



MONTREAL 2015
JULY 5 - JULY 10

BOOK OF ABSTRACTS

INTERNATIONAL
SOCIETY FOR THE
HISTORY
PHILOSOPHY AND
SOCIAL
STUDIES OF
BIOLOGY

Table of Contents

Schedule	2
Program	3
Sunday July 5	3
Monday July 6	5
Tuesday July 7	81
Wednesday July 8	169
Thursday July 9	229
Friday July 10	295
Index	328

Schedule

	SUNDAY JULY 5	MONDAY JULY 6	TUESDAY JULY 7	WEDNESDAY JULY 8	THURSDAY JULY 9	FRIDAY JULY 10
8H00 >		Registration				
9H00 >		Session 1	Session 4	Session 8	Session 11	Session 14
10H00 >		COFFEE BREAK	COFFEE BREAK	COFFEE BREAK	COFFEE BREAK	COFFEE BREAK
11H00 >		Session 2	Session 5	Session 9	Session 12	Session 15
12H00 >		LUNCH BREAK	LUNCH BREAK	LUNCH BREAK	LUNCH BREAK	LUNCH BREAK
13H00 >	Registration	Council meeting	Early career scholar mentoring lunch	Grad. student general meeting Membership diversity meeting	Council meeting	Council meeting
14H00 >						
15H00 >		Session 3	Session 6	Session 10	Session 13	Excursions in and around Montreal
16H00 >		COFFEE BREAK	COFFEE BREAK	COFFEE BREAK	COFFEE BREAK	
17H00 >	President's welcome	Plenary session Sandra Harding	Session 7	Plenary session W. Ford Doolittle	Awards ceremony and ISHPSSB general meeting	
18H00 >	Welcome to Montréal cocktail	Poster session and cocktail		Pub night cocktail and Montréal best poster prize		
19H00 >					Dining buffet ("Cocktail dinatoire")	
20H00 >						
21H00 >						
22H00 >						

SUNDAY JULY 5

13:00 - 17:00	LOBBY OF J.-A.-DESEVE (DS) BUILDING REGISTRATION
17:00 - 18:00	MARIE-GÉRIN-LAJOIE AUDITORIUM PRESIDENT'S WELCOME
18:00 - 20:00	MARIE-GÉRIN-LAJOIE AUDITORIUM WELCOME TO MONTRÉAL COCKTAIL

NOTE: the symbol ** indicates that, at time of publication, the attendance of this presenter has not been confirmed.

MONDAY JULY 6

08:00 - 09:00

LOBBY OF J.-A.-DESÈVE (DS) BUILDING
REGISTRATION

DS 1420

09:00 - 10:30

INDIVIDUAL PAPERS
ENVIRONMENTAL STUDIES: INTERDISCIPLINARY PERSPECTIVES

Evolution and (Aristotelian) virtue ethics

JOHN MIZZONI (Neumann University, United States)

It is well known that virtue ethics has become very popular among moral theorists. Even Aristotelian virtue ethics continues to have defenders. Bernard Williams (1983, 1995), though, has claimed that this “neo-Aristotelian enterprise” might “require us to feign amnesia about natural selection.” This paper looks at some recent work on virtue ethics as seen from an evolutionary perspective (Michael Ruse 1991, William Casebeer 2003, Donald J. Munro 2005, John Lemos 2008, and Jonathan Haidt & Craig Joseph 2007) and explores whether Williams’ evolutionary challenge can be met. Against Williams’ challenge, I argue that “the first and hardest lesson of Darwinism,” as Williams calls it, has indeed found “its way fully into ethical thought” (Williams 1983). And virtue ethics—in several varieties, not only Aristotelian—fits it rather well with an evolutionary perspective on human origins.

Environment and quantum Darwinism

DENİZ ÖLÇEK (Middle East Technical University, Turkey)

Environment is not a passive surrounding, but an active whole which consists of inter-related centers of life, individuals and subsystems. In Cartesian worldview, it is understood as a non-participatory structure which preserves its identity through time. It was perceived merely as a medium. Moreover, our interaction with it considered very limited and from an anthropocentric point of view. Today, we know that such unevolving essential description is not significant as physics, biology, ecology, they are all underlining the entangled, temporal nature of the world. Quantum Darwinism addresses that all living and nonliving entities, from macro objects to DNAs and to subatomic particles are open for external influences and that environment is an active, organic web able to monitoring itself, and the natural selection is not occurring in the biological level but also in quantum level. Thus, in all the fragments of reality – environment as what we live in – there are many levels of selection. This paper aims to revise the idea of an active environment in the light of the concept of Quantum Darwinism, first described by the Polish Physicist W. H. Zurek (1993), showing how selection occurs in different levels. Addi-

tionally, it briefly aims to discuss if this active, relational view of environment linking physics, evolutionary biology and ecology may be inspirational to ecocentric ethics.

Ethical dimensions in contents linked to ecosystem services in ecology teaching

DALIA MELISSA CONRADO (Universidade Federal da Bahia, Brazil); **NEI NUNES-NETO** (Universidade Federal da Bahia, Brazil)

Although very much used in current conservation policies, the concept of ecosystem services present some problems, such as commodification of nature or different ethical perspectives and values underlying discourses on it. Besides, this concept can be considered value-laden, because it is dependent on ideologies and human judgments. In this work we will argue for a strong emphasis on the ethical dimensions of ecosystem services concept in the context of ecology teaching. As a step towards this, we support the argument that the content in science education, in general, and in ecology teaching, in particular, should be conceived in a wider way than is traditionally done. Traditionally, the content is restricted to a conceptual dimension. However, as some authors have argued, educational contents should include also other elements, such as values and attitudes. Based on this wider understanding of content, the following particular subject matters associated to ecosystem services, could be approached in ecology teaching: biodiversity, production of biomass and ecosystem stability, global changes, resilience, health and human well-being, monoculture and genetic variability, among others. This seems to imply, then, that to approach ecosystem services in ecology teaching, there should be an integration between, by one hand, scientific (ecological) concepts and theories, and, by the other, ethical values. Particularly, to understand ecosystem services in this way would have an interesting consequence to practices in ecology teaching, in general: ecology should be taught linked to ethics. As a more radical consequence, ecology teaching strategies should not only be designed to generate a better theoretical understanding or technical intervention on ecological and social-ecological systems, where ecosystem services are embedded, but, significantly, should also provide ways to act – in an ethically informed manner – in these very systems.

INDIVIDUAL PAPERS

MEASURING EVOLUTIONARY FORCES

Challenges for determining which traits are selected for and to what degree

WES ANDERSON (Arizona State University, United States)

Biologists often use selection gradients or selection differentials, not merely to determine that selection is occurring on traits, but also to determine which traits are selected for and to what degree. I hold that to make such determinations one must be able to make claims like: this trait is selected for in this context but selected against in that context. Modeling interactive causation is a necessary and sufficient condition for making claims of this kind. Selection gradients represent the expected effect of interactive variable or type causation. Selec-

tion differentials represent the covariance of a trait variable and a fitness variable, relative to a token context. Then either (1) selection is individuated at a type level and conceptualized as merely influencing the expectation over fitness or (2) selection is individuated at a token level and conceptualized as having to do with how two variables covary in a token context. I argue that neither consequence for determining which traits are selected for and to what degree is particularly appealing.

In search of invariance in evolutionary biology

JUN OTSUKA (Kobe University, Japan)

The ontological and epistemological status of evolutionary principles has long been a topic of various discussions in the philosophy of biology. Are they empirical laws or mathematical tautologies? Do they represent dynamical processes or statistical patterns? Equally controversial is the nature of the concepts used in these principles or of the objects to which they are supposed to apply. What is fitness, phenotype, or gene? Do evolutionary equations apply to groups as well as individuals? If so, do they represent the same or different process(es)? In physics, the nature of laws has been studied by using the concept of invariance. The principal idea is that the form of physical laws must be invariant through a specified group of transformations. In classical non-relativistic mechanics, for example, the Newtonian laws and the distance between two objects do not depend on frames of reference related to each other by the so-called Galilean transformations. It is such invariance through a transformation group that makes physical laws and properties objective. The centrality and success of invariance principle in contemporary physics suggests that a similar approach may be useful in understanding the nature of evolutionary laws or equations. In this presentation I try to portray the philosophical puzzles about evolutionary principles as different facets of the same problem: the lack of a definite invariance principle in evolutionary theory. If this is correct, an effective approach would be to find an appropriate group of transformations through which evolutionary principles remain invariant. With this prospect, I explore what these transformations might look like in some simple cases of evolutionary genetics.

Quantifying form versus function in current evolutionary transitions

ROGER SANSOM (Texas A & M University, United States)

I take the form/function debate to be an empirical issue about the relative contribution to evolution from (a) the bias in the production of variation (due to probabilistic developmental constraints) and (b) the bias in elimination of variation (due to probabilistic natural selection). I develop a model that combines these two influences to predict a population's current path through morphospace to a local optimum and calculate the relative contribution of each bias to that path. Any such analysis is relative to the traits concerned, but there is no upper limit to how many traits can be included in an analysis and increasing that number should improve objectivity. The most important predictor in this model is a fact about the relationship between extant trait values in a population that is relatively easy to discover. The reason for its importance shall be discussed.

DS 1520

09:00 – 10:30

DS 1545

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

RANDOMIZED CONTROLLED TRIALS : THE PLACEBO PERSPECTIVEORGANIZER(S): **JEAN-FELIX GROSS** (Université Jean Moulin Lyon 3, France); **HAJIME FUJIMORI** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

Randomized Controlled Trials (RCTs) are generally considered as the most reliable form of trial design for assessing the efficacy of a medical intervention. A crucial component of such trials is the use of a placebo-control group. In this session, each presenter will challenge the sufficiency of our understanding of placebos and in turn, the way they are implemented in assessing medical treatments. Conservatively, it can be shown that placebos often fail to play the role they are intended to play in the logic of RCT experimentation. This is shown empirically and compensatory alterations to our concept of a placebo and statistical practices are proposed. More fundamentally, in violation of the dominant understanding of placebos, recent research into placebo effects shows they have distinct neurobiological underpinnings and that they can be produced without deception. This raises the possibility that rather than being a sham treatment suitable for control, the (so-called) placebo effect may be a legitimate treatment in and of itself. Accordingly, it would be inappropriate to regard treatments that are especially effective at harnessing such effects (e.g. acupuncture) as ineffective rather than a legitimate treatment in its own right.

Why most sugar pills are not placebos**BENNETT HOLMAN** (University of California, Irvine, United States)

The standard philosophical definition of placebos offered by Grünbaum is incompatible with the experimental role they must play in randomized clinical trials as articulated by Cartwright. I offer a modified account of placebos that respects this role and clarifies why many current medical trials fail to warrant the conclusions they are typically seen as yielding. I then consider recent changes to guidelines for reporting medical trials and show that pessimism over parsing out the cause “unblinding” is premature. Specifically, using a trial of antidepressants, I show how more sophisticated statistical analyses can parse out the source of such effects and serve as an alternative to placebo control.

Placebo effect and randomized controlled trials on acupuncture**WENBO LIANG** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

In this talk I consider the placebo effect concept as it has been employed by a large quantity of randomized controlled trials (RCTs) in clinic studies. After reviewing the history of RCTs and its application to acupuncture studies, I argue that applying RCTs to acupuncture requires a double evaluation, both of the standards of RCTs and of traditional Chinese medicine, rather than a simple confirmation via RCTs. I suggest that the abstract debates about placebo effect should be set aside, a more practical question is how can acupuncture leads to successful treatments with “specific effects” in the framework of RCTs.

Do we learn from history?**JEAN-FELIX GROSS** (Université Jean Moulin Lyon 3, France)

The standard history of the development of the placebo traces the use of placebos from the Bible through its employment in modern medical trials. This narrative is repeated not just in the work of English-speaking authors (e.g. Kaptchuk and Shapiro), but in French-speaking authors as well (e.g. Lemoine, Maire and Boussageon). I will argue that this uniformity in historical accounts stresses a dated vision of the concept of a placebo. Specifically, the standard history paints a placebo as an agent of suggestion, deception with poor biological grounding. In contrast, recent research has showed (e.g. Benedetti, Kaptchuk) that placebos can trigger very specific neurobiological pathways and in some cases (e.g. analgesia) that the effect can be produced without deception. The ability to evoke such a response in absence of deception would seem to be a troubling case to fit into our standard notion of placebo effects. However, I will argue that this impulse to incorporate such diverse phenomena under the umbrella of “placebo” unintentionally reifies a multifarious concept under a single label and thus inhibits research by demanding a single unified account for a diverse set of neuro-pharmacological phenomena.

DS M220

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

BOUNDARIES AND LEVELS OF BIOLOGICAL ORGANIZATION (1)ORGANIZER(S): **JON UMEREZ** (University of the Basque Country, Spain)

This double session will discuss the notion of biological organization from a system-theoretical perspective. In particular it will focus on its intrinsic hierarchical dimension, and on the role organization plays in the understanding of the transition from pre-biotic to minimal living systems and of the evolution towards more complex forms of biological, cognitive and ecological systems. More specifically, it will also address issues regarding individuality and autonomy at cellular and multicellular levels, from developmental and ecological perspectives as well as from genetic and evolutionary ones. Formation of boundaries at prebiotic scenarios and complex interactions at individual versus environment interfaces are also dealt with. The conceptual framework involves clarification of such general concepts as those of organization or level in terms of constraints, the characterization of regulation at its minimal instances or the assessment of diverse attempts to naturalize teleology. The double session is divided into two parts: a more general and conceptual one first, followed by another more specific and field centered.

From levels of organization to the organization of levels

MAEL MONTÉVIL (Université Paris Diderot - Paris 7, France); **MATTEO MOSSIO** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

We propose a theoretical and formal way to account for the various levels of organization that biological systems may realize. Our key assumption is that levels of organization are to be understood as specific networks of interdependences among the functional constituents. More precisely, we will rely on the notion of organizational closure, which refers to the mutual construction and stabilization of constituents playing the role of constraints within the system. A level of biological organization, we will argue, is a level of closure of constraints. With this characterization in hand, we will first discuss those situations in which different levels of organization can be distinguished, and hierarchically articulated, by relying on sharp discontinuities. In particular, this is the case of cells within multicellular organisms. We will then focus on those more complex cases in which the description of a level of organization requires appealing to the notion of “tendency to closure”, which aims to deal with the qualitative notion of level of organization by quantitative means. In particular, the tendency to closure involves a quantitative measure of functional interdependences at the relevant spatial scale at which constraints operate. We conclude with a preliminary discussion of the spatiotemporal conditions (in particular: the dependence on large space scale and small time scale) that enable the coherence of organisms realizing high levels of organization (e.g. mammals).

Regulation in biological systems

LEONARDO BICH (Instituto de Filosofía y Ciencias de la Complejidad, Chile); **ALVARO MORENO** (University of the Basque Country, Spain)

The appeal to the notion of regulation is widespread in biology. This property is usually ascribed to a variety of mechanisms and behaviours involved in living systems' responses to perturbations. Yet, the meaning of this notion is left somehow vague, very dissimilar types of phenomena are gathered under this label, and its relationship with akin concepts, such as control, homeostasis, robustness, and feedback is hardly stated in clear terms. To contribute to a deeper understanding of this notion, we will propose an organisational account of regulation by focusing on the mechanisms underlying compensations for perturbations in minimal living systems. In the first place, we will analyse different forms of control in the cell, and how they contribute to the maintenance of a biological organization. In the second place we will analyse how basic biological organisation can recruit forms of control to viably compensate to internal or external perturbations. It does so in two main ways: through holistic responses as networks or by means of the action of specific subsystems dedicated to handle perturbations. On this basis we will distinguish between two different classes of responses, respectively: dynamical stability and regulation. We will describe the limits of stability as an adaptive response, and we will provide a definition and a minimal set of organizational requirements for regulation, by pointing out the differences with similar concepts such as feedback, robustness and homeostasis. Finally, we will discuss the importance of the invention of regulation for the evolution in complexity in biological systems.

Teleology and biology: A scientific alternative to naturalization

NICOLE PERRET (École Normale Supérieure, Centre Cavailles, France)

In this paper we address the problem of teleological language in biology. In particular, we explore a scientific alternative to what is generally known as the solution of naturalization that consist in deriving teleology from efficient causation. We first take into account some classical attempts of naturalization in order to show their weaknesses and problems. Above all we analyze three ways of naturalization: the naturalization of teleology by the process of evolution, the reduction of teleology to fundamental matter by the notion of genetic program and the naturalization of teleology by its role in a proper organized system. We point out the fact that, in these solutions, teleology is never completely derived from efficient causation. On the contrary, some teleological notion seems always added as a special theoretical condition, hidden under other concepts. However these concepts are derived from a teleological logic. In order to overcome this problem, we suggest an alternative way that consist in legitimate this addition in a scientific sense as a constitutive condition. Starting from a brief analysis of the Kantian third critique, we explore the possibility of a constitutive place for teleology, in a peculiar different sense than a simple heuristic usage. We analyze some analogies with the conceptualization of causes in physics and we finally detail a naturalistic usage of teleology as a constitutive principle.

DS M280

09:00 - 10:30

INDIVIDUAL PAPERS

TECHNOLOGY, CONSTRAINTS, AND EXAPTATION

Two kinds of exaptation: Structures and functions in an extended taxonomy of fitness

TELMO PIEVANI (Università degli Studi di Padova, Italy); **ANDREA PARRAVICINI** (Università degli Studi di Padova, Italy)

Palaeontologists Stephen J. Gould and Elisabeth Vrba introduced the term “exaptation” to improve and enlarge the scientific language available to researchers studying the evolution of any useful character, instead of calling it an “adaptation” by default. Exaptation is neither a “saltationist” nor an “anti-Darwinian” concept and, since 1982, has been adopted by many researchers in evolutionary and molecular biology. In our talk, we firstly analyze the meaning of the term “exaptation” and its possible operationalization, in order to test “adaptive vs. exaptive” evolutionary hypotheses. Then, we differentiate two kinds of exaptation: 1) functional shift, i.e. the re-use by natural selection of a structure with previously different functions; 2) functional co-optation from non-adaptive structures (“spandrels”). Furthermore, we stress the importance of the exaptive mechanisms in order to philosophically rethink the evolutionary relationships between structures and functions. The benefits of an “extended taxonomy of fitness” emerge today in different studies, from the research in metabolic systems to the research in human evolution (i.e. language evolution within a mosaic evolution model).

Patented technology as a model system for cultural evolution

MARK BEDAU (Reed College, United States)

I argue that patented technology promises to be a good model system for the study of cultural evolution. My argument has three steps. First, from recent discussion I enumerate the main epistemic benefits of model organisms for biology. Second, I argue that analogous model systems for cultural evolution would provide analogous epistemic benefits, with one difference. The third step is to show that patented technology has all the hallmarks of a good model system for the study of cultural evolution. Published patent records provide clean and accurate data about every patented invention, including textual descriptions of the nature of the invention (title, abstract, and claims), the time it originated (filing and issue date), its “prior art” (citations to prior patents), and much more. Contemporary language-processing and machine-learning techniques enable one to extract each trait of each patent and to reconstruct the entire genealogy of each patented invention, and then to track how each trait flows through down lineage. Since patented inventions typically cite many prior patents, the genealogy of patented inventions is multi-parental (or “reticulated”). Highly multi-parental lineages are an important hallmark of cultural versus biological evolution, and patented technology provides an especially clean and crisp window into massive multi-parental trait flow in the population of all patented technologies. One important epistemic difference from model biological organisms is that model cultural systems lack the epistemic benefits that come only from experiments, for the study of actual cultural populations is empirically grounded in observations rather than experimental manipulations. Nevertheless, detailed and precisely controlled observations in masses of data from real cultural populations disclose many characteristics of multi-parental evolution that can be extrapolated to other multi-parental cultural populations, as patented technology shows.

Biological constraints do not entail cognitive closure

MICHAEL VLERICK (University of Johannesburg, South Africa)

From the premise that our biology imposes cognitive constraints on our epistemic activities, a series of prominent authors – most notably Fodor, Chomsky and McGinn – have argued that we are cognitively closed to certain aspects and properties of the world. Cognitive constraints, they argue, entail cognitive closure. I argue that this is not the case. More precisely, I detect two unwarranted conflation at the core of arguments deriving closure from constraints. The first is a conflation of what I will refer to as “representation” and “object of representation”. The second confuses the cognitive scope of the assisted mind for that of the unassisted mind. Cognitive closure, I conclude, cannot be established from pointing out the (uncontroversial) existence of cognitive constraints.

DS M320

09:00 – 10:30

INDIVIDUAL PAPERS

INTERDISCIPLINARY PERSPECTIVES ON HUMAN NATURE

Social studies of science meet development: DOHaD and medicalization

FABRIZIO GUERRERO MC MANUS (Universidad Nacional Autónoma de México, Mexico)

Within the myriad of topics discussed in the philosophy, history and sociology of medicine, certainly the concepts of “health” and “disease” are the most controversial. On the one hand, realists have attempted to defend robust, transcultural and objective notions of “health” and “disease” while constructivists have claimed that by necessity these notions are always inscribed in regimes of Power and Surveillance. Nevertheless, a new developmental approach to these notions -the so called Developmental Origins of Health and Disease (DOHaD)- seems to offer a different framework in which plasticity and cultural embeddedness can be fully recognized without relinquishing the goal of seeking an objective definition of these concepts. Be this as it may, the aim of this talk is to show that even if we accept that DOHaD admits a less dualistic view on human nature, it is still prone to serve as a tool for medicalizing human beings and, thus, it shows that the central arguments of sociologists do not require a commitment to an antirealist position of the structuredness of the body but only a recognition of how bodies can be inscribed by social practices.

Traditions of research on the definition of contagious disease

RUY JOSE HENRIQUEZ GARRIDO (Universidad Complutense de Madrid, Spain)

The conception of contagious disease that Girolamo Fracastoro provides in his work *De contagione et contagiosis morbis* (1546), marks the origin of modern epidemiology and microbiology. This conception puts into play the Galenic and Aristotelian traditions of research, faced with its own conceptual limitations of the growing mechanistic thought of the time. According to Fracastoro, epidemic diseases spread by invisible living germs called *seminaria* (seedbed), begotten by corrupted humours. Fracastoro resorted to the old notions of “sympathy” and “antipathy” to respond to questions about how *seminaria* is transmitted from one body to another, and what is the specificity that limits its transmission to certain species and organs. Like Galileo and Descartes, Fracastoro tries to establish a dialogue in the field of medicine between the Aristotelian vitalism and the modern mechanistic perspective. The purpose of this paper is to highlight the ideological, theoretical and conceptual assumptions, both philosophical and scientific, assumed by Fracastoro with regard to the problem of contagion.

Phenotypic regeneration and the inheritance of acquired characteristics: Obesity and type II diabetes mellitus as exemplars

EDWARD ARCHER (University of Alabama at Birmingham, United States)

While inheritance and evolution affect both physiologic and social outcomes (e.g., health and wealth), the prevailing biomedical and social scientific paradigms have limited explanatory or predictive power with respect to global epidemiologic trends and phenotypic evolution over the past century (e.g., increases in height, body

mass, precocious menarche, and chronic non-communicable diseases). I posit that by defining inheritance and evolution in strictly gene-centric terms or abstract conceptualizations (e.g., wealth, status), these frameworks impede interdisciplinary collaboration and effective research by imposing a limited, speculative dichotomy (nature vs. nurture) on non-dichotomous, complex, non-linear concrete processes. If science is the pursuit of lawful relations, then progress necessitates dissent when current paradigms fail to explain extant evidence. My recent work demonstrates that physiologic vectors of inheritance (e.g., maternal effects) lead to phenotypic evolution and have significant consequences for health and disease. Importantly, this work suggests that the “missing heritability” of the prevailing paradigms will not be found in the genome/epigenome or abstract conceptualizations (e.g., social status). As such, scientific progress necessitates a framework of inheritance and evolution that integrates: 1) the socio-environmental influences on ancestral behavioral and physiologic phenotypes, and 2) the inheritance of acquired characteristics and subsequent phenotypic evolution. This paper presents conceptual and empirical support for a heterodox framework that defines inheritance and evolution as the regeneration of ancestral phenotypes and social histories in present and future offspring. This conceptualization subsumes and overcomes the significant limitations of the hyper-reductionist DNA-centric paradigm and delineates mechanistic pathways that bridge sociologic conceptualizations (e.g., wealth) with biologic realities and relevant outcomes (e.g., health).

INDIVIDUAL PAPERS

EXPLANATION, COMPLEXITY, AND FUNCTION

Forms of explanation in genetics and embryology around 1900

ROBERT MEUNIER (Universität Kassel, Germany)

Genetics did not integrate well with experimental embryology around 1900, despite the fact that they were both concerned with reproduction. This can be explained by showing that the fields were governed by different epistemic modes, which were embodied in different types of experiments and yielded different types of explanation. I distinguish decomposition and differentiating modes of acting and reasoning in biology. One renders the organism as composed of parts, the other as different from other organisms. Accordingly, features of organisms appear as parts of wholes in the decomposition mode, whereas they figure as differences (“characters”) among kinds in the differentiating mode. These modes yield different forms of causal reasoning. In philosophical discussions of causation a distinction is made between the physical production of an event and the dependence relation between cause and effect. I argue that this distinction maps on the two modes in the following way. Under a decomposition interpretation causes are identified through a decomposition of a causal situation. Parts of a causal process are rendered as material agents in physical interaction with other parts. This interpretation corresponds to production theories of causation. In a differentiating mode of reasoning

causes are derived from the comparison of causal situations. Thus causal reasoning as described by dependence theories can be reconstructed as derived from classificatory reasoning in which causes and effects are “characteristics” of contrasted kinds of causal situations. It can be shown that in genetics characters and genes are first differential properties of organisms and gametes before they are seen as causally dependent variables. In embryology, instead, features of organisms are construed as parts, which are the outcome of growth processes. The causation of parts is investigated by distinguishing different subparts within an organism and following their productive interaction over time.

