own interactive animation work. I am a visual designer and animator currently studying the History of Science and Medicine at Yale University, and I want to merge my design work with more traditional forms of scholarship. I am experimenting with hybrid visual presentations that incorporate novel forms of visualization and interaction. I study creature design from the perspectives of historian and designer simultaneously, and I hope this presentation will serve as a model for potential future hybrid work in design/scholarship.

An analysis of Louis Guillaume Figuier's (1819–1894) contestation on the experiments of Claude Bernard (1813–1878)

Alan Dantas dos Santos Felisberto, University of São Paulo, Brazil
Silvia Fernanda de Mendonça Figueirôa, University of Campinas, Brazil

The present study aims to present elements of the methodology of the physiologist Claude Bernard (1813-1878) and the pharmacist Louis Guillaume Figuier (1819-1894) on the problem of the glycogenic function of the liver. In a communication of 1855 presented to the Académie des Sciences, Bernard claimed to have "incontrovertible" arguments about his experiments (Bernard 1855, 461). In his *Memoir on the Pancreas* of 1848 he conducted four sets of experiments and stated that animals are capable of producing sugar independent of food (Bernard, 1855, p.462). To state the glycogenic functions of the liver, he found that blood from the portal vein has no trace of sugar, and blood from the hepatic vein contains considerable proportions of glucose.

Louis Figuier presented three communications in the *Comptes Rendus de l'Académie des Sciences* (Bernard, 1855, p.462). According to the physiologist, in the first experiment analyzed, Figuier affirmed that sugar can not exist in animals without food, carnivores obtain such matter from herbivorous animals that assimilate this sugar (Bernard, 1855). According to Figuier himself, in his communication he emphasized the need for analysis of other organs, in order to determine the amount of sugar (Figuier, 1855a, 230). Figuier also argued the origin of the meat that Claude Bernard provided to the animals, because when acquired in the butchers had large proportions of sugar, because prior to slaughter the animals consumed foods rich in carbohydrate (Figuier, 1855a, 232). The pharmacist concluded that "the liver of animals does not have the function of making sugar and all the glucose in its tissue comes from food" (Figuier, 1855a, p.232).

According to Bernard, in the second *Memoir* of Figuier, the pharmacist states that the production of sugar in the animals is independent of the meal, for Figuier this sugar forms in the blood. As soon as it reaches the portal vein, this sugar is condensed and conveyed into the liver (Bernard, 1855, p. 462). According to Figuier, the liver functions as a reservoir of glucose from the portal vein blood, after digestion glucose is redistributed to the tissues of the body by circulation (Figuier, 1855b, p.675).

For his third *Memoir,* an evaluation committee of the experiments was set up which would judge which would be the most adequate to answer questions about the glycogenic function of the liver (Figuier, 1855c, p.352). Figuier maintained his claims based on about 30 experiments that he accomplished obtaining the same results (Figuier, 1855c, p.352). With this information, Claude Bernard repeated the experiment and found different results (Claude Bernard, 1855, p.463).

It was noted that the physiologist used a technique distinct from that of the pharmacist: fermentation rather than the reaction of Frommhertz. In the evaluation commissions composed by the physician Pierre Rayer (1793–1867) and the chemists Jean-Baptiste Dumas (1800–1884) and Theophile-Jules Pelouze (1807–1867), it was found that the members shared the same style of thinking of Claude Bernard, which could favor him, even if his conclusions were wrong about the method.

Irrational expectations: Rationality and mental health across cultures

Alexander Nicholas Lerner, University of Nevada Reno, USA

I will present a poster analyzing rationality associated with disorder categories in mental health across western and eastern medicine. The purpose is to clear up the confusion surrounding the everyday behavior associated with mental health disorders and to begin to establish a conceptual baseline or spectrum for what we deem healthful rationality. My approach is to conduct a bioinformatics study which reviews global disease categories across a host of contemporary diagnostic tools and where they draw the boundaries between rational and irrational behavior associated with dysfunction or disorder. The work stems from the fields of Philosophy of Mind, Neurobiology, and Psychology.

Rational behavior is a key component in the language of mental health diagnostics. The fuzzy boundaries between categories of diagnoses for patients are made up of our novice understanding of the phenomenology associated with various disease states. Contemporary work in the field of bioethics and philosophy of medicine is looking deeply into the social and cultural milieu that patients are steeped in. While advances in technology are allowing us a deeper insight into the hemodynamics and electrophysiological processes associated with certain behaviors, few researchers are considering how we attribute disease states to changes in rationality. Even less work is being done to include population data for behavior not associated with categories in western medicine.