Complexity, organization and life in the philosophy of Sir Kenelm Digby

DEREK SKILLINGS (City University of New York, United States)

One of the central themes of the history of early-modern philosophy and science is the rise of mechanical philosophy and the fall of Aristotelian views of the natural world. In this paper I look at the philosophy of Sir Kenelm Digby, a now mostly obscure figure who wrote early on in the transition to mechanical philosophy. Digby was a thorough-going mechanist in respect to matter and the physical world. He attempted to wed the emerging mechanical and corpuscular philosophies to the Aristotelian notion of composite substances in his most famous philosophical work, the 1644 *Two Treatises*. It is Digby’s views on living creatures and machines that concern me here, specifically the role of organization in delimiting the types of things in the world. Though he has not been very well appreciated, I hope to show that his views on life were quite insightful and bear some striking similarities to modern-day theories of the organism.

A better way to be a function pluralist

JUSTIN GARSON (City University of New York, United States)

I advocate a new version of function pluralism, which I call “within-discipline pluralism.” I will contrast it with the reigning view, which I call “between-discipline pluralism.” Pluralism, at the most general level, holds that there is more than one correct explication of “biological function.” However, many philosophers also maintain, I think incorrectly, that different theories of function are appropriate to different biological disciplines. For example, one prominent view is that the selected effects theory (SE) only reflects usage in evolutionary biology; in genetics, ecology, neuroscience, and so on, the causal role theory (CR) reigns supreme (unless those disciplines pose specifically evolutionary questions). This is a version of “between-discipline pluralism,” as it emphasizes conceptual variation between disciplines. This version of between-discipline pluralism (according to which SE is appropriate to evolutionary biology, and CR otherwise) is mistaken, however, for the following reason. SE holds that the function of a trait is just the effect it was selected for. It is natural to assume that “selection” refers only to natural selection operating over an evolutionary time scale, and hence, that SE is only relevant when evolutionary questions are being posed. However, SE theorists have typically maintained that there are many different kinds of function bestowing “selection” processes, some of which operate over ontogenetic time scales. These

DS M340

09:00 – 10:30

DS M440

09:00 – 10:30

include learning by trial-and-error, antibody selection, and even neural selection, all of which take place over the lifetime of the individual. So, there is no a priori reason to restrict the applicability of SE to evolutionary biology. SE functions are applicable whenever scientists use “function” in the “why-is-it-there” sense. As an alternative, I advocate “within-discipline pluralism.” It is a form of pluralism that recognizes how different concepts of function coexist within the same disciplines. I will illustrate this sort of pluralism with an example from neuroscience.

INDIVIDUAL PAPERS

SPECIES OF CONSEQUENCE? MULTIPLE PERSPECTIVES**Animals of consequence: Natural symbols****EMILY HUTCHESON** (Florida State University, United States)

Are some non-human animals more consequential than others? Or, on the other hand, are they merely tools within the human toolbox which man uses to subdue and lessen the grandeur of nature? The first portion of the paper explores how nature writers - namely David Thoreau and Aldo Leopold - utilized animals to portray their thoughts on the distinction between wild and unwild- things worth protecting and things worth altering. Most authors who engaged with the idea of nature writing in previous eras conceived of animals as consequential beings, symbols of our evolutionary history and of the ideal communion with nature. Synecdochically, Thoreau in *Walden* and Leopold in *Sand County Almanac* repeatedly feature animals, both wild and domestic, to symbolize quintessential nature. Far from being the only authors to do so, their not identical literary usage of “animals of consequence” highlights their personal philosophies of nature, wildness, and the man to nature relationship. Conversely, more recent nature-writers, even those who esteem to follow Thoreauvian values, utilize animals only as objects of nature-subjugation. The optimal purpose of Nature, and the human position in relation to Nature in the American mind can be clearly found in the author’s position on animals, and reflects the preservation versus management philosophies of the authors and the time periods. This paper explores the historic precedent in nature-writing and biological research - namely genetics and neuroscience - through which some species are deemed consequential and others considered to be useless. The semantics of species - and speciation - combined with the capricious tendencies of some historical actors pair to create an interesting story of how we humans have valued and devalued some creatures to the point of no return.

Contrasting approaches in mitochondrial evolution: Implications for the tree of life debate**THOMAS BONNIN** (University of Exeter, United Kingdom)

Through this talk I will reflect upon a controversy in evolutionary biology: the origin of mitochondria. This ongoing debate has been polarized between two camps. On one side, the proponents of the “hydrogen hypothesis” led by William Martin, opposing Thomas Cavalier-Smith and his “phagotrophic hypothesis” on the

other. The discussion of the origin of this organelle is not an isolated scientific theory. Instead, both camps have their scenario embedded in an interdependent set of stories they defend, that browse from the origin of life to the origin of eukaryotes. These ensembles, to which the origin of mitochondria comes as a conclusion, are supported by different kinds of data, common data being interpreted differently and incompatible assumptions. Philosophy of biology discussions could also be influenced by one of the camp, as is the case with the numerous interventions of William Martin and colleagues on the tree of life debate. Taking a close look at the scientific and philosophical discussions stemming from this controversy, my work tries to demarcate and contrast both camps’ philosophical assumptions. This will allow us to determine on which philosophical ground both positions are built in the “evolution of mitochondria” scenario and why they have been so far incompatible. This will also help us achieving a reappraisal of Cavalier-Smith’s mostly neglected work in the discussions of the tree of life topic, and see what his position can bring to the current discussions.

Species, scientific realism, and historical essences**MARION GODMAN** (Cambridge University, United Kingdom)

Natural kinds are thought to be an important asset for those who want to defend scientific realism in the special science domains (e.g. Kornblith 1991, Boyd 1991; Khalidi 2012). Essential natures are less in vogue. Many scientific realists want to dispense of essentialist requirements for natural kinds, while only a few dissidents maintain that abandoning essential natures might actually undermine scientific realism (Devitt 2005). The key case for the debate is biological species. While a dominant view holds that species might be natural kinds but lack essential natures (e.g. Sober 1980; Dupré 1993), some have argued that species do in fact have historical rather than intrinsic essential natures (Griffiths 1999; Millikan 1999). However replacing intrinsic essences with historical essences might come at a price since historical essences are relational. As such it has been suggested that they fail to do the epistemic and ontological work traditionally assigned to intrinsic essences and which is required for a scientific realism (Okasha 2002; Devitt 2008). This paper tries to counter this pessimism with respect to historical essences by arguing that they do have the right epistemic and ontological credentials that can underwrite defences of scientific realism. I begin by motivating why natural kinds with essential natures should matter for those wishing to defend a scientific realism. This also leads to specifying two basic jobs for essential natures: one which has to do with providing individuation criteria of kinds and the other for offering causal explanations of projectable properties. This sets the scene for asking: do species have any properties that can perform these roles? I argue that while the intrinsic essentialist strategy falls short with respect to both individuating and causally explaining kinds, the historical essentialist strategy is fit for task. I conclude that historical essential natures of natural kinds like species can support a scientific realism.

DS M460

09:00 – 10:30

INDIVIDUAL PAPERS

FREE WILL, EPISTEMIC LEVERS AND NORMATIVE IMPLICATIONS IN EVOLUTIONARY PSYCHOLOGY**Epistemic levers: Biological levers and knowledge in nonhuman species****GUILLAUME BEAULAC** (Yale University, United States); **FRÉDÉRIC-ISMAËL BANVILLE** (University of Western Ontario, Canada)

We provide a biologically-informed argument for the existence and philosophical relevance of a concept of knowledge in nonhuman species. Then, we show that such knowledge and the cognitive systems underpinning it should be used to better understand what human knowledge is. A well-known strand of arguments for the relevance of a notion of animal knowledge rests on demonstrating the explanatory usefulness of such a concept (e.g., Kornblith 2002). These arguments only support the claim that attributing knowledge to non-human animals may prove useful when our explanatory target is non-human animal behavior. They are at pains to push the thesis much further than the idea of a heuristically useful attribution of knowledge-like states to animals. One way to support the stronger claim that, not only do animals have knowledge, but that a fully naturalized epistemology should take into account the type of knowledge exhibited by nonhuman minds as well as specifically human forms of knowledge is to approach animal knowledge as a biological lever. Barker (2007) defines biological (or behavioral) levers as biological features playing a crucial role in the regulation of certain processes, and especially behavior. We begin with a general characterization of biological levers, and show how this notion can provide a solid basis to explain widespread epistemic capacities in the animal realm, such as those embodied by some danger detection mechanisms. These mechanisms rely on limited sets of cues to regulate the animals behavior. An analysis of this case in terms of biologically adequate truth-tracking capacities (similar to Millikan's approach) links this kind of capacities to knowledge as it is found in the human species. We then discuss the implications of this argument for naturalized approaches to knowledge, especially with regards to how the idea that animal knowledge can be seen as evolutionary scaffolding for human knowledge.

Clarifying contradictory results in free will belief measurements**MATTHEW SMITHDEAL** (University of British Columbia, Canada)

Recent work measuring individuals' intuitions concerning free will, determinism, and related beliefs finds increasingly complex and contradictory results. Some of these results seem to support the notion that individuals have compatibilist intuitions, while other results seem to support the notion that individuals have incompatibilist intuitions. Often these contradictory results stem from the exact same studies. One might reasonably expect that individuals construct beliefs regarding these subjects which fit together in at least a coherent manner; however, these studies show that conflicting beliefs are being held at the same time. This paper suggests that we need to draw a distinction between one's belief in personal free will versus one's belief in free will generally and that doing so will enable us to make better sense of the complexities and contradictions in individuals'

beliefs concerning free will and determinism. To this end, we should regard belief in personal free will as an ungrounded belief, where one holds a belief in personal free will as a result of experiencing oneself performing actions in a certain manner.

Historical functions and their normative implications**LOUISE DAOUST** (University of Pennsylvania, United States)

Experimental psychologists, such as those who adopt computational theories of mind, often appeal to ahistorical conceptions of function in their scientific explanations. In this paper, I argue that, in certain cases, treatments that privilege historical functions ought to be more systematically prioritized over those that privilege ahistorical functions. Use of historical functions in cognitive science is sometimes defended by appeal to explanatory power. These defences are often successful, but in certain cases indecisive, or insufficient to justify appeal to historical function. I show that historical functions provide not only a reasonable starting point for understanding a mechanism and how it works, they are also critical to our conceptions of how well a particular adaptation functions. I illustrate the relevant contrast in normative consequences by exploring the case of color vision. Which conception of function one employs to think about color vision entails significant consequences for the degree of accuracy one can associate with human color vision. I conclude by briefly exploring how this lesson applies to cognitive science more broadly.

DS R340

09:00 – 10:30

INDIVIDUAL PAPERS

EPISTEMOLOGY, OBJECTIVITY AND MARKETING IN BIOMEDICINE**Applying epistemology to help bridge the translational gap****JESSICA BOLKER** (University of New Hampshire, United States)

While epistemological perspectives can't answer biological questions, they can clarify questions, identify assumptions, and examine how the practices of scientific research shape its direction and findings. As in biology itself, however, global abstractions about how things might work have limited value: we learn more by studying particulars. In this talk, I focus on the intersection of epistemology and translational research (that is, research aimed at closing the gap between basic biomedical science and its clinical application). I point out a few key epistemological issues that arise in the domain of translational research, some ways philosophy might begin to address them, and how doing so could help bridge the "translational gap" between bench and bedside. One set of questions centers on representation and modeling, particularly the ways animal models and clinical trial participants represent the diseases and patient populations they're used to study. A second concern is the epistemological ramifications of current biomedical research practices, some of which may ultimately impede translation. The most effective way to address such issues is for philosophers and scientists to work together; both can contribute to bridging the gap, and both disciplines stand to benefit.

The objectivity of clinical trials outcomes

ROGER STANEV** (University of Ottawa, Canada)

Composite outcomes, wherein different outcome measures are combined, are becoming frequent in clinical trials. They are used to increase statistical power by obtaining more outcome events. Advocates argue their appropriate use is more patient relevant than single endpoints (e.g. death), while reducing sample size and cost requirements, thus improving trial efficiency and availability of new treatments. Critics, on the other hand, argue their use is problematic, since components are often unreasonably combined, inconsistently defined, and inadequately reported. Here, I examine common use of composite outcomes in cardiovascular trials and how composite results can be misleading, threatening the objectivity of the trial, particularly when treatment effects vary across components making the net effect on the composite difficult to interpret.

Profitable little pills: Marketing biological sex and gender

KATE GRAUVOGEL (Indiana University Bloomington, United States)

Hormone therapies are a popular treatment option marketed towards individuals for problems associated with biological sex, such as menopause. Pharmaceutical companies, however, often cash in on hormone treatment by attempting to convince doctors, patients, and non-patient consumers that such products are necessary to maintain good health. This paper examines the relationship between pharmaceutical companies and consumers, with an eye toward the effect that implicit biases about gender, sex, and medicine may have upon treatment options. Joining larger, ongoing debates about the roles of biological sex and gender in medicine as well as the characterization of health as the absence of disease, I suggest that the marketing techniques implemented by pharmaceutical companies have skewed perceptions about gender and biological sex, suggesting a symbiotic relationship where one does not necessarily exist. Conversely, health and disease are often depicted as extremes on a spectrum instead of as having a symbiotic relationship. Rethinking these relationships might lead to improved treatment outcomes.

ORGANIZED SESSION / STANDARD TALKS

PROBABILITY AND CHANCE IN BIOLOGY

Organizer(s): **JOEL VELASCO** (Texas Tech University, United States)

Statements about probability and chance occur all throughout the biological sciences and philosophers have long been interested in how to interpret such statements. As our empirical knowledge grows, the complexity of our models grow and philosophical understanding becomes more difficult and more important at the same time. Sometimes, these questions are approached by detailed examination of the science itself, other times with a focus on general considerations about the nature of probability. Often both. In this symposium, the three presenters will interact by approaching similar questions from different places.

First, **Charles Pence** will discuss recent work in biology on adaptive population dynamics and how these result fit within his account of fitness (co-authored with **Grant Ramsey**). Arguing against any conception of individual fitness, **Marshall Abrams** will defend his own account of type fitness by defining it in terms of a particular interpretation of probability, a “complex causal structure” interpretation. **Joel Velasco** will then step back and argue that we should not be thinking about probabilities in biology generically, but rather, that in different sub-disciplines and in different contexts even within the same problem, the role of probability statements is quite different.

Adaptive dynamics, chaos, chance, and fitness

CHARLES PENCE (Louisiana State University, United States)

In recent work, Grant Ramsey and I (2013) defended a picture of individual fitness which, while drawing on the same intuitions as the propensity interpretation of fitness (PIF), manages to resolve many of the counterexamples to that model which philosophers have offered in the intervening thirty years since its proposal. A crucial role in that argument was played by results from mathematical population modeling, particularly from a research tradition known as adaptive dynamics. While adaptive dynamics offered the mathematical resources necessary to resolve several problems with the PIF, it also offers more than this – in particular, it provides a broader formalism which we can use to think about the trajectory of evolving populations over time. In another recent paper, Michael Doebeli and Iaroslav Ispolatov (2014) demonstrate a surprising result: using models very similar to ours, they derive that, as the dimensionality of the evolving system increases, the probability of chaotic behavior goes very rapidly to 1. They argue that on the basis of these results, we should doubt that the current phenotypic state of a population can ever “be understood as the result of an equilibrium or optimisation process” (2014, p.1369). In this talk, I will explore the intersection of these two sets of results. If adaptive dynamics does offer us a fruitful way to understand individual fitness, what is the impact on that model of these results concerning long-term chaos? What does it say about our understanding of the sense in which individual fitness, and by extension, natural selection, is probabilistic? Do these results contradict our earlier claim that adaptive dynamics can provide stable values for individual fitnesses? Things are not, I will argue, that dire. But they do necessitate a rethink in the conceptual role of fitness and its close cousin, the principle of natural selection.

Resolving puzzles about types and tokens in evolution with new probability concepts

MARSHALL ABRAMS (University of Alabama at Birmingham, United States)

Philosophers concerned with whether natural selection is a cause typically assume that if fitness differences are in some sense causal, they must be defined as “token fitnesses” in terms of propensities of outcomes for token organisms (lineages, etc.) in particular circumstances. On the view that natural selection concerns heritable biological types (Lewontin 1970; Godfrey-Smith 2009), advocates of this view typically assume that fitnesses of types (“type fitnesses”) are averages of token fitnesses of those organisms actually in a population. That this is the received view despite significant, unaddressed challenges known for several years (Abrams 2006, 2012,

DS R515

09:00 – 10:30

2014; Ariew & Ernst 2009; Sober 1984, 2001, 2013) may be due the lack of an alternative, causal conception of type fitness. The goal of this talk is to describe such an alternative—one that makes type fitnesses fundamental, and causal—by defining fitnesses in terms of a “complex causal structure” (CCS) interpretation of probability (Rosenthal 2010, 2012; Strevens 2011; Abrams 2012a,b). I treat recurrent realizations of heritable biological traits in a population and environment as defining a kind of causal process or device, with states of organisms and their environment as inputs, and instances of outcomes relevant to evolution as outputs. Such a device can realize CCS probabilities if it has the kind of internal structure underlying Strevens’ “microconstancy” or my “bubbliness”. I argue that biological populations are likely to generate such causal structure, and that other conditions for my “FFF mechanistic probability” are likely to be satisfied. Importantly, fitnesses defined in terms of these probabilities, though causal, attach to types rather than tokens or particular trials (Rosenthal 2010, 2012; Abrams 2012a,b). My strategy doesn’t require biologically questionable assumptions about physical properties, as Strevens’ (2003, 2008, 2011, 2013) discussions of evolutionary processes do.

A disunified account of objective probability in biology

JOEL VELASCO (Texas Tech University, United States)

I will be examining the use of probability as it appears in three different subdisciplines in biology. First, within phylogenetics where we use and infer molecular clocks and various rates of evolution, as well as make pronouncements about the likely age of various clades or fossils. Second, in ecology and evolution where models of foraging behavior and genetic drift are used to explain the distribution of traits in species. And third, in molecular biology where stochastic models of molecular movements and processes are used to explain stochastic gene expression and “noisy” development. Questions of interpretation have arisen in each of these cases and typically, questions focus on whether such probabilities must be subjective or can be understood in an objective way. I will argue that while some useful distinctions can be made, classifying any of these as “subjective” or “objective” can be misleading and is mostly unhelpful. While all three cases are different, each has some elements (different between the three) that are typical for “objective” claims about the world and all share some aspects typical of “subjective” (or much better, “epistemic”) interpretations. I will then use these cases as the basis for an argument that we are unlikely to be able to have a unified account of probability even in relatively narrow domains such as “explanatory models in biology”, much less a unified account across all of the sciences.

DS R520

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

NEW PERSPECTIVES ON BIOLOGICAL INFORMATION

Organizer(s): **BRETT CALCOTT**** (Arizona State University, United States); **KAROLA STOTZ** (Macquarie University, Australia)

The topic of biological information continues to captivate philosophers of biology. The aim of this session is to showcase new research in this area, specifically (though not necessarily limited to) research on genes and gene action. In the view of many philosophers, crucial advances have recently been made in our general understanding of sign use and of causation. How can these theoretical advances be exploited to deepen our understanding of information and its causal and functional role in biological systems?

What makes causal relationships in biology “informational” relationships?

KAROLA STOTZ (Macquarie University, Australia)

James Woodward has remarked that, “biologists tend to think of structures as carrying information when they are involved in causally specific relationships” (2010, 314). My collaborators and I agree, and think this needs documenting and explaining by analyzing key examples of biologists distinguishing information from non-information. One example is Crick’s use of the idea of information to state the Central Dogma and sequence hypothesis. Crick believed that three factors were involved in protein synthesis, “the flow of energy, the flow of matter, and the flow of information” (1958, 144). I will elucidate the epistemic payoff of introducing information in this context. Another example is the distinction sometimes drawn in developmental biology between “instructive” and “permissive” causes (Gilbert 2003). I will show how the distinction between informational and other causal processes does real explanatory work and how it flows naturally from the pre-existing concept of information. Previous attempts to do this have focused on the analogy between aspects of biology and signaling systems. I argue that the analogy between biological information and human signaling points to an objective property of causal structure, and that it is this structure that justifies picking out some causal processes as informational. The work presented constitutes an explication of the idea of information, which maintains intellectual continuity with a vernacular concept but is prepared to depart from the original concept when this serves the goal of understanding the distinctive nature of living systems.

Biological specificity and biological information

ARNAUD POCHEVILLE (University of Sydney, Australia)

In recent years a number of information theorists have constructed information theoretic measures of causal influence. In earlier work my collaborators and I have constructed such a measure designed to give a quantitative account of causal specificity. Here I give an overview of these measures and show how this apparatus can be used to analyse the linear or “informational” specificity between nucleic acids and their products, and also the specificity of regulatory RNAs. A different set of information theoretic tools have been used by biologists to analyse the stereochemical specificity between biomolecules. I examine the relationship between these two

projects. Amongst other connections, these two information-theoretic approaches to specificity are related by the fact that stereochemical specificity can be encoded and transmitted as linear specificity.

Crick information: In genomes and elsewhere

PAUL GRIFFITHS (Sydney University, Australia)

Francis Crick's "sequence hypothesis" proposed "that the specificity of a piece of nucleic acid is expressed solely by the sequence of its bases, and that this sequence is a (simple) code" (1958, 152). Crick was right. However, most gene products are not fully specified in this way. Instead, the specificity for a product is distributed between the original coding sequence, cis-regulatory sequences and trans-acting factors that bind to those regulatory sequences and to one another. In earlier work my collaborators and I have proposed an information-theoretic measure of specificity. I apply this measure to the sources of the "distributed specificity" for a gene product. This work gives a precise meaning to Francis Crick's insight that coding sequence contain the "information" that specifies their products, reveals that information in precisely the same sense can be found in gene regulatory mechanisms, and lets us trace some of the information contributed by those mechanisms back to its sources in environmental drivers of gene expression.

ORGANIZED SESSION / STANDARD TALKS

ROBUSTNESS AND EMERGENCE

Organizer(s): **MARTA BERTOLASO** (Università Campus Bio-Medico, Italy); **SILVIA CAIANIELLO** (Istituto per la storia del pensiero filosofico e scientifico moderno, Italy)

Robustness, the ability of a system to maintain its functions despite external and internal perturbations, is nowadays a key-concept in the study of biological systems. This property has in fact become the major "conceptual and theoretical bridge" (Csete Doyle 2002) linking sophisticated systems engineering and systems biology, both committed to a non-reductionist view of the dynamics of complex systems structured by (engineered or evolved) functional optimization. However, the epistemological and ontological implications of the robustness perspective on biological systems are still in need of further clarification. Main questions to be addressed: On what kind of regulatory dynamics does biological robustness rely? How should higher-level robustness be understood in causal terms? How far can robustness be considered an emergent property? Which is the relationship between self-organization and robustness? How has robustness evolved?

Emergence and robustness: Explainable novelty

SANDRA D. MITCHELL (University of Pittsburgh, United States)

The options for strategies of explanation, prediction and intervention have often been presented as a mutually exclusive dichotomy: emergence or reduction, predictability or non-predictability. Robustness in evolved,

complex biological systems exposes the poverty of this contrast. Protein function, for example, includes both predictable and unpredictable effects and explanations appeal necessarily to both lower-level and higher-level properties, as well as to causal factors in the often unexplicated context. As emergence has become a legitimate scientific category it has dropped the strictly epistemic characterization of "that which cannot be explained/predicted" to an ontological understanding of types of stable, higher-level properties that are explainable by the integration of top-down and bottom-up causal inferences.

Robustness and novelty: Contradictions or complementary features of complex systems

MANFRED LAUBICHLER (Arizona State University, United States); **GUIDO CANIGLIA** (Arizona State University, United States)

Where does novelty come from? The ability to innovate (i.e., to generate novel features or behaviors) is a defining characteristic of complex systems. Biological, technological, socioeconomic, political and cultural transformations all presuppose that at some point in time "novelties" occur. The big theoretical question is: Are there commonalities in the underlying processes generating novelty across domains? This talk will explore this question in the context of similar discussions about robustness, often seen as an antithesis to innovation. It will sketch a theoretical framework that (a) ascertains whether the putative commonalities in the origins of novelty in the biological and social domains help explain innovation in a way that goes beyond the metaphorical; (b) elucidates how a "theory of the origins of novelty" (or a less ambitious but still general explanatory framework) would advance an understanding of biological evolution, cultural evolution and technological change; and (c) identifies specific questions whose answer could advance the construction of a general framework for understanding the origins of novelty.

Robustness as organized heterogeneity

MARTA BERTOLASO (Università Campus Bio-Medico, Italy); **SILVIA CAIANIELLO** (Istituto per la storia del pensiero filosofico e scientifico moderno, Italy)

Robustness is currently one of the most powerful cross-disciplinary concepts relating both living and engineering systems and their shared design principles. We investigate the status of biological robustness at the organismal level as an emergent property, for which specific topological properties of regulatory networks are a necessary, but not sufficient condition of possibility. Paradigmatic for this discussion is the biology of cancer, in which many of the conditions for organismal robustness are disrupted, in such a way that a different kind of robustness, the one of cancer, seems to take its place. Cancer, in fact, enacts the disruption of the hierarchical regulatory control of the biological organization, whose outcome is the high degree of phenotypic heterogeneity of tumor cells. The outcome of such disruption is the uncoupling of cell proliferation and differentiation, which accounts for the failure of the veritable systemic control at the organismal level. The substantial difference between the "unorganized heterogeneity" exhibited by cancer cells and the "organized dynamic functional heterogeneity" of healthy organisms lays therefore in the impairment of the dynamics of co-determination that characterizes the relational ontology of levels in healthy organisms, a dynamics which involves different types of causality and ensures the

DS R525

09:00 – 10:30

robustness of macrostates of functional integration. Understanding regulatory dynamics in relational terms, i.e. in terms of relationships among elements that are epistemologically and ontologically dependent on their context, offers the conceptual tools to contrast the pathological robustness of cancer with the veritable robustness that allows biological systems to orchestrate stability and novelty in face of perturbations.

10:30 – 11:00

COFFEE BREAK

DS 1420

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

ARE YOU A ROMANTIC OR KILLJOY? (1) ISSUES IN COMPARATIVE PSYCHOLOGYOrganizer(s): **RACHAEL BROWN** (Macquarie University, Australia)

Comparative psychology has been disparagingly described by some as a field of “romantics” and “killjoys”; some researchers being keen to attribute human-like mental states and cognition to non-human animals, and others arguing that to do so is anthropocentrism. This session brings together five researchers working in the philosophy of comparative psychology offering different perspectives on “romantic” and “killjoy” explanations and how to arbitrate between them. Each of the researchers will present an aspect of their most recent work followed by an open panel discussion.

Even a fish could do it: Outgroup species and killjoy explanations**HAYLEY CLATTERBUCK** (University of Wisconsin-Madison, United States)

I examine a common dialectic in contemporary debates about the kinds and degrees of cognitive continuity between humans and our closest primate relatives. When great apes demonstrate behavior that, in humans, is caused by sophisticated, abstract reasoning, this is often (correctly) offered as evidence that the apes' behavior has the same underlying mental causes. One common response has been to show that outgroup species (e.g., fish or birds) demonstrate the same behavior, and this is taken to significantly undermine the claim that the apes' behavior resulted from human-like mental causes. I first examine a prima facie problem with this “killjoy” argument which is that given the close phylogenetic relationship between humans and apes, facts about human cognition should provide much stronger evidence about ape cognition than do facts about distant outgroup species. Then, I consider several possible justifications for the killjoy argument, concluding that such phylogenetic considerations alone do not yield decisive answers about continuity between humans and our closest living relatives, and they must be paired with substantive theories of the mental causes in question.

Field and lab: Different methods, different questions, and different answers**KRISTIN ANDREWS** (York University, Canada)

While animal minds are typically studied in controlled experimental situations such as a laboratory, zoo, or sanctuary, some cognition research is done with wild animals in a messier natural environment. The benefits and problems associated with each method have been much discussed. Laboratory settings allow for better controls for experiments, but lack ecological validity. In wild settings, experiments, if performed, have fewer controls, and much of the research is not experimental. However, wild animals enjoy a typical ecological and psychological environment. What hasn't been discussed as much is what sort of information is better gained in the lab and in the field. Appealing to my notion of folk expertise (Andrews 2009), methods in classical and cognitive ethology, and comparative cognition, I sketch a program that combines lab and field research that we can use to gain a better understanding of animal cognition. The proposed program is a modification of the methods we use with human animals in psychology and anthropology. I appeal to the methods in these fields, and especially in cross-cultural psychology, and apply the lessons learned from these fields to the research we do with other animals. Finally, I show how the current state of research on ape cognition that attempts to compare apes with human children fails to make an adequate comparison given the differences in subject pools and methods used with each group.

Romantics and killjoys on animal morality**SIMON FITZPATRICK** (John Carroll University, United States)

In recent years, there has been much philosophical and scientific interest in whether some non-human animal species are capable of moral reasoning or moral agency, with various “romantic” and “killjoy” positions being occupied—for instance, that some animals possess full-fledged moral capacity, that they possess the “evolutionary building blocks” or “precursors” to morality, but not quite the genuine article, and that nothing remotely resembling moral capacity can be found in non-humans. However, like many debates in the animal cognition literature, this one often seems to hang more on how the relevant terms are to be defined than on particular empirical details about animal behaviour. In particular, much ink has been spilt on what should count as “true” or “genuine” morality (or moral reasoning), with protagonists proposing quite different accounts. I defend the sceptical position that it is there is likely no defensible definition of “morality” that provides a principled distinction between “genuine” morality and something that falls short of it, and hence that much of the existing literature on animal morality has been on a fool's errand. I then make some suggestions about how the debate might be best re-situated. This includes making more precise the question of whether animals possess a mechanism for internalizing and applying social norms.

DS 1520

11:00–12:30

ORGANIZED SESSION / DIVERSE FORMAT

NATURAL EXPERIMENTSOrganizer(s): **CARLOS MARISCAL** (Dalhousie University, Canada); **S. ANDREW INKPEN** (Harvard University, United States)

Participant(s):

CARLOS MARISCAL (Dalhousie University, Canada)**S. ANDREW INKPEN** (Harvard University, United States)**YOEL STUART** (University of Texas, Austin, United States)**ADRIAN CURRIE** (University of Calgary, Canada)

For understandable reasons, the laboratory experiment—in particular the replicated laboratory experiment in which the investigator intervenes and manipulates variables—has become a hallmark of the modern scientific method. It has been a powerful tool of inquiry for many modern sciences and is directly responsible for many important discoveries and technologies. But in other sciences, such as evolutionary biology and ecology, manipulative experiments are often impossible, impractical, would be ethically questionable to perform, or are simply misleading with regard to the questions being asked. In these sciences, many investigators have drawn attention to the importance of so-called “natural” experiments, in which scientists position themselves to observe the outcome of processes like economic meltdowns, hurricanes, or mass extinctions. This session will explore natural experiments from a variety of historical, conceptual, and empirical approaches. The speakers are two philosophers, a historian, and a biologist.

ORGANIZED SESSION / STANDARD TALKS

WHERE BIOLOGY MEETS ANTHROPOLOGY (1): PHILOSOPHICAL DISCUSSIONSOrganizer(s): **JAY ODENBAUGH** (Lewis & Clark College, United States)

Human behavioral ecologists and anthropologists seek evolutionarily grounded explanations of human social behaviors on the expectation that such behaviors will tend to optimize fitness. They've been “successful” in the sense that many current and recent social behaviors do seem to have optimized fitness. There are other cases—especially involving changes in family size—where the expectation seems to have been wrong. What should we say about the future of human behavioral ecology and anthropology in the light of such cases? How can we integrate the causal contributions of very different processes? Do humans have a robust enough life history to sustain causal generalizations?

Causation in evolutionary anthropology**STEPHEN DOWNES** (University of Utah, United States)

Evolutionary anthropologists aim to explain human behavior. Many Evolutionary Anthropologists claim to be providing accounts of the ultimate causes of human behavior, appealing to Mayr's proximate/ultimate cause distinction. Others claim that their approaches are guided by Tinbergen's four questions and their explanations are couched in terms of Tinbergen's four causes. There is a considerable amount of discussion about the merits of the proximate/ultimate cause distinction and a little discussion about the merits of Tinbergen's four questions approach but there is very little discussion about relations between these approaches to causation and those discussed and defended in philosophy of science (Jun Otsuka, 2014) presents one way of beginning this latter discussion.). I plan to begin the process of assessing whether there is any overlap between approaches to causation invoked by Evolutionary Anthropologists and those presented and defended by Philosophers of Science. I use a few examples from work in Evolutionary Anthropology to anchor my discussion in scientific practice.

It's all in the game: Optimality models and the rules of behavior**KENNETH BLAKE VERNON** (University of Utah, United States)

Behavioral ecologists often claim that “optimality models themselves are never tested.” This claim, although in one respect highly misleading, is nevertheless deeply insightful. Yet many still fail to appreciate its significance. This failure has unfortunate consequences. For proponents of behavioral ecology, it has often led to the need-less adoption of a crude sort of instrumentalism about models. For critics, it has led to the hasty and unwarranted assimilation of behavioral ecology to other kinds of evolutionary analysis. To remedy this confusion, I explore the role optimality models play in behavioral ecology. I argue that optimality models, in addition to representing actual behavior, specify rules in accordance with which an individual must act in order to count as performing that behavior. In a word, they explicate the behavior's meaning or nature. It is this nature that is never tested by any application of the model, at least not directly. Once this role of optimality models is recognized, the way is cleared for a more nuanced account of the possibility for the successful integration of behavioral ecology with other evolutionary approaches to the study of human behavior.

Human nature, anthropology and the problem of variation**JAY ODENBAUGH** (Lewis & Clark College, United States)

Philosophers of biology have largely agreed that species lack traditional essences. However, many have embraced Richard Boyd's Homeostatic Property Cluster (HPC) account of natural kinds as a successor. In this talk, I consider whether the amount of variation in the life history exhibited by *Homo sapiens* is consistent with this approach. Specifically, I examine cases studies from anthropology to determine whether we possess nature robust enough for inductive projection. That is, do inductive projections regarding our life history require us to consider groupings larger or smaller than the level of species?

DS M220

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

BOUNDARIES AND LEVELS OF BIOLOGICAL ORGANIZATION (2)Organizer(s): **JON UMEREZ** (University of the Basque Country, Spain)

This double session will discuss the notion of biological organization from a system-theoretical perspective. In particular it will focus on its intrinsic hierarchical dimension, and on the role organization plays in the understanding of the transition from pre-biotic to minimal living systems and of the evolution towards more complex forms of biological, cognitive and ecological systems. More specifically, it will also address issues regarding individuality and autonomy at cellular and multicellular levels, from developmental and ecological perspectives as well as from genetic and evolutionary ones. Formation of boundaries at prebiotic scenarios and complex interactions at individual versus environment interfaces are also dealt with. The conceptual framework involves clarification of such general concepts as those of organization or level in terms of constraints, the characterization of regulation at its minimal instances or the assessment of diverse attempts to naturalize teleology. The double session is divided into two parts: a more general and conceptual one first, followed by another more specific and field centered.

Developmental and ecological processes of multicellular organization**ARANTZA ETXEBERRIA** (University of the Basque Country, Spain)

Philosophy of biology is exploring different ways of being an individual organism. At the cellular level, free living single cells are viewed as autonomous individuals, whereas those in a multicellular organism appear to be just parts of it. The extent to which microbes and multicellular entities can be compared as organismal entities is challenged by the role of microbes in multicellular organisms. According to models such as Buss's, individual cells give up their autonomy and independence, which is subdued by a larger organization for which cells lineages divide and differentiate following developmental processes and rules. Recent evidences of the role of the microbiota in multicellular organization suggest that processes beyond genealogical lineages, plausibly of an ecological character, play a constitutive role. Yet, how do multispecies cells populating the organism acquire their roles in the multicellular whole? How are relations among microbial components constrained by the multicellular organization? How do rules of development (division and differentiation) and ecological/economical rules governing the interactions (symbiosis, etc.) integrate? In sum, an important issue of multicellular individuality is how biological levels of cellular organization are conceived. This paper considers that levels of multicellular organization can be explored both in terms of developmental and of ecological interactions among cells, with conflicting consequences about the individuality of multicellulars, as at least two levels of organization and interactions appear to coexist, one regulated by the upper level of organization and developmental rules and a second one regulated different evolutionary and ecological rules, and in which the boundaries of the individual organism will appear blurred. In what concerns multicellular autonomy, this view is coherent with the perspective that autonomy is not a fact of the living condition but a norm being pursued under contingent conditions of life.

Extended inheritance and extended organizational boundaries**GAËLLE PONTAROTTI** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

In this presentation, I argue that the increasing data about non-genetic inheritance requires the construction of a renewed conceptual framework that should complement the inclusive approaches already discussed in the literature. More precisely, I hold that this framework should be epistemologically relevant for evolutionary biologists: in capturing the limits of extended inheritance and of extended biological systems transmitting traits to their offspring, it should open an alternative way to apprehend the impacts of extended inheritance on evolutionary thinking. I outline the first elements of an organizational account of extended inheritance, based on earlier works on biological organization (Mossio et al., 2009, 2010) and extended physiology (Turner, 2004). In such an account, the category of inherited factors is neither restricted to genes nor extended to ill-defined stable resources related to trans-generational patterns of variation. Instead, it includes multifarious elements whose specific role is to harness flows of matter and energy – and thereby to maintain extended metabolic and functional networks – across generations of clearly delimited extended organized systems. This both inclusive and restrictive framework is therefore tightly associated to the conceptualization of new levels of organization, appearing as various levels at which evolutionary causality can take place.

“Proto-cell autonomy”: Constructing boundaries to organise basic biological processes and interactions**KEPA RUIZ-MIRAZO** (University of the Basque Country, Spain)

Autonomy does not mean independence. It refers, rather, to the capacity of a system to generate its own rules of operation as such a system, including the rules of interaction with its environment. This applies to biological systems, which are able to build their boundaries (selectively permeable lipid membranes) and other functional components (proteins, sugars, nucleic acids...) through the transformation of externally available material and energetic resources. They manage to do so by putting together and coordinating (both spatially and temporally) a complex network of reaction processes that take place in non-homogeneous, far-from-equilibrium thermodynamic conditions. Thus, biological systems, being necessarily open systems, constitute a dynamic organisation of processes that becomes clearly distinct from the inert environment that nurtures them and, at the same time, collects the products of their ongoing activity. In this contribution, I will argue that autonomy, in its most basic and minimal sense, had to be developed quite early in the sequence of transitions that led from complex physical-chemical systems to the simplest biological ones. Apart from relevant experimental evidence provided in present days by several labs, a theoretical model will be introduced to show how this could be achieved: namely, through the coupling of autocatalytic chemical reaction networks with processes of lipid self-assembly forming the membrane of the system. This marks an important transition, in which “vesicles” (closed lipid bilayers) transform into “protocells”, for they gain control on the production of their own boundaries, a crucial step for autonomous individuation and system-level coordination. In this context, autonomy will be claimed as a necessary but not sufficient theoretical construct to account for living phenomena, whose evolutionary-historical-collective dimensions also need to be taken specifically into account.

DS M280

11:00 – 12:30

INDIVIDUAL PAPERS

ECOLOGY, EVOLUTION AND PHILOSOPHY**The relationship between ecology and evolutionary biology: A transpositional thesis****STEPHEN FRIESEN** (Indiana University Bloomington, United States)

Understanding the relationship between evolutionary biology and ecology is an intriguing problem. Ecology and evolutionary biology share a deep interest in biological populations. Why and how have these two sciences produced such different conceptual tools? What kinds of concepts and assumptions in ecology have led to images of biological nature in which notions of stability, balance, and sustainability are foregrounded? Meanwhile concepts and assumptions in evolutionary biology have led to a very different picture of biological reality; a Heraclitean image of incessant flux, ever directed by natural selection. Practicing biologists in both disciplines have also struggled to articulate the relation and the relative interpenetration of evolutionary biology and ecology - but often aphoristically. Dobzhansky's sub specie evolutionis is chief among these generalizations, though other prominent biologists have attempted to improve upon this formulation. While an intriguing problem, an understanding of this relationship has resisted analytical transparency. Collectively, the historical and philosophical accounts of evolutionary biology and ecology, along with the reflective musings of biologists themselves has led to a problem of understanding the two sciences conjointly. I offer an account of these two sciences in terms of a transpositional thesis. The relationship between ecology and evolution rests on the relationship between concepts of biological stability and change. I support this thesis through a comparative analysis of the core mathematical models in population genetics and population ecology; the Hardy-Weinberg model and the logistic model respectively. Ecology and evolutionary biology are related in terms of transpositional explanatory targets, methodological strategies, and representational values. The Hardy-Weinberg model derives changes in gene frequencies from conditions of genetical equilibrium, while the logistic model derives stable population size from the dynamics of geometrical growth. The critical difference rests on the transpositional functions concepts of stability and change possess in these respective models.

Hull and Ruse on positivism, historicism, and Darwin's debt to philosophy**PHILLIP HONENBERGER** (Consortium for History of Science, Technology, and Medicine, United States)

This paper reconstructs the divergent paths taken by David Hull and Michael Ruse, in the late 1960s and 1970s, on three questions that (surprisingly) turn out to be closely related: (1) Darwin's intellectual relationship to the philosophy of science of his day (in particular, the views of Herschel and Whewell); (2) the promise of logical positivist philosophies of science, as applied to biology; and (3) the terms of what might be called "epistemic authority" between histories of science, on the one hand, and philosophies of science, on the other. I argue that these three divergences can be systematically related to one another in the following way: By the early 70s, Hull was beginning to view the Western philosophical heritage as generally retrograde and in need of radical reconstruction along lines consistent with Darwin's anti-essentialism and anti-teleological historicism – a position

that put him in qualified agreement with the new Kuhn-inspired, "historical" philosophy of science, and pitted him against the positivist legacy. Ruse, on the other hand, adopted both the Kuhnian and positivist legacies as providing insights that demanded qualification but not rejection, and that were not necessarily incompatible, and viewed Darwin as a member and contributor to an empiricist philosophical and scientific tradition, shared by the British philosophers of science of Darwin's day (though Herschel more than Whewell, obviously) and the logical empiricists several generations later, and thus not incompatible or orthogonal to Darwinian projects. I close with discussion of a few possible historiographical objections to this portrayal of Hull and Ruse's divergences, and reflections on the strengths and weaknesses of the reconstructed positions from a contemporary standpoint.

Constructing causal models in biology: What are the rules?**BRIAN MCLOONE** (University of Wisconsin-Madison, United States)

Recently, there has been much effort to "causalify" evolutionary biology – to take processes and equations from evolutionary biology and render them in explicitly causal language. Generally, the causal language that is used is that which comes from the interventionist/manipulationist approach to causation, as articulated by, for instance, Judea Pearl. I welcome these efforts enthusiastically; however, as I argue in this paper, too little attention has been paid to what counts as a legitimate causal model. In particular, I claim that the variables in a causal model, as well as the relationships between these variables, should satisfy certain desiderata. These desiderata should largely derive from the interventionist/manipulations framework itself. The three desiderata I defend in my presentation are these. INT: It should be possible in principle to intervene on each of the variables in a causal model; DIS: The variables in a causal model should be logically distinct; and MARK: The model should satisfy the causal Markov condition. I show why these desiderata are justified and discuss some recent causal models of evolutionary processes that do not satisfy them.

INDIVIDUAL PAPERS

UNDERSTANDING FITNESS PHILOSOPHICALLY**Honest propensities: Is there a crack in the new foundation?****PETER TAKACS**** (Florida State University, United States)

While answering early concerns about purported explanatory circularity, the propensity interpretation of fitness as originally stated by Brandon (1978) and Mills and Beatty (1979) foundered upon issues pertaining to the measurement of fitness as a scalar value in the face of demographic and environmental stochasticity (Gillespie 1977, Beatty and Finsen 1989, Brandon 1990, Sober 2001). Staunch critics of the propensity interpretation (Ariew, Matthen, Walsh, Lewens, Lewontin) and self-conscious proponents of propensities (Abrams 2007, 2009) alike have taken the inability of the propensity interpretation to overcome such measurement problems as

a decisive reason for concluding that the concept of fitness cannot be both explanatorily relevant and a probabilistic dispositional property of individuals. By reconfiguring the mathematical foundations of the propensity interpretation, Pence and Ramsey (2013) have effectively countered the aforementioned measurement worries. In importing the methods of calculus, however, the new foundation they have laid for the propensity interpretation runs the risk of losing sight of the basic reference class or population for which explanation of adaptation and ultimately speciation is sought. I will examine a biologically realistic case involving non-monogamous species of bean weevil and argue that the mathematical formalization which best describes the behavior of this model system is potentially problematic even for the revamped interpretation of fitness as a propensity.

Rejecting replicators

KAREN KOVAKA (University of Pennsylvania, United States)

According to the dominant view of biological inheritance, powerful inheritance processes require replicators. On this view, cumulative selection cannot occur without high-fidelity copying mechanisms. I argue that this is an insufficient justification for accepting a replicator analysis of inheritance. There are other essential elements of biological inheritance that the replicator view cannot capture. I focus on two examples. First, the replicator view sidelines the role of developmental plasticity in evolution. Second, the replicator view cannot accommodate ecological contributions to the evolvability of populations. On the basis of these examples, I suggest some features that a satisfactory account of biological inheritance must have.

Hypothetical biological spaces and genetic accessibility

JASON ZINSER (University of Wisconsin-Marathon County, United States)

Hypothetical biological spaces, such as “phenotypic space”, “design space”, or “morphospace” are employed for a variety of explanatory reasons. However, it is unclear exactly what these spaces refer to and how they function within specific theories. In this paper, I will provide a critical assessment of these spaces and specifically address whether these spaces reflect what is actually genetically accessible.

INDIVIDUAL PAPERS

GENES, INDIVIDUALS AND CONTINGENCY

Can genes be Darwinian individuals?

HAIXIN DANG (University of Pittsburgh, United States)

In this paper, I will answer affirmatively the question posed in the title. Darwinian individuals (DI) are members of a Darwinian population (DP), which is a collection of things that has the capacity to undergo evolution by natural selection (Godfrey-Smith 2009, 6). Godfrey-Smith argues that genes cannot be DIs. DIs are bounded

and countable objects and genes do not meet these criteria. I argue that under a molecular conception, the gene do in fact fulfill the criteria to be a DI. In doing so, I will be building from the molecular gene concept of Waters (1994) as well as recent research in molecular biology. I will show that genes, like macroscopic organisms, vary greatly in how Darwinian they behave. Not all genes are the same. Some genes, in fact, make paradigmatic DIs, while some fall in the middle, and some are indeed marginal. The Darwinian space, as introduced by Godfrey-Smith, can accommodate genes and can be used to understand the complex molecular world of the genome, while still maintaining that selection happens at other levels. The key argument I develop in this paper is that we should consider the more problematic cases of genes as analogous to collective entities that is, the gene can be conceived as one coherent object with discontinuous parts, like a colonial organism. Since the DI is dependent on a higher population concept, I will also argue that molecular genes can form a DP. I will also consider some possible objections and replies. In the final section of the paper, I will discuss the metaphysical aspect of the concept of individuals in biology. Many philosophers of biology privilege objects with natural boundaries as individuals that can be selected for. I argue that we ought to adapt our concept of individuality to accommodate molecular genes.

Gene regulatory models with evolutionary genetics models: Two cases

STEVE ELLIOTT (Arizona State University, United States)

Researchers have developed gene regulatory network (GRN) models partly to explain how major novelties arise within evolving lineages. Now biologists and philosophers debate about how those models will impact evolutionary theory. Some say that extant formal models of evolution can usefully accommodate GRN models. Others say that the GRN models are so different and powerful that they require us to drastically rethink how we model the causes of any variation within populations, and thus they require us to build a new formal structure for evolutionary mathematics. At the core of the debate is the status of formal models of evolutionary genetics, and as proponents of both sides have entrenched themselves, it's doubtful that current argumentative strategies will settle anything. Often lost in the debate, however, is the actual work of recent biologists who work to incorporate GRN models with evolutionary genetic models. I present two case studies of recent research groups, one that uses simulated populations and the other that uses actual populations. The case studies show the epistemic aims of each research group, their integrated models, and the limits of their research. Given those results, I encourage the construction of similar studies, and I suggest how we might use those cases to help adjudicate the debate about the status of evolutionary genetics.

Biological individuality and the evolutionary contingency thesis

ALISON MCCONWELL (University of Calgary, Canada)

John Beatty (1995; 1982) cites the dynamic nature of evolution as responsible for the contingency of biological generalizations. Beatty's Evolutionary Contingency Thesis (ECT) is originally discussed within the context of laws, but I wish to explore implications it may have for individuals relevant to natural selection. I will suggest that the impermanent character of evolution indicates a framework to think about individuals in biology, particularly evolutionary individuality. If biological laws and the mechanisms they govern are dependent on the outcomes of evolution, then it makes sense to ascribe contingency to mechanisms that underpin evolutionary individuality. In other words, if genetically-grounded mechanisms described and explained by biological laws are contingent and biological individuals emerge and are maintained by such mechanisms, then it follows that individuals are contingent too. *Mutatis Mutandis* for evolutionary individuality specifically. Examining evolutionary individuality through the lens of Beatty's ECT may provide insight into the viability of pluralism and evolutionary individuals. For evolutionary individuality to be highly contingent, not only would individuals be subject to change over time, but the individual visible to selection could have been otherwise. This yields pluralism in the form of a temporal succession. It implies that a given definition of evolutionary individuality may no longer hold true at a later time. Thus, the coupling of pluralism with the notion of individuality may be supported by what one finds in nature, which suggests that a more open-ended view of individuality is required.