Currently, our folk biological understanding of what it means to think clearly is left wholly up to the patient's discretion at intake and the doctors clinical opinion during treatment. This ensures that patients and doctors are both struggling to understand each others expectations for rational thinking. It also confuses the global statement on expectations for patient-life after treatment. Diagnoses can be daunting to patients as they assume their new identity as a disordered member of society instead of more rightly as a person who happens to suffer from a potentially recurring dysfunction.

Epistemic experimentation: Tools to evolve research practices

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Leïla Perié, Atelier des Jours à Venir, France and Institut Curie, France
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In this session, we invite participants to experiment three tools to step back and revisit their research practices. Our epistemic practices – our ways of building knowledge – constantly need to be questioned, e.g. when we feel locked into a way of thinking, or when the scientific community calls for evolving research practices towards more societal accountability. While science studies have proved to be of great use to understand the human, social, institutional dimensions of scientific research practices, it remains difficult for researchers to go beyond self-reflection. How to actually evolve our research practices, how to imagine, implement, experience new research practices? We propose here three practical tools, grounded in science studies, to reflect upon and experiment research practices. These tools result from three years of collaborative woork through regular workshops gathering academic researchers, artists and a non-profit research company dedicated to reflexive & responsible practices. This atypical collaboration in itself is an example of how bringing together different stakeholders can fruitfully lead to new research productions, practices and perspectives.

After a brief presentation of the way the three tools have been produced, participants will be divided in three groups, each experimenting one of the three tools below.

1. Shake Your Metaphors. Metaphors are pervasive in scientific research, and are sometimes considered as hindering research, biasing representations, especially when they remain unquestioned. However, metaphors also have a heuristic function : they can be used to generate new research questions. This protocol, designed as a 1h activity, guides the exploration of a metaphor of your choice, to prompt research questions.

2. What are you wondering at? This text is written as a script, where the reader engages into a scientific research process. In this script, the scientific research process is not limited to a scientific method. The scientific activity is considered as inseparable from its institutional framework, its social aspects, its articulation with other stakeholders, and the intimate experience of the researcher activity. This script can be used by researchers as a tool to reflect on their existing practices and imagine new ones, but it is also designed to be used by readers with no scientific background to get a glimpse at scientific research.

3. Asymmetry. Asymmetry is a participatory performance designed for a group of 8 to 12 people that questions the concept of dynamic balance when sharing elements within a group. It uses a minimal scenography and simple rules which are directly inspired by biological processes such as cell divisions and inheritances mechanisms. Each participant acts upon elements that can stand for particles, hereditary factors, cells. When one of these is moved, the whole equilibrium is impacted. Rules may exclude removing elements, invite for the search of equilibriums situation, etc. After witnessing the dynamics, participants can use the experience to question models used in their own research domains. They can also suggest new rules to adapt the performance and use it to witness other dynamical properties of the systems they investigate.

The neuroscientific case against retributive justice

Robert C. Robinson, Georgia State University, USA
Stephen G. Morris, City University of New York, USA

Retributive Justice is the theory of justice according to which individuals are either rewarded or punished as payback for the moral rights/wrongs they have committed. Consequentialist considerations such as deterrence and prevention do not figure into justifications for treatment from this perspective. This theory also holds that the severity of the punishment ought to be in proportion to the severity of the crime. The central tenant of the retributive model of justice – namely, that reward/punishment gives people what they deserve – relies crucially upon the intuition that people are sometimes accountable for their actions in some strong metaphysical sense. In particular, we may intuitively feel justified in holding someone morally responsible if her actions were intentional, rather than accidental or coerced. This common view is captured by what we call the "Principle of Retribution": i.e., the view that it is fair to hold an agent morally responsible, and therefore punish her for her crimes, only if her actions were freely willed, intentional, and uncoerced.
It follows from this that unless free will exists for human beings, retributivist justice (at least insofar as human beings are concerned) cannot be justified.

We provide empirical evidence that determinism is – for all intents and purposes – the correct position with regard to human cognition, decision making, and choice. We then argue that insofar as retributive justice seems to require that some actions depend on actions that are non-determined, neuroscience suggests that retributive justice is unjustifiable.