INDIVIDUAL PAPERS

CAUSATION, EXPLANATION AND INFORMATION IN BIOLOGY

Limiting cases for the new mechanists: Intralevel causation is insufficient for modeling complex biological systems

SARAH ROE (Southern Connecticut State University, United States); Bert Baumgaertner (University of Idaho, United States)

Mechanistic accounts of explanation pervade the philosophy of science. Typically, however, such accounts struggle to explain complex biological systems. Craver and Bechtel offer one suggestion along these lines: levels of mechanisms are related by constitution, and causation only occurs intralevel (there is no interlevel causation; "bottom-up" or "top-down"). We argue that this suggestion leads to a difficulty when we take seriously the modeling practices involved in studying contemporary complex biological systems. Such explanations often involve multilevel, nonlinear dynamic mechanisms, in which the mechanistic environment frequently plays an important organizational role. Our suggestion is that the New Mechanists should go the route of allowing for interlevel causation, because it better reflects modeling practices, and broadens the scope for mechanistic explanations.

Causal explanation in genetics and the pathway concept

LAUREN ROSS (University of Pittsburgh, United States)

In this paper I examine the concept of a causal pathway and how it is used to provide explanations in both classical Mendelian genetics and modern biochemical genetics. I indicate how the pathway concept is used to explain phenotypes that are causally complex in the sense that: (1) the phenotype is caused by multiple causal factors that work in aggregate in individual systems and (2) the phenotype is caused by heterogeneous causal factors in different systems with the same phenotype. In both cases, the numerous causal factors can be integrated on the basis of their causal influence on a shared or common pathway, which leads to the specific phenotype of interest. Shared pathways are appealed to in explaining these phenotypes, in part, because they represent sets of causal factors that make a difference to the phenotype of interest. As these common pathways often represent causal factors more upstream from gene variants, these cases clarify the rationale behind abstracting from genetic factors in explaining some phenotypes. Extant accounts of explanation in biology often assume that all complex causal factors can be characterized in terms of mechanisms. In this paper I will give reasons for doubting this assumption. To do so, I discuss the relation of pathway explanations in genetics to Batterman's work on minimal model explanations and multiple-realizability (Batterman 2001, 2002). I argue that when the concept of a causal pathway is invoked in these explanations, it differs in important ways from the philosophical concept of a mechanism. The central aim of this paper is to begin clarifying the differences among these complex causal concepts and why they find their respective application in particular contexts.

On the impossibility of measuring biological information

AGUSTÍN MERCADO-REYES (Universidad Nacional Autónoma de México, Mexico)

Since the inception of Shannon's theory of information, there have been several attempts to elaborate a method for measuring semantic information. This is a concern especially relevant in present day biological sciences, not only because of the enormous amount of data that has been produced in the past decades, but also because of the increasing interest to integrate the raw data into a broader picture of the processes of life. However, in order to measure biological information one must make the necessary presupposition that its semantic dimension is quantifiable. I analyse this presupposition and find that it is based on a series of idealizations which are detrimental to our understanding of living systems. On the one hand, semantic meaning is assumed to emerge out of a previously defined and fixed structure, on which there is a finite number of possible outcomes. Meaning is thus reduced to a correspondence between data and states of affairs. On the other hand, semantic processes are deprived of their temporal dimension, as they are analysed based solely on the formal structure. I argue that the reductionist programmes do not fully account for the complexity of biological systems, a fact which is especially evident when confronted with concepts like information and meaning. I suggest that a more appropriate theoretic framework must take into account different temporal descriptions, which would allow us to include phenomena such as the historical establishment of meaning and the repetitiveness of the outcome of informational processes. In this view, mechanicism need not be discarded, but rather included in a larger theory which more closely resembles biological reality.

DS M460

11:00 - 12:30

DS R340

11:00–12:30

INDIVIDUAL PAPERS

SPECIES QUESTIONS: MISSING LINKS, NEW CONCEPTS, AND METAPHYSICS**Hypothetical common ancestors and the search for missing links****RICHARD JAVIER STEPHENSON** (University of Cincinnati, United States)

In trying to reconstruct the evolutionary history of life, biologists and paleontologists often come across many instances of missing links. The characteristics of these ancestral forms is important for understanding the history of taxa and the attributes of descendent organisms. However, hypothesis about the characteristics these common ancestors can be problematic if these ancestors are interpreted as descriptions of some potential actual organism. Lindberg and Ghiselin demonstrated this issue in 2003 with their evaluation of the hypothetical ancestral mollusc or HAM. This paper looks to expand Lindberg and Ghiselin's criticisms of the HAM to issues in regards to the use hypothetical common ancestors in finding actual common ancestors in the fossil and genetic records. It will focus on the assumptions made for such projects, and bring to question what role if any hypothetical ancestors play in the investigation of missing links and transitional forms.

The mechanism of neo-biological species concept: From reproductive isolation to communicative isolation**BO-CHI G. LAI** (Da-Yeh University, Taiwan)

The debates of different species concepts proposed by the major biological scholars in 2000 have been regarded as the modern species concepts formed. In the debates, the biological species concept (BSC) proposed by Ernst Mayr was one of popular species concepts in decades. In *Species Concepts and Phylogenetic Theory* (2000), there are important debates among 4 major species concepts: "The Biological Species Concept", "The Hennigian Species Concept", "The Phylogenetic Species Concept" and "The Evolutionary Species Concept". Ernst Mayr not only modify the BSC to more molecular evolutionary theories and phylogenetic concerns but also defense that the BSC is the only concept can illustrate the meanings of species referring to both species as taxa and the category species. The mechanism of BSC concept is based on "reproductive isolation": members of biological species are united by being reproductively compatible and at least potentially. However, there are several critiques on the BSC, such as the concept of species will be limited in because the reproductive isolation mechanism will fail to identify species in evolutionary process. The communicative isolation mechanism, the basis of Neo-Biological Species Concept (Neo-BSC), is modified from the idea of reproductive isolation. The communication is grounded on the successful response to the signal between individuals, and the signal is in a broad meaning from gene level to individual level. The mechanism will not only try to answer the critiques but also to solve the problem of applying the Neo-BSC on the asexually reproductive organisms. Just as Mayr's claimed, "... since this is often misunderstood, that species taxa are multidimensional, but the nondimensional situation is required to determine the crucial biological properties of the species concept", my work is trying to continue to develop the BSC consummately.

The relevance of the metaphysics of time and temporal persistence for the species problem and the organism problem**AUGUST MARTIN** (Universiteit Leiden, Netherlands)

I argue in favor of the view that biological entities occupying distinct levels of biological organization can exhibit distinct modes of temporal persistence. I call this the "disparate persistence" (DP) thesis. Its relevance becomes apparent when considering implications of the organism problem and the species problem. The "species problem" (Richards 2010) is propelled by disagreements over the metaphysical status of species, and whether species are sets, kinds, or individuals. The "organism problem" (Pepper and Herron 2008), part of the problem of biological individuality (J. Wilson 1999; Clarke 2010), is propelled by disagreements over resolutions to unclear cases of biological entities that exhibit poor integration and unclear boundaries. I will show how these problems are related. Pluralistic accounts (J. Wilson 1999) advance multiple kinds of biological individuals, each potentially requiring a species concept, and so necessitating species pluralism. Furthermore, species concepts and organism concepts harbor underlying assumptions about the temporal persistence of species and organisms. Crane (2004) and Reydon (2004, 2008) demonstrate that different species concepts imply different models of temporal persistence. Some species concepts model species as 4D perduring objects, while other species concepts model species as 3D enduring objects. Importantly, Hull (1989) argues that 4D perduring objects must have perduring parts; therefore, the organisms of 4D perduring species must also be 4D perduring objects. Organism concepts and concepts of biological individuals themselves entail endurantism or perdurantism. A resolution to the organism problem that necessitates 3D enduring organisms, given Hull's claim, would lead to the unwelcome imposition that a resolution to the species problem would be restricted to 3D endurantist species concepts. The DP thesis dissolves this tension by allowing species and organisms to exhibit distinct modes of temporal persistence.

DS R510

11:00–12:30

ORGANIZED SESSION / DIVERSE FORMAT

BOOK SYMPOSIUM: GÜNTER WAGNER'S *HOMOLOGY, GENES, AND EVOLUTIONARY INNOVATION* (2014)Organizer(s): **VALERIE RACINE** (Arizona State University, United States)

Participant(s):

GUNTER WAGNER (Yale University, United States)**EHAB ABOUHEIF** (McGill University, Canada)**DOUGLAS H. ERWIN** (Smithsonian National Museum of Natural History, United States)**MANFRED LAUBICHLER** (Arizona State University, United States)**VALERIE RACINE** (Arizona State University, United States)

We propose an “author meets critics” session on Günter Wagner’s recently published book, *Homology, Genes, and Evolutionary Innovation*. Wagner’s book is the product of two decades of work in developmental evolution. His goal is to provide a conceptual framework to study the evolution of developmental types, such as homologies, body plans, and cell types, and to explain the historical continuity of characters, or character identity, as well as the observed variation of these characters, or character states. He argues that this class of phenomena has not, and cannot, be accounted for within an evolutionary theory founded on population genetics. Instead, he proposes that this class of phenomena can be explained by appeal to character identity networks (ChINs). ChINs are networks of regulatory genes that generate homologous morphological traits. Wagner’s ChIN concept is not a definition of homology, but a concept designed to help organize an empirical research agenda that attempts to provide mechanistic explanations of both the evolution of homologous types and the origin of evolutionary novelties.

Wagner’s work raises many conceptual questions that will be of interest to philosophers, historians, and biologists. How can the ChIN concept explain the stability and historical continuity, as well as the variational modalities, of homology? How does it compare to other accounts of homology? Can it provide mechanistic explanations of homology and the origins of evolutionary innovation? Can the ChIN concept contribute to the development of a quantification and measurement theory in phenotypic evolution? We hope that this session will provoke discussions around these questions and other issues in developmental evolution.

DS R515

11:00–12:30

ORGANIZED SESSION / DIVERSE FORMAT

ASPECTS OF BIOLOGICAL ORGANIZATION

Organizer(s): **DEREK SKILLINGS** (City University of New York, United States); **JOHN MATTHEWSON** (Massey University, New Zealand)

Participant(s):

LAURA FRANKLIN-HALL (New York University, United States)

JOHN MATTHEWSON (Massey University, New Zealand)

DEREK SKILLINGS (City University of New York, United States)

The organizational structure of a biological system is important in many ways and contexts. The way a cell, tissue, or organism is organized is a core determinant of its particular traits and features. Generic features such as robustness and reliability often depend on organization as well. While important, the notion of organization has remained under-explored in philosophy of biology, both conceptually and in terms of its significance within the life sciences.

One reason for this may have to do with the centrality of evolutionary theory, in which organization is (arguably) less important. However, increased philosophical focus on other parts of the life sciences, especially those that do not specifically deal in populations, means that organization requires more of our attention. Organization – or lack thereof – is a key concern in fields such as cellular, molecular and developmental biology and neuroscience. Accordingly, this concept has begun to receive more attention following the explosion of interest in mech-

anistic explanation. Organization is central here, but until recently philosophers have paid comparatively little attention to the character and specific roles a system’s organization plays in this type of explanation.

This session will bring together different perspectives on the theme of biological organization. The papers will explore the role of different organizational patterns with respect to robustness; the contrast between organization and disorganization in early developmental processes, the ability of certain physical organizations to support useful abstraction, and when it may be appropriate to represent systems as more organized than they actually are. This session aims to bring into sharper focus the philosophical issues surrounding the varieties of biological organization, as well as the contexts in which organization should be a central consideration.

The Possibility of Organismal Biology

LAURA FRANKLIN-HALL

Our world is a physical one, made exclusively of physical stuff governed by physical law. Yet many of the biological sciences—from ecology to molecular, developmental and evolutionary biology—with varying amounts of success, describe the workings of living systems by omitting many if not most of these physical details. Were these systems simple in either of two ways—had they only a small number of parts, or were those parts organized only loosely—it would be easy to understand how highly abstract, detail-sparse descriptions could be satisfactory. But it is not straightforward how real biological systems—particularly organismal systems—which possess a large number of parts, intricately organized, can be so described. While focusing on examples from contemporary systems biology, this paper aims to explain this possibility in two parts. Part one focuses on the causal architecture of organismal systems and catalogues the generic organizational features—among them hierarchical embedding and coordinated constraints—which underpin the robustness of organismal systems. In part two I suggest that these features also permit scientists to use iterative abstraction to neglect details in their predictive and explanatory models, thereby showing how simple models

Idealised Organisation

JOHN MATTHEWSON

The claim that a biological system exhibits a substantial degree of organisation usually involves some commitment to the idea that particular components within the system have particular roles to play. For example, intracellular processes will often be represented as organised sequences of functional roles discharged by a particular set of entities within the cell. However, many of these processes actually fail to approximate a straightforward role/occupier picture at all well. This means representing cells as composed of – and constituting – organised systems may require a significant level of idealisation and abstraction. This potential mismatch between depiction and reality is important to recognise if the representational goal is realism. However, it may be of less concern for other objectives such as prediction or even explanation. If this type of idealisation / abstraction leads to accurate predictions and enables us to account for the relevant counterfactuals, we might not need to care that much about whether cellular structures and processes are *actually* organised in some

straightforward manner, rather than merely *appearing as though* they are organised in this way. I will present some examples of mismatches between representation and actuality in this context, and consider whether anything general can be said about cases where this type of idealisation is likely to be benign, where it may be problematic, and ways in which it might be valuable.

Ways to be Robust

DEREK SKILLINGS

One striking feature of most biological processes and systems is their high degree of robustness, or the reliable production of a similar output under a wide range of circumstances. Despite the ubiquity and importance of robustness, many explanations in biology pass over the organizational details that give rise to it. This may be problematic because most of the biomolecular processes that underlie biological phenomena are robust in a way that is quite different from the robustness seen in macro-level processes. Because of this, I will suggest, our causal explanatory habits have the potential to mislead us when thinking about some aspects of biology. In this talk I will explore some of the alternative patterns of causal organization that underlie robustness in physical systems. I start by contrasting causal organization in two types of biological systems: the nanoscale world inside the cell--where stochastic processes dominate-- versus the more familiar world of macroorganisms. I suggest that when robustness is present, a good explanation must differentiate the way in which a causal process or system is robust. I finish by introducing a framework for doing so--co-opting and modifying the concepts of redundancy, resistance and resilience from ecology and structural engineering.

ORGANIZED SESSION / STANDARD TALKS

MODELING IN SYSTEMS BIOLOGY: SIMPLICITY VERSUS COMPLETENESS

Organizer(s): **SARA GREEN** (University of Copenhagen, Denmark); **MELINDA FAGAN** (University of Utah, United States)

All things considered, it would seem obvious that a mathematical model of a biological system that is more complete in terms characterizing the parts and operations of a mechanism would be preferable to one that simplifies. After all, the components and processes that are left out in the simplified model may make a difference to the behavior of the mechanism that cannot be detected except through use of a complete model. While systems biologists do employ models that attempt to be as complete as possible to determine whether the hypothesized mechanism will behave as anticipated, when the focus is on explanation they often prefer simpler models. This symposium will examine specific contexts in which the question of completeness versus simplicity has arisen in systems biology and examine the reasons the modelers advance for their strategy and the understanding of phenomena they offer.

Ingo Brigandt will set out the key issue for the symposium of what the complete modeling of a phenomenon involves, and contrast this with different types of mathematical models currently being deployed in systems

biology and the particular explanatory insight each provides. **William Bechtel** will then examine a specific case involving circadian rhythms in cyanobacteria in which, in order to understand how such rhythms were produced, the researchers developed a simplified model and searched for parameters that would generate sustained oscillations in the model. Finally, **Sara Green** will consider cases in which investigators are aiming to generate complete models, but focus on the critics and the shortcomings they identify in the pursuit of such models.

Different types of explanatory mathematical analysis in systems biology

INGO BRIGANDT (University of Alberta, Canada)

A mechanistic explanation cites the components of a mechanism, including the entities, activities, and their organizational features that underlie the phenomenon to be explained. But in addition to mentioning relevant components, the explanation also has to lay out how the operation of the mechanism generates the phenomenon of interest. This explanatory understanding often comes from mentally simulating the behavior of the components and overall mechanism, facilitated by a mechanism diagram. But complex mechanisms cannot be mentally simulated. In contrast, systems biology studies such mechanisms using different types of mathematical models. The result of a computer simulation may entail that the mathematical model does in fact produce the phenomenon of interest, but this does not provide the explanatory understanding afforded by mental simulation (of how the phenomenon is produced). Moreover, several types of mathematical analysis used in systems biology do not explain by reproducing the complete behavior of the mechanism, but instead by analyzing certain aspects of the system. The upshot of such a mathematical analysis is often visualized in graphs, which provide explanatory understanding without being mechanism diagrams. Such explanatory analysis can also require reference to parameter values not found in the actual mechanism in nature. In this talk, I lay out and compare a few of the types of mathematical analysis found in systems biology, including steady state analysis, bifurcation analysis, and stability analysis. I discuss in what way and in what epistemic context they have explanatory import.

Discovering design with simplified computational models

WILLIAM BECHTEL (University of California, San Diego, United States)

Although some computational models in systems biology aim to characterize completely the mechanism responsible for a phenomenon, another important use of computational modeling is to determine basic design principles that enable a mechanism to exhibit the phenomenon. This is often best achieved by focusing on simplified models that abstract from many known components and operations to determine which are essential. This paper will illustrate this practice by focusing on the circadian clock in cyanobacteria. Unlike circadian clocks in other organisms that rely on feedback loops involving gene expression, the cyanobacterial clock employs just ATP and three proteins, one of which is cyclically phosphorylated and dephosphorylated. In a 2012 paper Jolley, Ode, and Ueda used this as a basis for investigating through computational modeling a basic design that would suffice for a biochemical circadian oscillator. They found that a kinase and a phosphat-

DS R525

11:00 - 12:30

ase operating at just one phosphorylation site will converge to a steady state, but with two sites, using some parameter values, sustained oscillations are possible. By sampling a large numbers of parameter sets they identified approximately 1,000,000 (~0.1% of those tested) that sustained oscillations. These fell into two distinct clusters, each of which realizes a design motif (one that forces an ordered sequence of phosphorylation states and another that generates checkpoints by enzyme sequestering). From this foundation, the researchers went on to address questions about how the motifs made the resulting oscillators robust and synchronized activity of enzymes of the same type. By constructing a model of a minimal network and searching for parameters that sufficed to generate circadian oscillations, this research exemplifies a strategy for discovering design principles that explain the behavior of empirically identified mechanisms by developing highly simplified modes.

Large-scale modeling and the ideal of completeness

SARA GREEN (University of Copenhagen, Denmark)

This paper examines the prospects for and challenges to large-scale modelling in systems biology. The dream of complete models of living systems has recently been turned into serious research projects, such as whole-cell projects (the Silicon Cell, E-cell), the Virtual Physiological Human and the Human Brain Project. Rather than drawing on problematic idealizations for the sake of simplicity, the hope is to create as complete representations as possible of biological systems. Complete should here be understood in terms of mathematical descriptions that are maximally fitted to experimental parameter values for as many causal processes as possible. If successful, such simulations will not only allow researchers to mimic the behavior of biological systems in silico but also to observe effects of interventions on the model, and thereby to access in simulations what cannot be obtained through experimental research due to practical challenges or ethical reasons. The expected outcomes of such projects for biological and biomedical research, and for the development of personalized medicine, are tantalizing. Many proponents envision that developing such models will revolutionize biomedical research and health practices. But others remain skeptical that the vast amount of information can be turned into clinically useful information through large-scale integration of data and models. In this paper I analyze the methodological and theoretical challenges that give rise to such controversies. In particular, I focus on the problem of integrating different types of models (ODEs, partial differential equations, agent based simulations etc.) and different types of data, conducted at different scales of biological organization and in different contexts. In addition, I address the more fundamental concern that large-scale modeling aiming for completeness merely reproduces biological complexity.

12:30 - 15:30

LUNCH BREAK

13:00 - 15:00

COUNCIL MEETING | Room DS-1955

DS 1420

15:30 - 17:00

ORGANIZED SESSION / STANDARD TALKS

ARE YOU A ROMANTIC OR KILLJOY? (2) ISSUES IN COMPARATIVE PSYCHOLOGY

Organizer(s): **RACHAEL BROWN** (Macquarie University, Australia)

Comparative psychology has been disparagingly described by some as a field of “romantics” and “killjoys”; some researchers being keen to attribute human-like mental states and cognition to non-human animals, and others arguing that to do so is anthropocentrism. This session brings together five researchers working in the philosophy of comparative psychology offering different perspectives on the “romantics” and “killjoys” debate. Each of the researchers will present an aspect of their most recent work followed by an open panel discussion.

STANDARD TALKS

Explanatory constraints in comparative psychology

MARTA HALINA

The problem of bias is central to discussions of research on nonhuman animal behavior and cognition. This problem is often framed in terms of how to identify and avoid anthropomorphic and anthropocentric tendencies in the interpretation of experimental results. In this talk, I draw on general work in mechanistic philosophy of science in order to reframe the problem of assessing bias within comparative psychology. Using research on visual perspective taking as a case study, I show how the constraints on good explanation are often greater than supposed in the literature. Evidence from recent studies in psychology and neuroscience allow us to narrow down the range of how-plausibly mechanisms available for explaining visual perspective taking abilities in nonhuman animals. In addition, comparative research facilitates the discovery of differences and similarities in the mechanisms underlying visual perspective taking in humans and nonhumans. When assessing the available explanations of experimental results in comparative psychology—whether romantic or killjoy—one would be remiss not to take these additional sources of evidence into account. Doing so, however, limits the role of bias in this domain.

What the crow cannot do: Assessing the “signature-testing” approach to comparative psychology

RACHAEL BROWN

New Caledonian Crows manufacture and use tools and have been shown to be impressive causal problem solvers. Though it is clear from empirical work to-date that neither a “romantic” nor “killjoy” explanation of this behavior is wholly vindicated, the exact nature of New Caledonian Crow cognition remains unclear. In an attempt to some empirical traction on this issue, a new approach to corvid research has been proposed – “signature testing” (Taylor, 2014; Taylor & Gray, 2014). In contrast to focusing on successes (i.e. what the crows can do), under this new approach experimenters explicitly set out to search for errors, biases and limits to the capacities of their subjects (i.e. what the crows can’t do), and then use both of these features of crow behaviour to look for cognitive similarities between corvids and humans. In this paper, I critically assess this approach and consider its broader utility for avoiding killjoy and romanticism disagreements in comparative psychology.

PANEL DISCUSSION

Romantic or killjoy: Where to from here?**KRISTIN ANDREWS, HAYLEY CLATTERBUCK, SIMON FITZPATRICK, MARTA HALINA, RACHAEL BROWN**

This 30 minute panel Q and A session will focus on general issues raised by the five preceding papers. It will offer the speakers and the audience a chance to give general comments and feedback on the session topic and further comments on particular papers.

Participant(s):

RACHAEL BROWN (Macquarie University, Australia)**MARTA HALINA** (University of Cambridge, United Kingdom)**HAYLEY CLATTERBUCK** (University of Wisconsin-Madison, United States)**KRISTIN ANDREWS** (York University, Canada)**SIMON FITZPATRICK** (John Carroll University, United States)

ORGANIZED SESSION / DIVERSE FORMAT

REPRESENTATIONS OF BIOLOGICAL INHERITANCE: A ROUNDTABLEOrganizer(s): **FRANCESCA MERLIN** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

Participant(s):

STAFFAN MÜLLER-WILLE (Exeter University, United Kingdom)**GREGORY RADICK** (University of Leeds, United Kingdom)**LEÍLA PERIÉ** (Institut Curie, France)**ANNE-CÉCILE DAGAEFF** (Université Toulouse 3, France)**GAËLLE PONTAROTTI** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)**LIVIO RIBOLI-SASCO** (L'Atelier des Jours à Venir, France)

The present roundtable aims at raising a multidisciplinary discussion about the evolution of representations of biological inheritance, since the introduction of this concept in biology in the first half of the nineteenth century, as well as about possible directions its representation could – and should – take in the light of recent advances in research on non-genetic forms of transmission. In fact, several non-genetic factors and mechanisms have been found to be transmitted between organisms, such as modifications in gene expression due to changes in histones and chromatin conformation and in methylation patterns, modifications in behaviours due to parental influences, changes in the selective pressures due to activities of niche construction, and variation transmitted via social learning.

The roundtable is composed of six short presentations (10 minute long each) followed by a general discussion (30

minutes). We intend to focus the presentations on graphical representations of inheritance (drawings, images, illustrations, graphs, etc.). However, the roundtable is also open to other kinds of representation broadly speaking, such as theoretical models and conceptions of inheritance, that actually are essential in order to describe the way representations of inheritance have evolved as well as to fuel the debate about future directions of its representation.

During this roundtable, we wish to open a multidisciplinary debate on the issue at stake. This is the reason why we have decided to put together researchers coming from different disciplines: history of biology, biology, and philosophy of biology. They will intervene in the following order:

1 – Staffan Müller-Wille will propose a classification of inheritance systems based on the variety of metaphors that have been employed to capture phenomena of transgenerational persistence and variation of traits.

2 – Gregory Radick will talk about some interpretive questions arising from Francis Galton's use of the quincunx in the 1870s and 80s as a representation of his ideas about how inheritance worked.

3 – Leïla Perié will talk about the similarities in the representation of cell differentiation and extended inheritance comparing their conceptual basis.

4 – Anne-Cécile Dagaëff will deal with the transmission of behaviors in animals, focusing on the transmission of female mate preferences and its representations.

5 – Gaëlle Pontarotti will introduce a physiological representation of extended inheritance, in which inherited items appear as heterogeneous agents of physiological exchanges, channeling flows of matter and energy across generations of composite organized systems.

6 – Livio Riboli-Sasco, in collaboration with **Francesca Merlin**, will present illustrations which are an attempt to facilitate the understanding of the separation between transmission mechanisms from mechanisms of inheritance. These illustrations shall make it clear that these different processes could be associated with different dynamics of adaptation, while current representations of extended inheritance often confound various evolutionary dynamical regimes.

DS 1520

15:30 – 17:00

DS 1540

15:30–17:00

ORGANIZED SESSION / DIVERSE FORMAT

WHERE BIOLOGY MEETS ANTHROPOLOGY (2): PHILOSOPHICAL DISCUSSIONSOrganizer(s): **MATT HABER** (University of Utah, United States); **JAY ODENBAUGH** (Lewis & Clark College, United States)

Participant(s):

RICHARD BOYD (Cornell University, United States)**HEIDI COLLERAN** (Institute for Advanced Study in Toulouse, France)**STEPHEN DOWNES** (University of Utah, United States)**KENNETH BLAKE VERNON** (University of Utah, United States)**JAY ODENBAUGH** (Lewis & Clark College, United States)

Human behavioral ecologists seek evolutionarily grounded explanations of human social behaviors on the expectation that such behaviors will tend to optimize fitness. They've been "successful" in the sense that many current and recent social behaviors do seem to have optimized fitness. There are other cases—especially involving changes in family size—where the expectation seems to have been wrong. What should we say about the future of human behavioral ecology in the light of such cases?

Following short presentations by philosopher **Richard Boyd** and evolutionary anthropologist **Heidi Colleran**, participants from the first session will commence for an open round table discussion of these and related issues:

- How can different research strategies from human behavioral ecology, evolutionary psychology, and gene-cultural coevolution be integrated to provide more accurate and rich explanations of human life history?
- How can phylogenetic techniques applied to taxa be used to understand the evolution of artifacts?
- Is culture something especially human? If not, what are the implications of this?
- How has recent anthropology escaped the criticisms that have been registered against sociology and evolutionary psychology? How has it been methodologically transformed?

DS 1545

15:30–17:00

ORGANIZED SESSION / STANDARD TALKS

EVOLUTION OF COOPERATION: NEW ROLES FOR SOCIAL, CULTURAL, AND COGNITIVE INTERACTIONSOrganizer(s): **MARSHALL ABRAMS** (University of Alabama at Birmingham, United States)

There has been a great deal of research on how cooperation and coordination evolves among humans. This research has focused primarily on relationships between individuals that have been simplified for the sake of modeling and experimentation. Our session focuses on extending theory, empirical methods, and modeling to deal with ways in which those real-world processes by which cooperative relationships evolve depend on subtle and complex interactions between cultural, social, and cognitive processes. Cases we'll discuss will include the evolution of the role of social identity in cooperation, the development of reciprocity among Arabian Bedouins, and the role of religious analogies in coordination of irrigation among Balinese rice farmers.

Bedouin hospitality: A case study in human altruism**BENJAMIN REILLY** (Carnegie Mellon University, Qatar)

The phenomenon of human altruism has inspired an enormous body of literature, most of it in the form of qualitative research based on computer modeling and controlled experimentation. This paper augments that literature with a quantitative case study of what appears to be an extreme example of human altruism, the hospitality practices of Arabian Bedouins. Overall this paper demonstrates that, while Bedouin hospitality is explicable in large part by current theories of indirect reciprocity these theories cannot explain the origins of hospitality. On the other hand, the theory of direct reciprocity, which in the case of Bedouin altruism consists of food/shelter/protection for information, does offer an explanation for the origins of Bedouin hospitality, and also helps to explain changes in Bedouin hospitality as Arabs settled or became more hierarchical in social structure. More broadly, this paper makes the case that historical, ethnographic, and anthropological materials are necessary in order to fully understand of human altruism, in particular to test the various theories of altruism that have appeared in field of evolutionary biology.

The evolving relationship between social identity and cooperative group formation through human cultural history**PAUL SMALDINO** (University of California, Davis, United States)

Although most research on the evolution of human cooperation has focused on overcoming the free rider problem, an equally important question is how the synergistic benefits of cooperation are generated. Here, I will draw attention to the evolving role of social identity in facilitating human cooperation. In contemporary industrialized societies, social identities serve a key function in cooperative group formation, enabling individuals with similar norms and complementary skills to assort. Importantly, we have not one social identity, but many, and how we express a social identity is highly dependent on context. However, the structure of the social environ-

ment has not stood still. In the small-scale societies of early *Homo sapiens*, most potential partners were known either directly or by reliable reputation, and the role of social identity was likely minimal. Since the rise of agriculture and hierarchical societies, social landscapes have grown increasingly varied as social organization placed new demands on individuals and offered new ways to identify oneself. Moreover, while increased diversity in skill sets and opportunities multiplied the set of possible cooperative interactions, increased population size and complexity meant that more and more initial interactions were with strangers. Due to the historical recency of these changes, the capacity for complex, variegated, and context-specific social identities is likely exapted from pre-existing psychological structures. I will present a coevolutionary model in which the complexity of individual social identities increases with the size and complexity of a population, corresponding to increased context-dependence of the psycho-social requisites for successful collaboration.

Modeling complex cultural interactions in cooperation: The coevolution of sustainable rice farming and religious practices in Bali

MARSHALL ABRAMS (University of Alabama at Birmingham, United States)

Using a computer model of success-biased cultural transmission of planting schedules in a network of Balinese farmers' "water temples", Lansing and Kremer (1993) showed how cooperative coordination for sustainable rice farming can evolve from local decisions: Niche construction and feedback involving water, crops, and pests led to local pockets of similarity and difference between planting schedules. Lansing (2006) later described psychological and cultural influences that routinely disrupt such coordination, along with religious practices that tend to suppress this sort of disruption. These religious practices bear both similarities and differences to those in other areas of Balinese society, yet seem to be tailored to the rice farming system. Why? How did this localized cultural harmony come about? I propose that religious practices in rice-growing regions in Bali also spread through success-biased cultural transmission: Religious practices that tended to suppress disruption of planting coordination spread because those who engaged in them were more successful at growing rice. I also suggest that analogies between religious practices and social factors in rice farming helped make the religious practices effective. To motivate these claims, I first extend a version of Lansing and Kremer's model by adding disruption of planting coordination, also adding a second channel of cultural transmission using a simplistic representation of religious practices. In a second modeling stage, I replace the simple religious representations with sets of propositionally structured beliefs, and incorporate a model of the role of analogies in cognitive processes. In this second stage, some sets of religious beliefs are made "plausible"- more likely to be believed -if they form analogies with existing beliefs about practices connected to rice growing. I argue that my models illustrate common patterns of interaction between real-world cultural variants, and illustrate processes by which cultural variants often come to exhibit subtle relations of harmony with each other.

DS M220

15:30 - 17:00

ORGANIZED SESSION / STANDARD TALKS

FORMAL EPISTEMOLOGY AND EVOLUTIONARY BIOLOGY

Organizer(s): **BENGT AUTZEN** (University of Bristol, United Kingdom)

Evolutionary biology raises a number of epistemological questions: How to test hypotheses about natural selection? How to infer evolutionary history? And, how to combine evidence from different sources? Formal epistemology has equipped philosophers with a number of tools to address these and other issues in evolutionary biology. The symposium will present current philosophical work at the intersection of the two disciplines. The purpose of the symposium is twofold. First, the session aims to provide new insights into epistemological problems in both Darwin's work and in contemporary biological research by applying formal methods. Second, the symposium will discuss conceptual issues arising from the application of formal methods to biological questions. That is, by applying formal methods to particular inference problems we can explore the implications and possible limitations of these techniques.

Is natural selection evidence for common ancestry?

ELLIOTT SOBER (University of Wisconsin-Madison, United States); **MIKE STEEL** (University of Canterbury, New Zealand)

Darwin thought that natural selection explains why all present-day life traces back to one or a few common ancestors. Here we investigate whether natural selection increases the probability of Darwin's thesis about common ancestry. We show that any such claim of probability raising is indefensible. We develop our argument by identifying the property of an evolutionary process that determines what its probabilistic impact on the common ancestry thesis will be. The point of this exercise is to understand how the parts of Darwin's powerful theory fit together, not to call into question common ancestry or natural selection, as these enjoy strong support.

Judgement aggregation and phylogenetics

JOEL VELASCO (Texas Tech University, United States)

Traditionally, phylogenetic inference has assumed as a background that there are unique histories for the particular taxa, species, organisms, or genes that you are examining. When you have multiple sources of evidence such as data from multiple genes, one possible class of methods for inferring that history is to treat the genes independently and try to aggregate the results in some manner. The realization that different genes quite often have different histories makes aggregation methods simultaneously more important if you are trying to build a unique tree and also less important since it opens up the possibility that we shouldn't be building a single tree at all. In this talk I will compare the situation in phylogenetics and in other aggregation contexts such as social choice theory and group deliberation to see what connections can be drawn and what can be learned from these connections and importantly, also how these contexts differ and why that matters.

Dissolving the star tree paradox in Bayesian phylogenetics

BENGT AUTZEN (University of Bristol, United Kingdom)

While Bayesian methods are widely used in phylogenetic systematics today, the foundations of this methodology are still debated among both biologists and philosophers. The "star tree paradox" in Bayesian phylogenetics refers to the phenomenon that a particular binary phylogenetic tree sometimes has a very high posterior probability even though a star tree generates the data. In this paper I discuss two proposals found in the biological literature of how to solve the star tree paradox. In particular, I defend the polytomy prior against some objections raised by biologists and argue that it is preferable to Yang's data-size dependent prior from a methodological perspective.

ORGANIZED SESSION / STANDARD TALKS

DISCOURSES ON ORIGINS: A PHILOSOPHICAL INQUIRY

Organizer(s): **PASCAL NOUVEL** (Université Paul Valéry Montpellier III, France); **GUILLAUME BAGNOLINI** (Université Paul Valéry Montpellier III, France)

As the mathematician and physicist Henri Poincaré said in his last series of lectures in Collège de France : "The problem of the origin of the world has always been a concern for all men who were thinking ; it is impossible to contemplate the spectacle of the stary universe without wondering how it has been formed." Indeed, the problem of origins does not pose itself only for the world as a whole but also for all of their components, including life, humans, language, techniques, and so on. In this session, we will present papers dealing with discourses on origins: discourse about the emergence of consciousness from the non-conscious (**Claus Halberg**), discourses on the origin of language and their relation with the origin of technics (**Arild Utaker**) as well as a typology of discourses on origins (**Pascal Nouvel**).

Origins without causes: On the phenomenological discourse on the origins of man

CLAUS HALBERG (Universitetet i Bergen, Norway)

The phenomenological movement emerged in European thought in opposition to what its pioneers perceived as the relativist threats involved in the contemporary attempts to explain human rational faculties along naturalist (psychological, physiological, and evolutionary) lines. However, the initial enthusiasm with the descriptions of the a priori structures of intentionality as a way to save rationality from the threat of relativism was tempered by an increasing sense that this "static" approach left important genetic matters out of consideration. The phenomenological, anti-naturalist discourse on the origins of man that ensued from this acknowledgment in key thinkers such as Husserl, Heidegger and Merleau-Ponty is very much alive among our present day's heirs to the phenomenological tradition. In this paper, I try to articulate what it is that distinguishes phenomenology as a contemporary discourse on the origins of man, the motivation and logic behind it, as well as the challenges it faces.

Paleoanthropology and the origins of man: The emergence of techniques and language according to André Leroi-Gourhan

ARILD UTAKER (Universitetet i Bergen, Norway)

Recent discoveries in paleoanthropology have put the question of the origins of man in a new empirical setting. Especially will the large time-scale of millions of years (creating different human species) cast doubt on the hypothesis of a sudden mutation leading to a talking being. Already in 1965 with his book *Gesture and Speech* Leroi-Gourhan argued for the slow development of human technics. Linking technics to the body and distinguishing between organs and functions of relations, he considered technics as the framework for the emergence speech. The paper will discuss this hypothesis by stressing how it is related to a general view on language as an exteriorization that belongs immanently to a human group.

A typology of discourses on origins

PASCAL NOUVEL (Université Paul Valéry Montpellier III, France)

Discourses on origins can be found in all and every cultures and at all and every times. Most of them consist in mythical or religious narrations, which are, as such, literary discourses. Our culture, however, did produce an other kind of narratives on origins, namely scientific discourses. These discourses present hypothetical theories on the origins (or, to use a more technical term, on the emergence) of things, plants, animals, humans, language, society, etc. Contemporary scientists, for instance Harold Morowitz, the author of *The emergence of everything: How the world became complex* (2004), are building narratives that tend to give a complete account of the things that exist based solely on scientific clues. In this paper we will discuss the diversity of discourses on origins and we will show that this diversity, although very broad, can nevertheless be understood with simple principles of analysis. Additionally we will suggest that the typology of four ontologies proposed by the French anthropologist Philippe Descola in his study on the diversity of human cultures (*Beyond nature and culture*, 2005) can also be found among discourses on origins. We will discuss the implications of such a striking similarity between the diversity of cultures and the diversity of discourses on origins.

DS M240

15:30 - 17:00

DS M320

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

TOPICS IN THE HISTORY OF GENETICS: MENDEL AND EXPERIMENTAL EVOLUTIONOrganizer(s): **YAFENG SHAN** (University College London, United Kingdom)

This session aims to reexamine the history of the origin of genetics, especially Gregor Mendel from philosophical, historical, and sociological perspectives.

Entwicklung or Vererbung? A new analysis of Mendel's Versuche**YAFENG SHAN** (University College London, United Kingdom)

The traditional understanding of Mendel's contribution as the discovery of the laws of heredity was seriously challenged in the late 1970s. Some (for example, Callender, 1988; Olby, 1979) develop the revisionist interpretation by postulating that Mendel's real concern is about the genesis of new species by hybridisation. Recently Müller-Wille and Orel (2007) tried to reconcile the two views by arguing that though Mendel's story is oversimplified by the traditional interpretation, it is right to maintain that Mendel's work is about inheritance. However, the debate goes murky especially when Mendel's contribution is not explicitly distinguished from what Mendel's objective is, and what was Mendel's understanding of his own work. I revisit Mendel's work on *Pisum* by focusing on three questions: What is Mendel's real concern in his paper *Versuche über Pflanzen-Hybriden* (1866)? What did Mendel believe that he achieved in the paper? Can Mendel's paper be understood as a study on heredity? And my answers are 1. Mendel's real concern in his paper is not about heredity. Rather, under Gärtner's influence, it is about development of hybrids in their progeny. 2. Mendel himself well confirmed in the 1866 paper and his correspondence with Nägeli that his key contribution is to discover the laws of development of hybrids. 3. Mendel's work on *Pisum* cannot be understood as a study on heredity, no matter how heredity is interpreted.

The great train crash of 1866**MICHAEL BUTTOLPH** (University College London, United Kingdom)

It is a fundamental objective of science to disseminate new work, so that it can be evaluated and used in later work. Mendel's paper on pea hybrids was published in 1866 but there was no significant discussion of this work until 1900. This can be explained if Mendel (1866) did not disclose anything that was of great value to science when it was published, in which case the system of science succeeded in adequately disseminating and evaluating Mendel's ideas (whether or not Mendel's ideas assumed a new significance in the changed intellectual climate of 1900). On the other hand, if at any time before 1900 a more widespread knowledge the work would have been beneficial for science, then it should have been accorded greater and earlier recognition. In that case the "long neglect" of Mendel (1866) was a failure of the system of science; being both unintended and undesired, it can be seen as an accident. Since 1900, there have been many suggestions as to the "cause" of this accident – obscurity of publication, mathematical analysis unfamiliar to botanists of the time, inconsistency with the ideas of Darwin, and so on. Generally each author contends for a single cause; but it is a basic tenet of

modern accident theory that significant accidents have multiple causes. Here each candidate "cause" is not considered as an explanation which could be sufficient in itself to explain what happened; instead each is regarded as one of many factors that made a greater or lesser contribution to the "long neglect". These many factors and their interrelations are mapped to produce a logical representation which sheds light on the immediate reception of Mendel (1866), and also provides new insights into the disputes about mendelism after 1900.

Purposes and implications of early experimental evolution**KELE CABLE** (University of Minnesota, United States)

With the experimental turn in biology at the turn of 19th/20th centuries, especially in the science of heredity, even evolutionary biology was folded into the experimental program. Scientists brought various organisms under their control in order to enact directed changes in domesticated animals and crops in addition to an array of laboratory-based experimental organisms. This creation – "experimental evolution" – replaced nature with humans, not only as the agent(s) of natural selection, but as the agent(s) that creates variation, controls genetics/heredity, and modifies the environment, with the purpose of developing not only an understanding of evolution, but also methods to control the process that underwrites life itself, so that humans could evolve organisms according to their own desires. My paper will focus on the issue of agency in experimental evolution, especially within the context of the work of various evolutionists and geneticists, such as Darwin and Mendel, Hugo de Vries, Charles Davenport, T.H. Morgan, and William Castle. I will discuss what they considered the purposes of experimental evolution to be and what wider implications they thought their work held, for both science and society.

ORGANIZED SESSION / STANDARD TALKS

WHAT ARE ECOLOGICAL COMMUNITIES, AND ARE THEY PRESERVABLE?Organizer(s): **CHRISTOPHER LEAN** (Australian National University, Australia); **ALKISTIS ELLIOTT-GRAVES** (Rotman Institute, Canada)

The aim of community ecology is to explain ecological communities (i.e., assemblages of populations), how they influence each other and how they co-exist. The ontological status of ecological communities has been energetically contested within the ecological sciences for almost 90 years, with battle lines drawn up between realist and anti-realist camps. Providing a substantive account of what ecological communities are has ramifications that extend beyond the practice of ecological science. Conservation efforts often focus on the preservation of ecological communities and/or describe ecological communities as nodes of normative worth. As a result, the philosophical debate over ecological communities has become a practical issue confronting conservation workers and governmental agencies attempting to preserve biotic communities. Recently, philosophers have started to take notice of these foundational debates within ecology and contribute. This session will further this inquiry with three new papers on ecological communities.

Ecological community identity is not a function of emergent properties

CHRISTOPHER ELIOT (Hofstra University, United States)

Ecological communities are units of description in biological ecology. They consist of more than one population and generally do not include abiotic components. Whether communities exist as such is of interest to conservation policy, conservation biology, and scientific realists. I'm aware of 6 general positions on whether ecological communities exist, and to the extent that something is a community, what criteria it can be recognized by: (1) eliminativist accounts (defended by Gleason, for one example, on one reading), suggesting that no communities exist as such; (2) co-occurrence accounts (Shrader-Frechette and McCoy), suggesting that communities are generally merely statistical associations; (3) place-based accounts (Odum), attending to location alone, to the exclusion of any membership or interaction criteria; (4) interaction strength accounts (Odenbaugh) recognizing communities above a threshold of interaction strength among populations; (5) causal-perspectival accounts (Lockwood, Eliot), embracing pluralism about kinds of communities based on the kinds of causation knitting them together; (6) emergentist accounts (Mikkelson, Sterelny, perhaps Mitchell), recognizing communities as such when they reveal emergent properties including top-down self-regulation. In this paper I assess the strengths of emergentist accounts of communities against the others. They are well-motivated, and I accept the capacity of emergent properties to ground identities, but I am skeptical that any naturally-occurring communities meet such criteria for identity or derive their identities from their possession of any emergent properties.

Ecological communities are robust population networks

CHRISTOPHER LEAN (Australian National University, Australia)

The task of providing a substantive description of ecological communities bears upon hypotheses in both ecology and conservation science. Ecologists have frequently questioned whether ecological communities “exist” or are just observer defined with the scientist or conservation worker dictating the boundaries of the community. Richard Levins and Richard Lewontin provided an early reply to such scepticism, proposing that ecological communities are causal networks of populations. I develop an allied view which recruits the Woodwardian “difference-making” account of causation to define ecological communities as causal networks of populations. I propose that a “real”, and distinguishable, ecological community is a robust causal network of populations. The network is identified via the counterfactual effects of intervention on a single population radiating through other local populations. This network is bound by the dissipation of the force of the initial intervention through the other populations. If intervention on different populations that are spatially and temporally proximate yield the same or similar population networks, then this network can be considered robust. Network robustness can also be identified through varying the type of intervention on a population and the strength of intervention. This account has the virtue of being able to exclude ephemeral networks that appear through transiently interacting populations and captures how communities appear to have a stable identity without being beholden to the stability-diversity hypothesis in its various guises. Accordingly, this account offers a schematic for distinguishing between simple aggregates of populations and communities. A distinction which, I argue, is supported by empirical evidence from community ecology.

Is Aldo Leopold's “Biotic Community” an individual?

ROBERTA L. MILLSTEIN (University of California, Davis, United States)

Aldo Leopold's Land Ethic has often been interpreted as ascribing intrinsic value to what he calls the biotic community. But what is the biotic community? Is it actually an entity at all, which might seem necessary (albeit not sufficient) for it to be intrinsically valuable; more precisely, is it an individual? Some authors equate Leopold's “biotic community” with “ecosystem.” It is true that Leopold's concept of “biotic community” is similar to that of “ecosystem,” since like an ecosystem it includes abiotic components and like an ecosystem it is at least partially characterized in terms of energy flow. However, Leopold also emphasizes that a biotic community is composed of interdependent parts. By underscoring the interactions between species and the way in which changes in some species affect other species, his concept of “biotic community” sounds a bit more like the concept of “community” studied by community ecologists. So, perhaps Leopold's “biotic community” blends the concepts of “ecosystem” and “community” in some fashion. But this blending raises a complication, which is illuminated nicely by considering a recent essay by Jay Odenbaugh. Odenbaugh invokes a “causal relations” criterion of individuality; the relevant causal relations for communities are interactions between species whereas the relevant causal relations for ecosystems consist of nutrient and energy cycling. If this is right, what sense can be made, if any, of a blended community-ecosystem? Would it be an individual as well? I explore answers to these questions, considering, e.g., recent attempts to integrate community and ecosystem ecology. My goal is to shed light on what an integrated community-ecosystem might look like and how to make sense of the relationship between a community-individual, an ecosystem-individual, and a community-ecosystem-individual, helping to provide a solid basis for Leopold's Land Ethic.

DS M460

15:30–17:00

ORGANIZED SESSION / STANDARD TALKS

FROM THE TISSUE ORGANIZATION FIELD THEORY OF CARCINOGENESIS TO A THEORY OF ORGANISMS AND BACK

Organizer(s): **MAEL MONTÉVIL** (Université Paris Diderot - Paris 7, France); **MATTEO MOSSIO** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France); **ANA SOTO** (Centre Cavailles, École Normale Supérieure, France); **CARLOS SONNENSCHN** (Tufts University, United States)

In 1999, C Sonnenschein and AM Soto proposed the tissue organization field theory (TOFT) that views cancer as a tissue-based disease akin to morphogenesis gone awry. Understanding cancer requires paradigmatic changes which are incompatible with the reductionist genocentric perspective of the molecular biology revolution. While the theory of evolution provides increasingly adequate explanations of phylogeny, biology still lacks a theory of organisms that would encompass ontogeny and life cycles. To achieve this goal we propose that theoretical extensions of physics are required in order to grasp the living state of matter. Such extensions will help to describe the proper biological observables, i.e. the phenotypes. Biological entities must also follow the underlying principles used to understand inert matter. However, these physical laws and principles do not make biological dynamics intelligible at the phenotypic level. We will propose a default state and a framing principle as basis for a theory of organisms.

The biological default state

ANA SOTO (Centre Cavaillès, École Normale Supérieure, France); **MAEL MONTÉVIL** (Université Paris Diderot - Paris 7, France); **CARLOS SONNENSCHNEIN** (Tufts University, United States)

A theoretical transition from physics to biology requires defining a default states that is a limit case. By describing inertia as the default state in mechanics, Galileo could focus on the analysis of the forces constraining it. Organisms are far-from-equilibrium systems that require a flow of energy and matter. More specifically, the “unconstrained” condition proper to the biological default state requires adequate physical conditions (temperature, pressure and pH). Sufficient nutrients provide a flow of energy and matter canalized through metabolic processes that keep cells alive regardless of whether cells are proliferating or quiescent, moving or immobile. In contrast, “a default state happens when nothing happens to prevent it”. The default state should not be conflated with conditions necessary for life. The biological default state is cell proliferation with variation and motility and represent the constitutive properties of the living. Variation is generated in particular by the mere fact that cell division generates two overall similar, but not identical cells. Darwin explicitly stated “...There is no exception to the rule that every organic being naturally increases at so high a rate, that, if not destroyed, the earth would soon be covered by the progeny of a single pair”. Reproduction comes with “modification” (descent with modification, in Darwin's words). Reproduction with variation is intrinsic to organisms regardless of whether they are unicellular or multicellular. Darwin's narrative implies that reproduction with variation is a default state. Motility, which encompasses cell and organismic movements as well as movement within cells is the most obvious manifestation of the agentivity of the living. The analysis of constraints to proliferation with variation and to motility are fundamental to organismal biology like the constraints to inertia (forces) are fundamental to mechanics. Finally, the default state provides a theoretical link between the theory of evolution and the theory of organisms.