We conclude by providing insight for revising our thinking about criminal justice and what we owe to those who commit crimes. In particular, we discuss how the common theory of distributive justice – which remains intact and includes principles guaranteeing individual liberty and equality of opportunity – gives advice on how we have failed people antecedent to their crimes, and how a person is best dealt with after her crime has been committed.

An evolutionary game theory approach to sex bias in drug research

Lida Sarafraz, University of Utah, USA

Despite slowly changing social norms and ample academic attention to sex bias in biomedical research, the disproportionate use of male human subjects and animal models has ongoing negative impacts on women's health. While evolutionary game theory (EGT) was developed to model natural selection, it also works as a model of cultural evolution. Players in evolutionary games change their strategies slowly to achieve their goals. EGT by its emphasis on the slow process of evolving traits and increasing them in populations is a perfect model for reflecting the slow process of eliminating sexism in drug research.

I use an EGT model to assess interventions at the level of funding, through publication constraints, and by increasing researcher diversity and show that a combination of funding strategies and policy changes is the most promising way to achieve sex parity in research subjects.

In my poster, I use two game models. The first model, illustrates sex bias in drug research as an evolutionary game played by the populations of researchers. The players of the game choose either using mostly male research subjects or using both sexes equally in their research as their game strategies. In the model, playing mostly with male subjects is the dominant strategy, as currently occurs in drug research. Then, in another game design, my second model illustrates, if my suggestions for more inclusion of women in drug research get adopted, by changing the payoffs of the game, sexism in drug research could be eliminated gradually. In my second model, I offer two main proposed interventions to change the payoffs of the game. First, funding agencies should mandate equal numbers of male and female test subjects as their conditions for funding research. Second, medical institutions and journals must have rules and policies for equal inclusion of male and female subjects to accept research proposals and papers. By applying both of these suggestions, since more researchers will use both sexes equally in drug research, it will change the payoffs of the game. Using both sexes equally in drug research will be the dominant strategy of the game, for both funding and regulatory benefits, which will push the male-dominant research strategy to be a less fit strategy to choose.

Memento alien, a tale from alterity

Alecks Volta, Independent Artist

Thomas Nagel (1974) and Peter Godfrey-Smith (2016) write about how it is like to be a bat or an octopus and about how different it could be from our common-day experience. On the other hand, biology has told us about differences and similarities which exist between human groups, either in terms of phenotypical or genetic traits. Also, ecology, bioethics, and biosemiotics let us reflect about our relationship to other nonhuman living beings. In summary, biology and philosophy of biology often reason through theoretical pathways of likeness and alterity. We depend on our own preconceptions and structural constraints in order to understand other cultures and species, but such constraints do not only limit our knowledge about such beings, instead, they also impinge on our ethical behavior toward them. On the other hand, an experience of the other usually turns into distrust and fear. This artistic installation will attempt to engage participants in order to gauge a gradient between familiarity and alienation regarding other living beings. Such a display will contribute to enlighten differences between stances or attitudes regarding our relationship to other species or human groups.

Reexamine the individuality of holobionts through a framework of evolutionary transitions

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Zhiping Cao, Xiamen University, China

A holobiont is a symbiotic collective formed by a multicellular animal/plant organism and the microbial community living inside its body. The individuality of holobionts has been a highly controversial issue. Zilber-Rosenberg and Rosenberg (2008) and Dupré and O'Malley (2012) insisted that holobionts are cohesive as organisms and units of natural selection, while Godfrey-Smith (2013) claimed that holobionts horizontally picking up their symibonts are organisms, but they have no clear parental lineage, thus are not reproducers and not qualified as units of natural selection. Booth (2014) argued that they are still qualified as interactors. On the other hand, Skillings (2016) insisted that most of holobonts should be viewed as ecological communities, rather than organisms or units of selection.

Here we argue that, if we examine the issue of holobiont individuality through a historical dimension, which has been commonly ignored in previous discussions, it can be found that different representation might corresponds to different stage in evolution of holobionts. Thus we propose a framework of evolutionary transitions for this issue. Theoretically, there might be three stages in evolution of holobionts, and there was a major transition of individuality in every stage: the first is from contemporary associations to anatomical individuals, the second is from anatomical individuals to physiological individuals, and thirdly, some horizontally transmitted holobionts evolved to vertically transmitted ones. Every transition produced holobionts with higher degree of individuality, and turned out to be a foundation for the next transition. If a holobiont is merely viewed as an ecological community, some significant evolutionary processes on the level of the whole system will be missed. In order to understand and explain the second and third transition, the holobiont as a whole should be better understood as a unit of selection.

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