A novel framing principle for biology

MAEL MONTÉVIL (Université Paris Diderot - Paris 7, France); **CARLOS SONNENSCHNEIN** (Tufts University, United States); **ANA SOTO** (Centre Cavaillès, École Normale Supérieure, France)

Biophysical approaches to biological phenomena have provided fruitful insights, yet they generally suffer from the direct transposition of physical paradigms and methods into biology, without the appropriate analysis of the deep theoretical implications of the transposed concept (for example, about the conservation of energy, or the symmetries involved). In this context, we are now proposing theoretical principles that are genuinely biological in order to discuss the mathematical analysis of biological processes. Namely, biological processes can be interpreted as the never-identical iteration of morphogenetic processes. This iteration takes place both a) at the level of tissues and organs, where for example, it can lead to fractal-like structures, and b) at the level of organisms (including cells), where it leads to the flow of generations, which phylogeny aims to reconstruct. The non-identical character of these iterations correspond to a specific form of variation, not just of a quantitative nature but of changes in the mathematical regularities that enable to study the corresponding processes. We will discuss how the concept of never-identical iteration of a morphogenetic process facilitates an understand-

ing of both ontogenetic and phylogenetic processes, and we will give examples of its usefulness when applied to the process of branching morphogenesis of the mammary gland epithelium. It is noteworthy that phylogenetic analyses are based on the notion that individuals that are afar in the genealogy have different relevant characters. Finally, we will briefly discuss the epistemological consequences of this proposal as for the nature of the articulation between mathematics and biological phenomena.

From a theory of organisms to carcinogenesis

CARLOS SONNENSCHNEIN (Tufts University, United States); **ANA SOTO** (Centre Cavaillès, École Normale Supérieure, France); **MAEL MONTÉVIL** (Université Paris Diderot - Paris 7, France)

The tissue organization field theory (TOFT) posits that cancer is a tissue-based disease akin to development and morphogenesis gone awry. Carcinogens (directly) and mutations in the germ-line (indirectly) may alter normal interactions between the different cellular components of the morphogenetic field, including the reciprocal interactions between stroma and adjacent epithelium. The principles we postulated for the construction of a theory of organisms provide novel insight into normal and neoplastic development. Regarding the latter, carcinogens alter and relax the constraints that operate from tissues to the cells inside them. This, in turn, allows the cells within tissues to regain their constitutive properties, which are proliferation with variation and motility. Because proliferation with variation and motility represents the fundamental postulate (i.e., the equivalent of inertia), they do not require an explanation. What requires an explanation are the constraints that limit the default state. This novel perspective makes useless the search stimulators of proliferation (i.e., the so-called growth factors) and cellular movement and migration. We will analyze experimental data obtained from this theoretical framework, including the normalization of “cancer cells” achieved when those cells are transplanted in the midst of normal tissues.

DS R340

15:30 - 17:00

ORGANIZED SESSION / STANDARD TALKS

NOVELTY AND DISCONTINUITY IN EVOLUTION

Organizer(s): **THIBAUT RACOVSKI** (University of Exeter, United Kingdom)

Evolutionary novelties as opposed to quantitative phenotypic variation and macroevolutionary patterns as opposed to microevolutionary events play strategic roles in current theoretical debates in evolutionary biology, especially with respect to the call for an “Extended Evolutionary Synthesis” (EES) (e.g. Müller & Pigliucci 2010). The core of the Modern Synthesis (MS) was a theory of microevolution, formalized by population genetics as changes of allele frequencies in populations under the influence of natural selection and other population-level forces. The claim that macroevolution can be extrapolated from microevolution (Simpson, 1953) could solve the problem of novelty. From the 1970s onwards, this picture has been challenged on several fronts: from paleontology, with the theory of “punctuated equilibria” (Gould and Eldredge 1972); from developmental biology, with the study of heterochrony (e.g., Gould 1977) and other regulatory phenomena studied in the

context of EvoDevo; from physical theories of self-organization (e.g., Kauffman 1993); and, from studies on the role of symbiosis in macroevolution (Margulis 1970). This session aims to assess the impact of these advances in different biological disciplines on issues related to novelty and macroevolution. These advances led some defenders of an EES to argue that the MS did not have the theoretical means to address these issues (e.g. Pigliucci and Müller 2010). While contributing to a deeper understanding of novelty and macroevolution, the variegated theoretical landscape makes it difficult to formulate a unified framework. A first talk (**Huneman**) addresses the respective impacts of different challenges (especially biological and mathematical) to the extrapolationist thesis. A second talk (**Love**) tackles the problem of integrating different approaches to the explanation of novelty, especially the historical and experimental approaches. A third talk (**Racovski**) addresses ambiguities in the definitions of evolutionary novelty and show how they weaken the case for an EES.

Macroevolution and microevolution: Timescale and modeling in evolutionary biology

PHILIPPE HUNEMAN (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

According to the Modern Synthesis, population genetics, as the science of the dynamics of changing allele frequencies in a population, is the core of evolutionary biology since it explains the arising of adaptations by cumulative selection. Its scale is microevolution, namely, evolution of the population of one species within a timescale not too large, defined by a small window of variations and environmental changes. Microevolution contrasts with macroevolution, that is, a longer timescale that involves large environmental changes such as the extinction or emergence of species and clades. MS claimed that macroevolution is not different from macroevolution. This “extrapolationist” thesis formulated by Simpson (1953) is challenged: by the “punctuated equilibrium” thesis, recently by Evo-Devo, or by biologists highlighting that symbioses – sometimes occurring at the microevolutionary scale - have major macroevolutionary effects (Margulis, 1970). This talk questions why the extrapolationist thesis is threatened by advances in ecology and developmental theory. It essentially distinguishes between biological and mathematical reasons why there could be principled differences between microevolution and macroevolution. The former concern the nature of variation, which fuels natural selection: whether it’s only made up by mutations and sexual recombination, or whether other developmental features should account for phenotypic variation. Mathematical reasons concern the modeling of chance events in microevolution: at larger timescales, models of chance (such as Gaussian distribution of fluctuations) may not be any more justified, and other models would be required, though at microevolutionary timescales all models would be in practice equivalent. This argument relies on the distinction made by mathematician Mandelbrot between “wild randomness” and “mild randomness” as two distinct structures of randomness. I conclude by showing that the mathematical differences between micro and macroevolution are more general, and therefore may challenge the extrapolation thesis even if empirical facts do not support the biological differences.

The centrality of experiment in the historical science research program on evolutionary novelties

ALAN LOVE (University of Minnesota, United States)

Most evolutionary novelties originated long ago in the history of life. Some philosophers have argued that there are key differences between experimental and historical science, such as the latter exhibiting confirmation that relies on explanatory power rather than predictive success (Cleland 2011). Investigations of evolutionary novelties, such as the origin of the tetrapod limb or angiosperm flower, fall into historical science as they concern past events and require an explicit reconstruction of the phylogenetic juncture relevant to the period of origination for a trait (Love 2008). At the same time, most biologists working on explanations of the origin of novelties see their research program as experimental, and this experimental aspect is crucial to its viability as a developmental contribution to evolutionary theory (Wagner 2001). This paper will explore what it means for a historical science research program to be experimental by scrutinizing two different approaches to the origin of novelties developmental genetics and generic, physical mechanisms (Wagner 2014 Newman 2012). The lines that have been drawn between historical and experimental science do not capture the nature of these research programs and the associated scientific inquiry is better interpreted as organized by structured problem agendas that encourage an explicit combination of historical, experimental, and comparative dimensions.

On ambiguities in the definition of evolutionary novelties and their consequences for the debate on the extended evolutionary synthesis

THIBAUT RACOVSKI (University of Exeter, United Kingdom)

A commonly accepted intuitive definition of evolutionary novelty exists: a new phenotypic trait bringing a qualitative difference, rather than a quantitative one, compared to traits already present in the lineage. However, there are currently several technical definitions of evolutionary novelty in use, some incompatible with each other. In recent years, the search for a unique definition has been criticized as harmful for research (Brigandt & Love 2012). In this framework, the diversity of definitions corresponds to diverse explanatory goals. Furthermore, this search for a unique definition has been overcome by devising typologies of novelties (e.g. Müller 2010). There is however one important reason to be careful in assessing this diversity: the concept of evolutionary novelty is closely related to the debate over the need for an Extended Evolutionary Synthesis (EES). Novelty is often presented as a class of phenomena that is allegedly not fully covered by explanations from traditional evolutionary biology and that demands theoretical changes to be fully addressed (Pigliucci and Müller 2010). In this talk, I argue that the plurality of definitions of novelty is a sign of the weakness of the concept of novelty itself. I focus on the prominent definition of novelties as traits with no homologs (Müller and Wagner 1991), and on subsequent variants of it. I show that among different proponents of this single definition, there are explicit or implicit disagreements on the essential properties of evolutionary novelties (developmental independence, lack of evolutionary intermediates, specific processes of origination). I then argue that these properties are actually independent (one often comes without the others) and that some are not specific to novelties. I end by analyzing the role of the concept of novelty in the defense of an EES and how a weakened concept of novelty affects this defense.

DS R510

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

CANCER CAUSATION AND EXPLANATIONOrganizer(s): **KATHERINE LIU** (University of Minnesota, United States); **ANYA PLUTYNSKI** (Washington University in St Louis, United States)

Cancer presents a fascinating case study for exploring a variety of questions about demarcating biological processes and entities, and the complimentary roles of molecular genetics, evolution and development in explaining disease. In this session, longstanding issues in philosophy of biology surrounding the unit or level of organization, the demarcation of biological kinds, the theoretical and practical relationships between molecular biology, evolution, and development, and the scope and limits of methodological reductionism overlap with longstanding issues in philosophy of medicine concerning disease classification and debates about how best to move from "bench to bedside." Some questions we investigate are: Is cancer a process or product? How is cancer a product or by-product of developmental processes? What are the scope and limits of molecular genetic explanations of cancer initiation and progression? How can evolutionary and developmental perspectives on cancer be integrated? This session will explore these questions, drawing upon current research in the sciences, situating the discussion *vis-a-vis* current philosophical work on the metaphysics and epistemology of the biomedical sciences.

Rethinking cancer through modularity**KATHERINE LIU** (University of Minnesota, United States)

Cancer research is guided by two main conceptual models: (1) a molecular, biomarker approach focused on individuals; and (2) an evolutionary approach based in populations. In both cases, these models are meant to inform us about causal relationships in cancer such that researchers can develop clinical interventions. I argue that these conceptual models are not sufficient for cancer translational research, even when considered jointly. This is because they fall along the proximate-ultimate distinction, and it has been shown that maintaining this distinction is problematic. Taking a more integrated approach gives a more thorough causal picture. I offer a novel conceptual model for understanding cancer that based in modularity – the relationships between parts and wholes. This model helps us to understand the evolutionary dynamics of cancer by emphasizing changes in the degree of modularity over time as a major causal factor. This model helps bridge the proximate-ultimate distinction since modularity is about the relationships between hierarchical levels. I will end with a plan for how we can study this using microbial experimental evolution. Together this conceptual model and experimental approach will help clarify the complexity of causal factors in cancer and hopefully lead to the successful development of new clinical interventions.

Cancer as a process**JOHN DUPRE** (University of Exeter, United Kingdom); **MARTA BERTOLASO** (Università Campus Bio-Medico, Italy)

Everyone knows that the idea of seeking "the cause" of cancer is a mistake, since cancers are diverse and different cancers have different etiologies. A more unified perspective on the subject can nonetheless be discerned by taking seriously the fact that cancer is a process rather than a thing. Cancer is, indeed, a malfunction of a quite normal process, cell division or even, more broadly, development. This simple distinction has at least two significant implications. First, there is no reason to expect there to be any essential difference between cancerous and non-cancerous parts of an organism. There may be distinctive cancer cells or cancer genes in some or all cancers, but this cannot be assumed. Second, our understanding of development remains quite limited. In particular, we need a deep understanding of the exquisite regulation of cell development that allows particular cell lineages within an organism to reach and maintain a functional size. Without such an understanding the fundamental question that we need to address is not why we sometimes develop cancer (misregulation of cell division), but why we so often fail to develop cancer.

Sexual conflict or genial genes? The seductive temptations of evolutionary explanations of gender disparities in cancer**ANYA PLUTYNSKI** (Washington University in St Louis, United States)

Is better science necessarily sexist science? Epidemiologists have long known that there are significant differences in cancer susceptibility between males and females even in early childhood, males have a higher incidence of cancer, and higher mortality (Dorak, et. al., 2012). This has led some advocates of evolutionary medicine to argue that there are sex-specific genetic, developmental and evolutionary causes of this difference. For instance, short repeats of the CAG region of the androgen receptor are associated with increased trans-activation of the receptor and increased body size, but also increased risk of prostate cancer, and more aggressive forms of disease. This has led to the suggestion that differential susceptibility to cancer could be driven by antagonistic pleiotropy enhanced reproductive success early in life at the expense of reduced survivorship later in life (Summers Crespi, 2008). Genes associated with antagonistic pleiotropy are expected to drive sexual conflict, where sexual conflict is when aspects of one sex's behavior, physiology, or phenotypic traits enhance that sex's fitness but impose a cost on the fitness of the opposite sex. Sexual conflict, it's argued, is expected because the sexes maximize their fitness via different and mutually incompatible strategies. Sex-specific optimization of reproductive strategies could result in different life spans and aging rates, and this could cause sexually antagonistic selection on shared genetic architecture. Is the disparity in cancer incidence and mortality driven by sexual conflict? This paper considers a variety of evidence and alternative explanatory strategies (e.g., immune surveillance differences, and/or differences due to the laboratory environment and gene x phenotype interactive effects in resource rich environments). In addition, I consider the broader import of such work for cancer treatment and prevention. How, if at all, does the study of sex difference in causes of cancer enhance our understanding of how to intervene on the disease?

DS R515

15:30–17:00

ORGANIZED SESSION / STANDARD TALKS

ARE HALF OF AMERICANS REALLY CREATIONISTS?Organizer(s): **MICHAEL WEISBERG** (University of Pennsylvania, United States)

The American public seems strongly resistant to evolutionary theory. Some polls suggest that almost 50% of Americans are young earth creationists. The participants in this section are actively engaged in studying and trying to explain acceptance of and understanding of evolution in the US. Each paper builds a more nuanced picture about exactly what Americans accept and reject, the extent of their biological understanding, and what could explain deviations from the overwhelming biological consensus about evolution.

Creationists' criteria for credence: An account of the conflicting frameworks of evolution and creationism**EMLÉN METZ** (University of Pennsylvania, United States)

Interviews with a cross section of Americans suggest that the conflict between creationists and proponents of evolution arises in part from their allegiance to different criteria for what makes a belief more likely to be true. This may be one reason that deeper cognitive reflection can increase ideologically motivated reasoning (Kahan, 2013). Kahan suggests that reasoning about controversial beliefs is often not purely truth directed, but used to signal loyalty to ideological affinity groups. However, interviews with creationists and evolutionists suggest that the frameworks of creationism and science themselves include different conceptions of ideal reasoning even as directed at truth-finding. Philosophy of science acknowledges multiple epistemic values which sometimes conflict, such as simplicity, scope, and generativity. Within contemporary science, different epistemic values are emphasized in different disciplines. Creationists and non-creationists also seem to hold different epistemic values. Those who believe in evolution emphasize openness to empirical evidence (i.e. responsiveness to publicly accessible reasons), while the creationists emphasize the knowledge of the heart (i.e. faith or revelation). Each considers their own way of thinking more disciplined, because their notion of what counts as epistemic discipline is different. Each view is thus supported by its own internally specified criteria for what makes a good view. Insofar as creationists' confidence is founded on their preference for alternative modes of reasoning, an accumulation of scientific evidence will have little effect. Changing minds would require a conversion of ideals of reasoning.

The disentanglement project**DAN KAHAN** (Yale University, United States)

"Evolution" refers not only to a scientifically grounded account of the natural history of life on earth but also to a symbolic issue positions on which signify membership in one or another cultural group. The confounding of the former and the latter are at the root of a cluster of related societal problems. One is simply how to measure individual comprehension of evolutionary science and science generally. Another is how to impart collective knowledge on terms that avoid needlessly conditioning its acquisition on an abandonment or denigration of cultural commitments collateral to science. And a final problem is how to insulate the enterprise of acquiring,

assessing, and transmitting knowledge from dynamics of cultural status competition corrosive of the reciprocal benefits that science and liberal democratic governance naturally confer on one another. My paper will discuss the "disentanglement project," an empirical research program aimed at identifying an integrated set of practices for unconfounding the status of evolution as a token of collective knowledge and as a symbol of cultural identity within the institutions of the liberal state.

Probing public understanding and acceptance of evolution**MICHAEL WEISBERG** (University of Pennsylvania, United States); **DEENA SKOLNICK WEISBERG** (University of Pennsylvania, United States); **JANE REZNIK** (University of Pennsylvania, United States)

In a recent Gallup Poll, 46% of Americans reported that they believe humans were created in their present form within the last 10,000 years. These responses stand in sharp contrast to those of biologists, who overwhelmingly accept evolution. Why do Americans overwhelmingly fail to accept that humans have a purely naturalistic origin? And what do they believe about other species and other aspects of evolutionary theory? Although it is tempting to think that Americans' resistance to evolution is explained solely by ignorance or religious fundamentalism, previous research suggests that this issue is considerably more complex. For example, people's understanding of evolution is not correlated with their acceptance of it, but their understanding the provisional nature of scientific theories is. We report on an ongoing project that systematically investigates the public's knowledge about and attitudes towards evolution by presenting probative, psychologically sophisticated instruments to a demographically representative national sample. We will discuss the range of evolutionary ideas accepted and rejected by our subjects, the extent to which these ideas are understood, and some hypotheses about what might explain our results.

DS R520

15:30–17:00

ORGANIZED SESSION / DIVERSE FORMAT

NORMS, KINDS, AND BIOLOGICAL PRACTICEOrganizer(s): **THOMAS REYDON** (Leibniz Universität Hannover, Germany)

Participant(s):

MATTHEW BARKER (Concordia University, Canada)**MARC ERESHEFSKY** (University of Calgary, Canada)**P.D. MAGNUS** (University at Albany, United States)**MATTHEW SLATER** (Bucknell University, United States)**THOMAS REYDON** (Leibniz Universität Hannover, Germany)

Philosophers of science have long been searching for an account of kinds and classification that does justice to the plurality of classificatory practices in the various sciences. Especially in the biological sciences considerable differences between classificatory practices can be found, for example between classifications of microbes and "macrobes", between classifications of plants and animals, or between classifications in different research contexts, for example ecology and evolutionary biology.

This session aims at presenting recent advances in formulating such accounts, as well as assessing the directions in which further research should be going. In doing so, it discusses concrete biological cases such as the kinds polygenomic organism and living thing, type specimen methodology, frog and spider taxa proposed for classificatory revision within integrative taxonomy, and microbial classification. The session takes the form of a panel of four speakers plus a commentator. All five participants are working on accounts of classification and kinds with close attention to biological practice, and the four speakers are currently working on the topic in teams of two.

Thomas Reydon will set the stage by asking why the philosophy of biology (and of science more generally) needs an account of natural kinds in the first place. He examines the various aims of biological classifications, and in what ways philosophical accounts of kinds might come closer to providing a faithful picture of actual classificatory practice in the biological sciences. This involves examining which criteria any acceptable account of natural kinds should meet. **Marc Ereshefsky** points out that while philosophers tend to posit monistic theories of natural kinds, many successful classificatory practices in science are inconsistent with such monistic theories of natural kinds. According to Ereshefsky, given the diversity of epistemic aims scientists have for positing classifications we need a non-monistic account of natural kinds that is sensitive to the diversity of classificatory practices in science. Nevertheless, such an account should not merely say that any group of entities highlighted by a scientific classification is a natural kind. Consequently, we need a pluralistic theory of natural kinds that has a normative component. Ereshefsky proposes a pluralistic account of natural kinds, based on Laudan's normative naturalism.

Matthew Slater examines classificatory practices to distill from them several specific classificatory norms that they explicitly or implicitly imply. Scientists' appeals to norms are motivated by both empirical and extra-empirical factors, and Slater argues that good arguments for classification claims must appeal to both factors. This raises questions about the extents to which different classificatory norms are rationally evaluable. **Matthew Barker** addresses these questions with an eye to how empirical and philosophical methods should coordinate when answering them. He argues that there are different types of classificatory norms, including both epistemic and pragmatic, and clarifies how these operate in parallel within a layered view of rational evaluability. On this view, if an epistemic norm helps justify a classification claim, then some pragmatic norm does too. And if a pragmatic norm itself receives any further justification, then pragmatic appeal to further goals of ours is among the further justifiers. This leaves open that successful justification for a classification claim may have empirically derived epistemic parts to it, but insists that in such cases the success of the justification must depend on pragmatic parts too. Science typically provides any empirically derived epistemic parts of justifications; philosophy can and should help with the pragmatic parts by clarifying classificatory norms, our goals, and relations between these.

P.D. Magnus closes by giving an overall commentary on the four talks and opening the discussion between the panel and the audience.

DS R525

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

ETHICAL DIMENSIONS OF PHILOSOPHY OF RACEOrganizer(s): **ADAM HOCHMAN** (Macquarie University, Australia); **JON RØYNE KYLLINGSTAD** (Norsk Teknisk Museum, Norway)

In this session we explore some of the ethical dimensions of philosophy of race, with a focus on the contemporary biologically and psychologically informed literatures. First, what role should moral and political considerations play in racial ontology? Should we understand the reality of race as primarily a normative issue? Can normative considerations be part of the metaphysics of race? Second, what is the relationship between morally loaded biological racial realism and mere “misreadings” of the biological evidence surrounding human population structure? Are those people misusing the science to support racial classifications (in for example ways that seem racist) morally culpable even if they are sincere in their misreading of the evidence? Under what conditions is it reasonable to consider the possibility that some misreadings of the contemporary evidence might not be innocent? Finally, in what sense can we hold those people who hold implicit (unconscious) biases against racialized groups morally responsible for those biases, and/or for the actions which arise out of them? What strategies might be deployed to minimize the effects of these biases?

In defence of the metaphysics of race**ADAM HOCHMAN** (Macquarie University, Australia)

Philosophers have been increasingly active in the debate about the reality of race since it heated up in the new millennium. Some argue against the reality of biological race. Some argue that race is biologically real. A few – and it is with these scholars that this talk is concerned – have defended a deflationist position which would subvert the debate about the reality of race. These deflationists are against metaphysical approaches to the debate. While the anti-metaphysicians do not all agree on what the metaphysics of race actually entails, they do agree that the ontological status of race should be determined on normative, rather than metaphysical, grounds. In this talk I argue that we should understand the metaphysics of race as being concerned, quite simply, with the following question: “what is race, and is race real?” On this understanding of the metaphysics of race one can include normative, semantic, and pragmatic considerations when answering the above question, but still be doing the metaphysics of race. Yet the issue remains, “how should we answer our metaphysical question?” The anti-metaphysicians argue that it should be answered on pragmatic and normative grounds, and that the answer(s) should be context specific (we might want to say that race is real in contexts where race is socially or biomedically useful, for instance). I will argue, on pragmatic grounds, that this line of argument ought to be run alongside arguments in which the normative commitments of authors play a less explicit role.

Human races, biological realism, and “slippage”**JONATHAN KAPLAN** (Oregon State University, United States)

There are at least two distinct elements to answering questions about the biological reality of human races: first, what is required for “races” to be biologically real entities, and second, what the biological facts can support. Put this way, the project might seem straightforward: propose a defensible definition of “race” in humans, and see whether the biological facts support or speak against that definition being instantiated in the world. But things are not so simple. There is often a kind of “slippage” – a weak definition of race will be proposed in order to show that biological facts can support it, and then a stronger definition “snuck in.” In such cases, what seems to be driving the process is the desire for easy shortcuts to social/political or moral conclusions. Race naturalists who affirm a weak version of racial realism, but then slip into a strong version, may be helping themselves to what would otherwise seem like obviously racist positions without explicitly defending them. Keeping clear about what, precisely, one means by the claim that human “races” are (or are not) biologically real is one way to counter this kind of slippage.

Agential technologies and implicitly biased behaviors**NATALIA WASHINGTON** (Purdue University, United States)

In this paper I discuss the moral significance of our increasing empirical knowledge about implicit racial biases, asking how we as agents can use these gains to actively shape our own moral ecology I aim to defend two claims: first, that people can be responsible for actions that are influenced by biases they do not know they have and that they would disavow if they were made aware of, and second, that the kind of agency involved in taking responsibility for bias is best conceived from an externalist perspective. My defense of these claims will involve framing the issue in terms of kinds of control-based and knowledge-based exculpating conditions commonly taken to excuse actions, laying out the core features of implicit biases, and considering whether anything about the character or operation of implicit biases themselves satisfies those conditions, or guarantees that actions influenced by them should be excused. Finally I comment on how bias is addressed by individuals in institutional contexts such as policing, hospitals, and schools.

17:00 – 17:30

COFFEE BREAK

17:30 – 19:00

PLENARY SESSION – SANDRA HARDING | Marie-Gérin-Lajoie auditorium

19:00 – 20:30

POSTER SESSION AND COCKTAIL | Lobby of Marie-Gérin-Lajoie auditorium

POSTER

CLAUDE BERNARD AND THE EXPERIMENTAL METHOD WITH LIVING ORGANISMS**ALAN DANTAS S. FELISBERTO** (Universidade Estadual de Campinas, Brazil)

Inserted into the search History of Biology line, this study aims to explore the epistemic context in which it was the doctor and physiologist Claude Bernard (1813-1878), and the evidence that led to the historiographical interpretation that appointed him “father” or “founder” of experimental physiology. Regarding the methods of investigation, it is known that Francis Bacon, René Descartes and other thinkers had formed the general principles of what is known as the scientific method (Schiller, 1967, p.118), but the consolidation of an experimental methodology living beings involved the integration of two elements: observation and experience (Schiller, 1967, p.118). Such concepts were found in the works of William Harvey (1578-1657), Franz Sylvius de le Boe (1614-1672), and Claude Perrault (1613-1688), no apparent systematic (Schiller, 1967, p.118-119). In the second half of the eighteenth century, three researchers showed the first attempts to systematize the methods of observation and experiment with living beings through his works: George Zimmermann (1728-1795), Samuel Georges Carrad (1740-?) and Jean Senebier (1742-1809), (Prestes, 2006, p. 227-228). Among them, in the mid-nineteenth century, the physiologist Claude Bernard was one of the experimenters who drew the attention of the scientific community of his time. Two relevant evidences about its reputation are: the large number of publications, especially of the book *Introduction à l'étude de la médecine expérimentale* in 1856, which established some formal basis for methods of experimentation with living beings; the applicant resumed his earliest experiments to remake them more systematic way and with greater depth of reflection and interpretation, which he did, at times, give up the established theories on such experiments (Holmes, 1974, p. 257).

POSTER

EDWARD O. WILSON'S “CONVERSION”: A CURRENT POLEMIC ABOUT GROUP SELECTION**LÍVIA ASSUNÇÃO** (Universidade Federal da Bahia, Brazil); **MARK BORRELLO** (University of Minnesota, United States);**JUAN MANUEL SÁNCHEZ ARTEAGA** (Universidade Federal da Bahia, Brazil)

Since the publication of *On The Origin of Species*, in 1859, the level of biological organization at which natural selection works has been under discussion by evolutionary biologists. The idea that natural selection could work in different biological hierarchies, more specifically at the level of individuals and at the level of the groups of individuals, was first proposed by Charles Darwin and was intensely discussed during the beginning of the 20th century. However, from the mid-1960s, the theory of group selection began to be widely rejected. One of the causes of this rejection was the decisive criticism by George C. Williams and the advent of alternative explan-

ations to the origin of social behaviours. Within this debate, one of the remarkable figures that opposed group selection theory was the biologist Edward O. Wilson. He began to be directly involved in the debate about the forces of social evolution since the beginning of the 1970s. For the next 40 years, Wilson opposed to the idea of group selection as a theoretical basis to explain the evolution of social behaviour. However, with the publication of "Rethinking the Theoretical Foundations of Sociobiology" (2007), in collaboration with David Sloan Wilson, E. O. Wilson changed his position. This project aims at analysing Wilson's conversion regarding the theory of group selection since his first publications about the topic until his current ones. In order to do so, it has been done a chronological analysis about his work that discusses group selection, the evolution of altruism and related topics. Some of the early results from this research (currently in progress) are that Wilson did not neglect the discussion about levels of selection. Wilson clearly changed his positioning regarding multilevel selection toward a more pluralist view, including group selection in his explanations about the evolution of social behaviours

POSTER

WHAT PHILOSOPHY OF BIOLOGY GOT WRONG ON THE GAIA HYPOTHESIS

SEBASTIEN DUTREUIL (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

The Gaia hypothesis (GH) was originally proposed by Lovelock and Margulis in the 1970's. It was famously criticized by Doolittle (1981) and Dawkins (1982). After these critiques a standard narrative has spread in various circles, and in particular in evolutionary biology and philosophy of biology. This narrative contains three claims: GH is nothing more than a metaphor comparing the Earth with an organism; it is pseudo-scientific or it has been abandoned by the scientific community at large; the relevant community when it comes to discussing GH is that of evolutionary biologists. Not surprisingly then, GH has not attracted the interest of philosophers of biology over the past thirty years (leaving aside Ruse (2013) and Doolittle (2013)). The first aim of this poster is to describe the extent to which this standard narrative has pervaded evolutionary biology and philosophy of biology. The second is to show that none of the claims of the narrative is warranted. Prior to the 1980's, all the evidences necessary to show that GH is not just a metaphor and did not aim to contribute to evolutionary biology are available. Besides, the demarcation claim conceals the fact that there has never been any serious demarcationist argument proposed and glosses over the development of the massive scientific literature on GH over the past forty years (involving geochemists, geophysicists, Earth historians, Earth system scientists and cyberneticians). Though the lack of interest from evolutionary biologists and philosophers of biology can be understood, the rest of the poster points out that philosophers of science have missed an opportunity to engage in the controversy and to discuss fascinating questions raised therein: the demarcation between science and pseudo-science, teleology and function, the epistemic role of computational models and of metaphors, the claim that GH may support an alternative conception of nature.

POSTER

THE SPACE OF EXPLANATIONS IN EVOLUTIONARY BIOLOGY AND ECOLOGY

PHILIPPE HUNEMAN (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

I present the project of a systematic investigation of explanatory modalities in evolutionary biology/ecology, aiming at assessing current attempts to revise the classical framework of the Modern Synthesis (MS), which often are named extended synthesis. Modern Synthesis was centered on the crucial explanatory role of population genetics as the science of the process of evolution by natural selection, and its centrality is challenged by the views alternative to MS, that doubt the hegemony of natural selection as explanans, and the population genetics view of variation as provided by mutation and recombination of alleles. The space of explanations in evolutionary biology appears structured along two axes, namely the two questions "How does selection proceed?", and "Why is there selection?", a difference exemplified by the difference population genetics/behavioural ecology. A third axis concerns the mechanistic or topological character of explanations topological meaning the explanatory character of properties of an abstract structure (like a phase space, or a fitness landscape) associated to the system under study. Whereas mechanistic explanations are familiar to philosophers of molecular biology and neuroscience, topological explanations belong to the more general set of structural explanations, in which mathematics play an explanatory rather than representative role, and appear pervasive in ecology or evolutionary biology (especially when robustness is explained). Four tasks therefore emerge investigating the explananda of natural selection as population-level explanation exploring the modes of topological explanation at different levels and their articulation with mechanistic explanation questioning the status of neutral processes and neutral networks as pervasive explanatory tools in ecology (i.e. Hubbell's neutral theory of ecology) and evolution (i.e. Kimura's neutralist theory of molecular evolution), and thereby the explanatory status of neutrality and randomness.

POSTER

FROM DUALISM TO MULTIPLICITY: SEEING BCL-2 FAMILY PROTEINS AND CELL DEATH WITH NEW EYES

ABDEL AOUACHERIA (CNRS/ENS-Lyon, France); **GUSTAVE THEILHABER** (CNRS/ENS-Lyon, France)

Bcl-2 homologous proteins are extensively studied in cell and medical biology, as they represent essential regulators of the mitochondrial apoptotic pathway in metazoans. Their function is usually given as either pro-apoptotic or anti-apoptotic: an asymmetry in function. Nonetheless, these functionally opposed proteins find their origin in a single ancestor. As testament to this fact, they have maintained a strikingly similar tertiary structure over the course of evolution. We ask how a single protein ancestor could be the originator of homologs having diametrically opposed functions. We also assess if functional divergence reflects at the structural level through some topological asymmetry. Furthermore, some empirical evidence support the notion that certain Bcl-2 homologs are bifunctional, depending on changes in the expression level, alternative splicing and post-trans-

lational modifications. Thus, the difference between pro- and anti-apoptotic Bcl-2 proteins may not be a solid dichotomy. To what extent are our understandings of the Bcl-2-regulated pathway dependent on a perceived dichotomy? Recent discoveries found Bcl-2 homologs can display non-mitochondrial and even non-apoptotic roles, suggesting that these proteins are pleiotropically involved in a variety of cell processes. A deeper understanding of the concerned biology can be attained by moving beyond contrasting descriptions towards integrating the evolutionary history and peculiarities the proteins exhibit. The case of the Bcl-2 family might help us reconsider the way we model and define complex biological systems expressing an either/or relationship

POSTER

COULD IVAN IVANOVICH SCHMALHAUSEN'S CONCEPTIONS OF EVOLUTION IN THE 1940'S BE RELATED TO THE IDEA OF "PHENOTYPIC PLASTICITY"?

CINTIA GRAZIELA SANTOS (Universidade de São Paulo, Brazil)

According to some authors such as Massimo Pigliucci and Gerd B. Müller (2010) the phenomenon named today as phenotypic plasticity was not considered by the Modern Synthesis. Besides that, it is claimed that in the book first published in Russian by Ivan Ivanovich Schmalhausen (1884-1963), in 1947, there can be found some ideas closer to this phenomenon. This book was translated to English in 1949 by Isadore Dordick and edited by Theodosius Dobzhansky (1900-1975), one of the architects of the Modern Synthesis. At that time, it was considered that the book aimed to show the factors which could explain how evolution takes place. Schmalhausen was criticized for including in its bibliography only Russian-papers and presenting a language often obscure. Besides that, despite presenting interesting ideas he did not provide evidence for supporting them. The aim of this work is departing from the analysis of *Factors of evolution: the theory of stabilizing selection* to discuss Schmalhausen's ideas on evolution trying to elucidate whether it contains conceptions which could be related to what is known today as phenotypic plasticity. The present analysis showed that although this term was not present in the book and the author was main concerned with the roles of natural selection (stabilizing and dynamic) in evolution, it is possible to find some ideas related to phenotypic plasticity. For instance, Schmalhausen considered both internal and external factors as being relevant since they could enable or limit phenotypic evolution. He also considered the reaction norm in a similar way as Richard Woltereck's one. Relating the reaction norm to ecological and developmental components, he got closer to the current concept of developmental reaction norm. However, this was not his main concern in the book.

POSTER

ERASMUS DARWIN'S AND LAMARCK'S CONCEPTIONS ON EVOLUTION: A COMPARISON

PEDRITA DONDA (Universidade de São Paulo, Brazil)

Erasmus Darwin (1731-1802) is generally known by his works devoted to medicine. However, he also brought contributions to botany, heredity, and evolution. In the historical sketch of the 6th edition of *On the Origin of species* in a foot-note, Charles Darwin (1809-1892) commented: "It's curious how largely my grandfather, Dr. Erasmus Darwin, anticipated the views and erroneous grounds of opinion of Lamarck in his "Zoonomia," vol. I. pp. 500-510, published in 1794". The aim of the present presentation is departing from the analysis of Erasmus's and Lamarck's works in which they presented their conceptions on evolution elucidate the similarities and differences between their proposals. This study leads to the conclusion that both Lamarck and Erasmus tried to explain the origin of life through spontaneous generation. However, Erasmus mentioned that it happened in the oceans and considered heterogenesis contrary to Lamarck. Erasmus Darwin attributed the transformation of living beings to three great objects of desires: lust, hunger and security. This idea is not present in Lamarck's theory. Besides that, although both accepted the inheritance of acquired characteristics. Contrary to Lamarck, Erasmus believed that characteristics produced by diseases, weather changes, domestication and ways of life could be inherited. Whereas Lamarck dedicated several works to present his theory of evolution, trying to explain since the origin of life until the rise of man's high characteristics, evolution was not the main concern in Erasmus' works.

POSTER

REASSESSING THE STATUS OF HOLOBIONTS IN EVOLUTION

SHIJIAN YANG (Xiamen University, China); **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. How shall we properly characterize the operation of natural selection on holobionts? Holobionts vertically transmitting their endosymbionts, like aphid-Buchnera holobionts, have been widely accepted as units of natural selection. Now controversies lie on holobionts horizontally picking up their symbionts, like squid-Vibrio holobionts. Zilber-Rosenberg and Rosenberg (2008) and Dupré and O'Malley (2012) insisted that this kind of holobionts are cohesive as units of natural selection, while Godfrey-Smith (2012) claimed that they have no clear parental lineage, thus are not reproducers and not qualified as units of natural selection. This paper proposes that what has been missing in previous discussions is a careful examination on various levels of biological organization in the holobiont. On the cellular and physiological level, acquisition and replication of symbionts could be better viewed as a part of development of the holobiont, and on the organism level, the parental lineage can be tracked by following the lineage of the host organism. In this way a horizontally transmitted holobiont can still be viewed as a reproducer and hence a unit of natural selection.

POSTER

FROM CLASSIFICATORY TO QUANTITATIVE CONCEPTS IN THE STUDY OF SOCIALITY IN ANIMALS: AN EPISTEMOLOGIC VIEW

LUCIA C. NECO (Universidade de São Paulo, Brazil); **CHARBEL EL-HANI** (Universidade Federal da Bahia, Brazil); **HILTON F. JAPYASSÚ** (Universidade Federal da Bahia, Brazil)

In the book *The Insect Societies*, Edward O. Wilson proposes categories (or levels) of sociality that are presented as a landmark unification of terminology in the study of social behavior. Until the mid-1980s, the eusociality phenomenon was restricted to some bees, ants, wasps and termites. Since this decade, in many other species new sociality patterns have been found that could not be fitted in any of the available categories. Therefore, from these discoveries, the characterization of sociality in levels was set up as a problem in this field and several reevaluation of sociality categories were presented. Among the propositions, some maintain the form of discrete categorization using features considered important by the authors who proposed them, as in the Wilson's proposal, but others advance to a quantitative model of characterization of sociality, such as the continuous proposed by Sherman & co and Costa & Fitzgerald. These proposals have failed to clarify the use of the categories of sociality. None of them has become widely accepted and the confusion in social behavior classification continued to occur. The context points out to the understanding of the concept of sociality and the characteristics that can be used as a criterion for the classification of social behavior, resulting in a conceptual shift in the field. Thus, there is shown a need for an epistemological analysis of this shift that can understand the evolution of their categorization and propose a breakthrough in more practical and clear use of levels of sociality. Carnap's contribution in building concepts, from qualitative (classification and comparative) to quantitative concepts can be used as an epistemological basis for analyzing the development of these conceptual changes, as it reinforces the proposal to overcome the dichotomy between eusocial and social bodies in favor of a model of sociality gradients.

POSTER

GREEN TRAVELLING

DENİZ ÖLÇEK (Middle East Technical University, Turkey)

We are in an age where the possibility to travel for everyone is not a luxury anymore. It has become an activity every person imagines and easily realizes. With this fast growing industry, environments, places and communities visited are exposed to immense effect of their visitors. This situation brings great responsibility to travelers for them to get more conscious and environmental friendly concerning how they can contribute the preservation of natural environments or their involvement in local communities they are visiting. Many environmental friendly practices that we can perform while travelling are often similar to the ones we can perform in our everyday lives, such as using biodegradable products, considering garbage recycling regulations, using public transport, buying products from local producers, using solar battery chargers etc. As well as ecologically improving our habits

as an individual, existing travel agencies can help to create awareness on the issues too. Mutually, customers of such agencies can demand responsible holidays and eco-touristic trips. As an experienced long-term traveler, I would like to introduce numerous ethical ways of travelling in this poster and to have session with participants, if possible, to have further discussion on the issue in order to exchange opinions and different practices.

POSTER

AT THE BIO-ANTHROPOLOGICAL CROSSROADS: A COMPARISON OF THE USE OF NICHE CONSTRUCTION THEORY (NCT) IN ARCHAEOLOGY AND EVOLUTIONARY BIOLOGY

FRANCISCO VERGARA-SILVA (Universidad Nacional Autónoma de México, Mexico)

Recent trends in interdisciplinary research involving biological and anthropological components –such as “modern domestication studies” (MDS)– claim a prominent role as contributors to an “expanded/extended evolutionary synthesis” (EES). At the same time, MDS and related, emerging strands of theory place niche construction (NC) at the center of their conceptual schemes –for instance, eco-evo-devo, an ontogeny- and ecology-oriented evolutionary biology perspective whose projections upon a bio-anthropological realm share several explanatory goals with niche construction theory (NCT), as it applies to human/hominid evolution. Here, I investigate the reception, adoption and/or modification of NCT-based arguments in current archaeological theory, in order to contrast the corresponding results with those of human NCT (hNCT) and NCT-influenced MDS. On the archaeological side of the comparison, my analysis pays special attention to aspects of Ian Hodder's version of post-processual archaeology (PPA) –in particular, to his notion of “entanglements” between humans, other species, and things. After identifying ways in which ideas crucial to evolutionary discourse on both strictly biological and bio-anthropological issues –e.g. fitness, inheritance, ontogeny and variation– are differentially understood in hNCT-MDS and PPA, I discuss the implications that the co-existence of divergent theoretical standpoints incorporating NCT might have for the articulation of either one or more versions of the (many times promised) EES.

POSTER

PHYLOGENETIC ANALYSIS USING A NOVEL THEORETICAL MORPHOSPACE FOR FUNGI SHOWS MULTIPLE ORIGINS OF MULTICELLULARITY ACHIEVED BY MULTIPLE ROUTES

DAVID CRAWFORD** (University of Bristol, United Kingdom)

The project combines a novel theoretical morphospace with a contemporary phylogeny to map origins and routes of multicellularity in fungi. The morphospace decomposes fungal morphology according to numerous characters, some shared with theoretical morphospaces constructed for other groups (e.g., karyokinesis [a] synchronous with cytokinesis, or uni-/multinucleate cells), and some not (e.g., yeast-hyphal dimorphism, or [un] walled hyphal bodies). I discuss the resulting trait map in terms of transitions to multicellularity, transitions in individuality, and hierarchical transition theory more generally. I focus on three major results: (1) The fungi evolved multicellularity multiple times via two different hierarchical transition types - transition via isolation and transition via integration; (2) Many routes to multicellularity in fungi involved losses and/or gains of major morphological characters and sometimes the loss of one form of multicellularity preceding the gain of another form (e.g. routes from filamentous to yeast to filamentous multicellular forms); and (3) The fungi possess remarkable developmental and morphological plasticity that enables lineages to adapt even their basic hierarchical organization to ecological or macroenvironmental changes.

POSTER

HISTORY, INTEGRATION, AND THE BIOLOGICAL CHARACTER CONCEPT

SHARI MONNER (University of Western Ontario, Canada)

Characters are the units of change on which evolutionary theory is based. Implicit in concepts like homology, heredity, and adaptation are assumptions about characters; homology is a relationship among characters; heredity is the passing of characters from one generation to another; and adaptation refers to benefits characters afford the organisms to which they belong. However, a single character concept which can capture the many uses of “character,” has not been elaborated. An exemplar case of problems that arise in the absence of a single, unified character concept is the character individuation problem. Assumptions about characters guide analysis of data used to reconstruct evolutionary history; but differing assumptions by researchers result in conflicting conclusions about evolutionary events. I argue that the root of this problem is an inadvertent blending of two conceptions of biological characters. I introduce integrative characters and historical characters as importantly distinct notions of biological character which are both central to the study of evolution. Integrative characters are generally understood in terms of the organism which possess them—as parts or properties of biological entities. Historical characters are understood in terms of their use in classification—as points of comparison among biological entities. Historical characters are used to determine the evolutionary history and

interrelations among species while integrative characters are more prevalent in discussions of ontogeny, adaptation, and selection. Proposing a single biological character concept with these two distinct aspects, I show how the character individuation problem results from exclusive focus on the historical aspect of characters; the solution, thus, lies in a qualified re-introduction of the notion that characters are integrated parts of living systems. In this way, I show how my two-pronged character concept can provide solutions to problems like the character individuation problem.

POSTER

TWO WAYS OF THINKING ABOUT MODULARITY

LUCAS MATTHEWS (University of Utah, United States); **KENNETH BLAKE VERNON** (University of Utah, United States)

The concept of “modularity” plays distinctly important roles in both philosophy and science. Philosophers of mind, for example, theorize about “Fodorian” mental modules in efforts to explain conceptual challenges of human cognition while cognitive scientists invoke a similar sense of “Darwinian” massive modularity (Fodor 1978, Machery 2007, and Robbins 2009). These two kinds of mental modules capture a distinct sense of cognitive modularity, accompanied by a refined set of features and properties, such as information encapsulation, operational mandatoriness, superficiality, and domain specificity. On the other hand, however, biologists refer to at least three distinct kinds of modularity: structural, developmental, and functional (Schank and Wimsatt 2001; and Winther 2001). This sense of biological modularity is typically cast in efforts to solve the problem of evolvability (i.e., the evolution of highly complex biological systems) and accompanies a different set of properties (e.g., quasi-independence and continuity), applications (i.e., physiology and developmental biology), and empirical identificatory criteria (e.g., differential genetic specification, connectivity, repetition, and conservation). What is the relation between these two distinct ways of thinking about modularity? At first glance these dissonant concepts appear incompatible. In this poster presentation, however, we tease apart the key philosophical similarities and differences between biological modularity and cognitive modularity to make a case for two claims. On the one hand, we argue, there is an important sense in which most cognitive modules are merely a subset of functional biological modules (of the functional kind). On the other hand, however, we emphasize that cognitive modules exhibit unique properties related to information-processing that have no analogue in biological modularity and may be indispensable to theorizing about human cognition. The upshot of our analysis is motivation to revisit the concept of modularity with an eye for its explanatory value in both philosophy and biology.

POSTER

REMOTENESS, UNCERTAINTY, AND NATURAL INSTRUMENTS: THE INFERENTIAL STRUCTURE OF PROXY RECORDS

KIMBERLY BRUMBLE (Indiana University Bloomington, United States)

Historical sciences ranging from paleoclimatology to evolutionary biology to archeology rely on proxy records to “observe” or draw inferences about the past. Proxies are “natural instruments” that contain records of past geological and biological phenomena and patterns such as fossil records, ancient tree rings, or pollen captured in ice sheet bore holes. Among the set of proximate, or representative, systems used to make inferences about target systems, proxies have some unique inferential properties. Proxies do not rely on resemblance or representation of a target system as model organisms do. Instead, their epistemic connection to the target system is based on a historical causal story, and the record usually consists of a pattern that can be interpreted and measured. These characteristics allow them inferential reliability, even when latent properties between proxy and target system are posited or when the key structures of either are black boxed. The temporal and physical remoteness of the phenomena recorded by proxies results in additional challenges for characterizing uncertainty within the data. While proxy data share measurement uncertainty and data handling challenges with instrumental records, they also contain inherent uncertainties as a result of being the products of natural instruments (after all, no one was present to check recording conditions and such); all calibration must be done after the fact and by inferring qualities and sources of error and noise. For these reasons, uncertainty quantification and characterization are especially significant features of the inferential power and structure of scientific pursuits that rely on proxy data.

POSTER

MULTIPLE REALIZATION REVISITED: A MECHANISTIC SOLUTION

WEI FANG (University of Sydney, Australia)

The multiple realization thesis (MRT) was first introduced as an argument against reductionism from mental kinds (properties, states, events, etc.) to physical kinds in philosophy of mind, but later expanded into many other philosophical areas such as philosophy of biology, philosophy of psychology, philosophy of neuroscience, etc. In this paper, to set the stage, I first exam Fodor’s version of the thesis, and then discuss Shapiro’s objection to this thesis based on his “causally relevant differences” account of realization. Then I point out that Shapiro’s conception of realization (and many others rejecting the MRT) is problematic, for it confuses constitutive relationship with causal relationship. After this, I argue that to fully comprehend the MRT and its implications, a new framework is called for, and mechanistic realization is a good candidate on offer. With this new framework, a mechanistic multiple realization (MMR) account is provided in place of the old version. Finally, two examples drawn from biological sciences are scrutinized in support of the MMR account.

TUESDAY JULY 7

DS 1420

09:00 – 10:30

ORGANIZED SESSION / DIVERSE FORMAT

TRANSMISSION AND INHERITANCE

Organizer(s): **ANTONINE NICOGLOU** (LabEx “Who am I?”, France); **FRANCESCA MERLIN** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France); **ALEXANDRE PELUFFO** (LabEx, France); **OLIVIER PUTOIS** (LabEx “Who Am I?”, France)

Participant(s):

ANTONINE NICOGLOU (LabEx “Who am I?”, France)

FRANCESCA MERLIN (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

ALEXANDRE PELUFFO (LabEx, France)

OLIVIER PUTOIS (LabEx “Who Am I?”, France)

The purpose of the present symposium is to offer a redefinition of the “nature/culture” distinction – and, at a more technical level, of the contours of the “nature-nurture debate.” How are complex factors – psychological, behavioral or morphological traits, sometimes based on a “cultural” and/or “parental” environment transmitted, if not through the genes? In this session, we will examine the issue of an “extended” transmission of some traits, offering discussions on how early mechanisms of development – at the biological, psychological, cultural or symbolic level – could either associate or either oppose nature and nurture. Human sciences in general – including psychoanalysis – have often emphasized the relative autonomy of nurture (to put it quickly, the level of human interactions and sociality), and its importance for the determination of adult traits. For this reason, a gap often separates human sciences from biological sciences (e.g., neurosciences and evolutionary psychology) – which, in turn, insist on the “nature” of transmission. Therefore, the following question arises: does the promotion, in biology, of epigenetic mechanisms – or even non-genetic mechanisms – of inheritance require to go beyond (or at least to re-articulate in depth), the nature/nurture opposition, in order to adopt a concept of heredity which would integrate nurture? Or should we rather adopt a more “conservative” concept of heredity by restricting its use to the level of “nature”, defined by its difference with “cultural” modes of transmission? More specifically, such an issue will lead us, in the context of an interaction between biologists, philosophers and psychoanalysts, to address the modalities, timings and access points of nurture, and thus to look at the ways in which the notion of transmission is conceived throughout the disciplines.

Time-scales analysis as a way to distinguish transmission mechanisms from inheritance

FRANCESCA MERLIN & LIVIO RIBOLI SASCO

Recent proposals to redefine biological inheritance all come to suggest an extended concept which applies to traditional genetic mechanisms of inheritance as well as to different forms of non-genetic transmission, from epigenetic mechanisms to ecological and cultural ones. Our project is to take a step back with respect to the issue of the extension of inheritance. Rather than listing types of inheritances and their directions (to descendants or within generations, for example), we want to put into the fore the question of time-scales as regard the transmission of genetic and non-genetic factors. In particular, we will zoom out these processes at evolutionary time scales. Our aim is to show that a closer look at the mechanisms and pathways of transmission (e.g., passing through a bottleneck or not), combined with an analysis of the relationship between short term and long term transmission time-scales – measured in terms of number of generations – of genetic and non-genetic factors, allows to better understand evolutionary and adaptive dynamics. Moreover, this approach is fruitful in order to map among different organisms like bacteria, plants, and animals the relevant differences in modalities, or strategies, of both transmission and inheritance. A graphical representation of these different modalities and their deployment over time helps us to show more vividly that there are relevant discontinuities among what contemporary biologists and philosophers of biology put under the name of “extended inheritance”.

Distinction of the timings of development: A way to characterize inheritance?

ANTONINE NICOGLOU

It has become clear that knowing “how much” of the genetic part (population studies) is linked to the disease is not tantamount to knowing “how” (comprehension of the etiopathogenic process) a specific disease occurs. The distinction here is the same as the one in biology between the “genetic contribution to variation” and “contribution to the cause” – and thus to the development – of the trait. Such opposition is linked to the debate among theoreticians about inheritance where the major input of inheritance for evolution mainly concerns the former whereas the major input of inheritance for development concerns the latter. In this regard, the analysis of apparently “simple” genetic diseases revealed complex patterns of inheritance (Wagner 1999) and individuals with the same genotype at a specific locus might be affected to a quite different extent (Lewontin 2001). In this presentation, I will focus on developmental process. My hypothesis is that by comparing different timings of development within developmental process (i.e., the different morphogenetic stages but also the different kinds of phenomena of periodization), one can also compare different types of inheritance for development. Indeed, if one sees inheritance as the process of realization of a pattern of resemblance rather than the pattern of resemblance itself, inheritance might be conceived as a complex system including different time-scales. Therefore, by comparing different time periods of development, one can also compare different time-scales of inheritance and this might have a consequence for evolutionary explanation. For instance, environment may have more influ-

ence at certain time periods of development than at others time periods (e.g. canalization, plasticity). The final purpose of this approach will be to investigate if and how these types of inheritance for development might also be relevant to evolution – contrary to the traditional view that assumes that only genetic inheritance is important.

Finding genes: What does it mean and how can we do it? An illustration using an ongoing research project in genetics

ALEXANDRE PELUFFO

For more than a hundred years, there has been a debate over what genes are. At his Nobel lecture in 1933, Thomas Morgan said that it did not really matter for the geneticist. This seems to be the point of view adopted by many biologists. However, the concept of gene has evolved and diversified across the many fields that make up modern biology (Griffiths and Stotz, 2013). Therefore, what are genes can be an important question in the recent discussion about the definition of inheritance and its potential extension. Using my research as a geneticist in the field of Evo-Devo, I will show that current methods “to find genes” in biological research are based on different hypothesis of what a gene is. Hypothesis which do not only rely on experimental facts, but on epistemological heritage of each field, historical grounds and philosophical positions. After introducing some of the main methods in genetics today, such as QTL mapping, site specific mutagenesis and next-generation sequencing, I will show that these methods rely on different historical and philosophical grounds and lead to different kind of “genes.” This implies that philosophical and historical conceptions of genes are crucial to current research in biology.

How does early psychological development articulate inheritance and transmission? When psychoanalysis meets epigenetic models

OLIVIER PUTOIS

In his recent mapping of the various disciplinary fields which have drawn on Waddington-inspired modeling (esp. the “epigenetic landscape”), Baedke (2013) rapidly mentions psychology – and focuses mostly on the dynamic systems approach to human development. But within psychology, a psychodynamic/psychoanalytic trend (starting with Spitz [1959]) has explicitly relied on a waddingtonian modeling of psychological development in order to describe, in a morphogenetic fashion, the emergence of the psyche (or mind) in the course of the early nurturing individual-environment interactions. In this presentation, I will (1) sketch out a contemporary Waddington-inspired psychoanalytic model of the interactional emergence of the psyche, which will also draw on clinical material; and (2) indicate how this model of early-life development articulates the level of intergenerational, reproduction-based inheritance (what is “innate”) and that of interactional transmission. I thus want to stress how such modeling can help make sense of Freud’s boldest claims as to the biological articulation between ontogeny and phylogeny – these claims thus appear far from being an obsolete part of psychoanalysis, as some have claimed (Laplanche).

DS 1525

09:00 – 10:30

INDIVIDUAL PAPERS

SPECIES ORIGINS, MUTUAL AID AND ORGAN DONATION**Alfred Russel Wallace and the problems of the origin of species****KOEN TANGHE** (Universiteit Gent, Belgium)

John van Wyhe recently qualified the traditional assumption that Alfred Russel Wallace set out for the Amazon in 1848 with the aim of solving the problem of the origin of species as an anachronistic myth. In reaction, Charles H. Smith defends the traditional story by arguing that it is almost certain that Wallace left for the Amazon with the intention of considering evidential materials that might reveal the causal basis of organic evolution. This article presents a synthesis of these two theses by discerning six separate origin of species problems: three before 1859 and three after 1859. The main post-1859 origin of species question was indeed projected back into history and has colored the traditional account of the Amazon expedition ever since: it is doubtful whether Wallace in 1848 intended to find the causes of evolution. However, van Wyhe subsequently pushes his case too far by implicitly assuming that there existed no genuine pre-1859 origin of species problems at all and by interpreting both the Amazon expedition and pre-1859 origin of species talk through the lens of the main post-1859 origin of species problem. In reality, Wallace had, in the mid-1840s, become very interested in the budding evolutionary approach to two of the three pre-1859 problems. Ten years later, he became intrigued by the question that, after 1859, would become the main origin of species problem. It is in these senses and only in these senses that his expeditions can be interpreted in terms of evolutionary origin of species “problem-solving”.

Kropotkin's theory of mutual aid: Implications and current evidence**GEORGE STAMETS** (Florida State University, United States)

Charles Darwin recognized that success in the “struggle for existence” may be realized through different means, depending on the broad environmental context. But while he thus identified the possibility of success through intra- and inter-species cooperation and symbiosis, he was strongly influenced by Thomas Malthus, and his actual examples of struggle tended to favor the same “gladiatorial” view of nature that his disciple Thomas Huxley deployed in his writings in ethics – one that stressed competition and conflict between organisms. Peter Kropotkin and his Russian contemporaries accepted the picture of natural selection as driven by a metaphorical “struggle for existence”, but sought to undermine the increasing prominence accorded the Malthusian elements of Darwin's theory in both evolutionary and political theory in England. Kropotkin observed, in Siberia and elsewhere, widespread cooperative and altruistic behavior, with organisms of all kinds forming small groups that appeared to extend well beyond ties of blood kinship. While recognizing that there exists much “warfare and extermination” between various organisms across various environments, Kropotkin concluded that sociability – including the capacity for mutual aid and cooperation – is at least as much a factor in driving natural selection, on the whole, as conflict and competition. After outlining Kropotkin's theory of “mutual aid” and situating it as a response to the influence of Malthus on mainstream Darwinian thought, this paper first examines the strength of Kropotkin's

evidence in light of the current state of research in evolutionary biology and anthropology. It then considers the implications of that evidence for a theory of human nature – and thus also for normative theories of human social organization. Particular attention is paid to the question of whether, as Kropotkin believed, just and successful human communities must build upon humans' natural inclinations, rather than attempt to reverse them.

Ego depletion and organ donation**SARA KOLMES** (Florida State University, United States)

Many people have died while waiting for necessary organs to become available for transplantation. However, the treatment of the bodies of the deceased who house these organs is naturally important to many people. There are various religious and metaphysical reasons which make people unwilling to have organs removed after death. In the interest of balancing these concerns, we allow people to refuse to become organ donors without having to justify this decision. In order to reach a similar balance for those who die without expressing a preference, families of the deceased may refuse donation on their behalf. If we take these refusals seriously, then we must allow families an unimpeded opportunity to refuse donation. Both because of the pressing need for more organs for transplantation and because of the biological realities of how quickly organs must be removed in order to be useful for organ donation, Organ Procurement Organizations engage in practices such as asking the families about organ donation multiple times in a short period of time even if met with refusals, requesting donation at the same time as the family is informed of the patient's death, and approaching the family accompanied by multiple authority figures. I will argue that research on the psychological phenomenon known as ego depletion suggests these practices reduce the ability of families to refuse donation if they are against it. This is because it has been shown to be difficult to refuse medical authority figures, and repetition of the request as well as having to suppress immediate sadness in order to examine the request has been shown to make difficult refusals significantly more difficult. If legitimate agreement to donation is desirable, then the ego depletion inherent in donation requests should be minimized so that families are able to make their concerns known.

DS 1540

09:00 – 10:30

ORGANIZED SESSION / DIVERSE FORMAT

PHYSICAL SCIENCE APPROACHES TO ORGANISMAL DEVELOPMENTOrganizer(s): **ALAN LOVE** (University of Minnesota, United States); **WILLIAM C. WIMSATT** (University of Minnesota, United States)

Participant(s):

KARL NIKLAS (Cornell University, United States)**ROBERT BATTERMAN** (University of Pittsburgh, United States)**ALAN LOVE** (University of Minnesota, United States)**FRANCOIS FAGOTTO** (McGill University, Canada)

Developmental biology investigates how a variety of interacting processes generate the heterogeneous shapes, size, and structural features of an organism as it develops from embryo to adult. The primary explanatory approach has been genetic, with a special emphasis on how features internal to the developing embryo make a difference or contribute to the morphological features of the organism (e.g., cell-cell signaling and transcriptional regulation). In recent years there has been a growing interest in elucidating how physical factors (e.g., mechanical forces) play a causal role in ontogeny. Since explanations deriving from physical science remain in the minority among developmental biologists, this session aims to better understand these physical science approaches, the conceptual challenges they pose to extant genetic explanations, and the prospects for integrating approaches to achieve a deeper comprehension of developmental phenomena. The biologist **Karl Niklas** begins the session by reviewing some of the mechanical forces that are operative in plant development and shows how they can be linked up with molecular genetic signaling and developmental genetic networks in cellular contexts. The philosopher of physics **Robert Batterman** explores how multi-scale models frequently utilized in materials science can be applied to developmental phenomena, specifically epithelial sheets. The philosopher of biology **Alan Love** demonstrates how physical forces can be manipulated experimentally as difference makers in a manner analogous to mutational analysis—a central feature of successful genetic approaches—and illustrates it with studies of fluid flow during cardiogenesis. The biologist **Laura Nilson** completes the session with a commentary from the vantage point of a developmental biologist studying the mechanisms underlying the origin of axial asymmetries during the development of the fruit fly, *Drosophila melanogaster*.

DS M240

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

HETEROGENEITY AND THE PROBLEM OF ECOLOGICAL PREDICTION

Organizer(s): **ERIC DESJARDINS** (University of Western Ontario, Canada)

“The fundamental aim of many empirical studies is to predict” (Spirtes et al 2000). A common view in philosophy of science is that predictions are the ultimate measure of a theory’s success or, at the very least, that they are inextricably linked to successful explanations in a particular field (Salmon 1989). In the field of ecology, however, this relationship does not seem to hold. Even though ecologists in many subfields provide explanations which greatly increase our understanding of particular phenomena, predicting future instances of these phenomena remains largely elusive. This is particularly problematic in some subfields of ecology that deal with practical issues such as bioinvasion, conservation, restoration, epidemics, etc. The purpose of this symposium is to explore the issue of prediction in ecology from an interdisciplinary perspective, in order to uncover some of the underlying theoretical and methodological difficulties in making precise predictions. The first paper, by **Antoine Dussault**, will revisit the Clements/Gleason controversy about the formation of ecological communities and thus provide an historical viewpoint on early debates that shaped subsequent views about the law-like

vs. random nature of ecological succession. In the second paper, **Katie Marshall** will approach the issue from the standpoint of an insect ecologist, and give an account of the practical constraints faced by ecologists when making predictions about an invader’s response to environmental pressures, in the light of climate change. The third paper will provide a philosophical diagnosis of the problem of prediction in ecology. **Alkistis Elliott-Graves** will argue that some ecological phenomena are characterized by extreme causal heterogeneity, resulting in limits on the generalizability of results and a tradeoff between generality and predictive accuracy.

Rethinking the Clements-Gleason debate

ANTOINE C. DUSSAULT (Université de Montréal, Canada)

Discussions of F. Clements and H. Gleason in ecology are often presented in terms of polarities. Clements’ Climax theory of species succession for example is commonly conceived as law-like and supporting of the idea that ecologists should be able to consistently predict the evolution of ecological communities after perturbation. On the contrary, Gleason’s theory of species assembly is commonly presented as random and therefore not supporting of the idea that such predictions should be possible. However, recent historical and philosophical investigations have suggested that this polarization between these two authors is unrepresentative. On the one hand, Eliot (2011; 2007) and Hagen (1992; 1988) have demonstrated that Clements does not conceive of ecological succession as exceptionless. On the other hand, Nicolson and McIntosh (2002), McIntosh (1998; 1995; 1975) and Nicolson (1990), have shown that Gleason does not endorse a purely random picture of the ecological world. However, these conclusions are so far apart from the received view that they leave the reader wondering whether there was actually something at stake between Clements, Gleason and their followers, or why the triumph of the Gleasonian view in the 1950s was perceived by many ecologists as a radical shift in the discipline (Barbour 1996). The goal of my presentation is to propose a more subtle and accurate picture of the Clements/Gleason controversy, which explains the perception of a disciplinary shift, while not falling into the simplified readings criticized by Eliot and others. My suggestion, building on some observations by Allen, Mitman and Hoekstra (1993), will be that Clements’s commitment to neo-lamarckianism allowed him to reconcile mechanistic explanations for ecological succession and the origin of repeatable species association; and that Gleason and later Gleasonians were led to reject such mode of reconciliation by their commitment to neo-Darwinism and its genetic view of inheritance.

Why it’s so hard to model the response of the “average” insect to climate change

KATIE MARSHALL (University of British Columbia, Canada); **BRENT SINCLAIR** (University of Western Ontario, Canada)

Understanding the effects of climate change on organisms is a critical part of preparing for the future. Drawing on lab and field-acquired data, biologists produce models of the both the present and predicted future distribution and abundance of organisms. The models can either be “top down”, correlating current distributions to abiotic conditions and the extrapolating to future conditions, or “bottom up”, attempting to model current

distributions based on lab-measured physiological tolerance. Modelling animal distributions is generally based on three key assumptions: 1) that the limits of organismal tolerance are fixed, 2) that means, extremes, and variability of environmental factors have no additive physiological effects and therefore can be treated equally in models, and that 3) the environment that organisms experience is what is being measured by dataloggers. While some biological systems do not violate these assumptions, many others do. Using the economically and ecologically important example of insect overwintering biology, we demonstrate how all three of these assumptions are violated in this system. Overwintering insects have extremely plastic cold tolerance on both short and long time scales, variability of low temperature stress has additional effects on survival, energy use, and reproductive output, and snow cover can have a large effect on thermal environment leading to downstream potential fitness effects. Violating these assumptions leads to very differing model outcomes at both the individual and population level. We will discuss the relative merits of each of these approaches, framed as ways of understanding the emergent property of population distribution, and outline what empirical work and assumptions would be necessary to increase the accuracy of these models.

Causal heterogeneity constrains predictive power in ecology

ALKISTIS ELLIOTT-GRAVES (University of Western Ontario, Canada)

Ecologists study systems which are complex and are characterized by heterogeneous phenomena. In many cases, such as ecological succession and bioinvasions, part of the heterogeneity is causal as each particular instance of a phenomenon can be caused by a unique combination of factors. I argue that this has some important implications. First, it limits the generalizability of explanations and results. For example, the invasion of the north american lakes by the aquatic cattail *Typha angustifolia* was caused by the displacement of the native *Bolboschoenus fluviatilis*, fueled by allelopathy (the exudation of toxins from the roots of a plant). Even though this is generally considered to be a sufficient explanation of this particular invasion, the results cannot be generalized to other invasions, given that most other plants and animals are not allelopathic and toxins diffuse differently in other environments. Second, generality comes at the expense of causal detail. That is, a description or explanation of a phenomenon becomes general if we abstract away causal particulars. In the case of the aquatic cattail, the invasion could be explained in a more general way by abstracting allelopathy and conceptualizing it as an instance of interspecific competition. However, a significant subset of ecological predictions must be precise and localized in order to be useful. For instance, it is not sufficient to predict that allelopathic species tend to become invasive; the key is to determine when and where the next invasion is likely to occur. This leads to the third implication, namely that in these heterogeneous systems, the very causal factors which must be abstracted in order to generalize from a single case are the same factors which are necessary for making precise predictions. Thus, the key to successful predictions is to conceptualize each phenomenon with the right level of generality.

DS M280

09:00 - 10:30

ORGANIZED SESSION / STANDARD TALKS

DRAWN FROM LIFE: VISUAL CONSTRUCTIONS OF BIOLOGICAL KNOWLEDGE FROM EARLY MODERN ALCHEMY TO VICTORIAN BOTANY

Organizer(s): **DONALD OPITZ** (DePaul University, United States); **AGUSTÍN MERCADO-REYES** (Universidad Nacional Autónoma de México, Mexico)

Recent historiography has drawn attention to the role of visual art not only in representing scientific knowledge but also in its very construction. What we can know about natural phenomena gets mediated through processes of visual observation, as well as visual conceptualizations and figurations of phenomena. Understandings of nature are achieved through the very making of artworks, and these, in turn, are often rendered indistinguishable from the natural objects themselves. Visualizations of nature, too, enable the communication and transit of ideas, as well, at times, their obfuscation. The papers of this session explore these dimensions to the entanglement of art with biology in three European contexts: the early modern alchemical tradition, the romantic galvanic experimental tradition, and the imperial Victorian botanical tradition. The presenters address how visualizations of life within the cosmos, the symbolic figuration of experiments on life, and artistic embodiments of botanical specimens visually construct (authoritative) biological knowledge in distinctive ways.

The cosmography of my self: The exchange between microcosm and macrocosm in the tradition of alchemy

AGUSTÍN MERCADO-REYES (Universidad Nacional Autónoma de México, Mexico)

The Paracelsian tradition of alchemy, during the late 16th century and the first half of the 17th century, thrived in the complicated relationship between the human microcosm and the larger macrocosm. This relationship was highly paradoxical: humans were and were not a part of Nature. Furthermore, the individual person could create a sort of inner world through the lens of consciousness. The relationship between microcosm and macrocosm was clearly that of “otherness,” but the traces of opposition between them were dissolved by the alchemical tradition. In an operation of concordia discors, alchemy postulated a meshwork of correspondences which permitted the flow of knowledge between different levels. The present work aims to show how, using the meshwork of correspondences as common ground, art and science were allowed to closely interact. Embedded in this meshwork, specific animals, plants, colors and activities were appointed as the bearers of deep and complex meanings. Expressive arts in the alchemical tradition were focused on expressing these unseen relationships, and thus artistic representation guided specific modes of inquiry, practice and further representation. Art, then, was both an object of investigation and an instrument for understanding the phenomenon of life and organic matter. Although alchemy fell out of favor in the early 18th century, recent work on the historiography and philosophy of science can help us reassess the bond it created between knowledge representation and knowledge construction and, moreover, help us to evaluate this bond in its proper light.

Instrumental languages and symbolic scripts: Visualizing galvanic experiments

JOAN STEIGERWALD (York University, Canada)

Recent scholarship on romantic experiments has drawn attention to its methods of active empiricism. Novalis in particular gave expression to an epistemic emphasis on experimentation as a process of mediation between conceptual representation and empirical perception, enacted concretely through instruments and depicted symbolically in figures. Ritter's galvanic experiments with frog legs were regarded by Novalis as exemplary of active empiricism. Ritter's intense investigations of a range of galvanic phenomena made evident through different instrumental arrangements, and his dense descriptions of his experiments, showcased romantic experiments as concrete practices and active interactions with the living material world. Novalis depicted Ritter's experimenting as a means of making knowledge, open-ended and generative. But not only does it render material processes cognitively meaningful, it also renders our concepts concrete. Novalis held that it is not possible to arrive at determinate knowledge of the world, or ourselves, but rather one must remain in the space of appearances and the making of meanings. Ritter's figures of his experiments lie precisely in this space of mediation. Ritter called these figures experiments as well as formulae. They provide a visual representation of his experiments, but they are also abstractions from actual material experiments into the language of scientific formulae. Novalis regarded Ritter's figures as an instrumental language. Ritter's figures are amphibious schemata – both intuitive and conceptual, lying between experimental phenomena and their interpretation – that act as instruments for making and communicating meaning. Novalis held that the language of nature resists understanding because that understanding can only be expressed in another language one cannot get beyond signs and symbols to the thing itself. Ritter's galvanic experiments, and his figures, for all their mediations between phenomena and thought, do not provide a definite deciphering of nature's script, but only a refiguration of it in a symbolic script.

Size matters: Victoria Florilegia and the embodiment of botanical authority

DONALD OPITZ (DePaul University, United States)

The nineteenth-century imperial obsession over the gigantic South American water lily, best known as *Victoria regia* (Lindley), led to innovations in biological classification, horticultural and architectural design, and, indeed, visual artistry. In my paper, I will analyze the lily's role in creating an interdisciplinary space for science and art, with a particular focus on the production of nineteenth-century florilegia devoted to the species. What was the significance of this "boutiquish" genre of publication, one bearing all the marks of gentility, for the construction, representation, and transit of botanical knowledge about the lily? Here I will advance the idea that size indeed mattered: the mid-nineteenth-century practice of representing botanical specimens in artistic folios, within a flourishing marketplace of scientific publication formats, distinguished the subjects within a realm of noble science, and in doing so, imbued them with noble authority. This elevation of select departments of botany, in this case exotic floriculture, within noble realms fed into a more general aristocracy of knowledge that increasingly clashed with a growing democratization of science marked by its professionalization and, indeed, popularization. The entanglement of science with art not only influenced the fate of knowledge about the lily, but it also determined the very format of that knowledge and its circulation.

DS M320

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

THE QUEST FOR AFFINITY: FOUR PRE-DARWINIAN VIEWS OF NATURE

Organizer(s): **ALETA QUINN** (University of Pittsburgh, United States); **AARON NOVICK** (University of Pittsburgh, United States)

"I confess that this question as to the nature and foundation of our scientific classifications appears to me to have the deepest importance, an importance far greater indeed than is usually attached to it," Louis Agassiz wrote. We fully agree. That Darwinism did not put the question to permanent rest is shown by the bitter debates within systematic biology in recent decades. Appeals to philosophy and to history feature in these debates, but historians and philosophers have not yet responded adequately to this opportunity. For example, historians trace the concept of homology back to Richard Owen's definition, but Owen acknowledged his debt to the taxonomic concept of affinity. Never synonymous with similarity, this subtle and influential concept rose to prominence in Britain when William Sharp Macleay placed it at the heart of his quinarian system. Macleay's circular diagrams, though well-known to historians, remain poorly understood. Most taxonomists were notoriously unreflective about the theoretical basis of their work, but Macleay was an exception, as was his one-time admirer George Waterhouse and his articulate opponent Hugh Strickland. Across the Atlantic, Charles Girard, apostate student of Agassiz, also strove to make explicit his ideas on affinity. The writings of these four men demand from us careful and sympathetic reading, avoiding anachronism – but not only their writings, for they also conveyed their thoughts through diagrams. We must examine their various images with the same careful attention we give to their words, but should we also keep in mind the meanings assigned to diagrams by systematists today?

On the origins of the quinarian system

AARON NOVICK (University of Pittsburgh, United States)

William Sharp MacLeay developed the quinarian system of classification in his *Horae Entomologicae*, published in two parts in 1819 and 1821. For two decades, the quinarian system was widely discussed in Britain and influenced such naturalists as Charles Darwin, Richard Owen, and Thomas Huxley. This paper offers the first detailed account of MacLeay's development of the quinarian system. I show that MacLeay had two primary motivations in developing his system: (1) to reconcile the continuity of organic nature with the failure of linear classification schemes, and (2) to overcome what he perceived as dogmatism and indolence on the part of British Linneans. The paper also argues against two myths widely accepted in the historiography of the quinarian system: (a) that MacLeay developed his system as a modification of Lamarck's twin series, and (b) that the quinarian system was an "idealist" system of classification.

Comparing Strickland

MARY P. WINSOR (University of Toronto, Canada)

In 1843 Hugh Strickland created a huge chart on which hundreds of genera of birds are linked to one another as a vast network. He unrolled this remarkable object at the annual meeting of the British Association for the

Advancement of Science, held that year in Cork, Ireland. At that same meeting George Waterhouse presented a diagram of ten circles representing the orders of mammals. Strickland judged Waterhouse's project as similar to his own, even though major differences are obvious to us. Macleay's distinction between affinity and analogy, and his diagrams, had greatly influenced both men. Although all these naturalists rejected transmutation, for a 21st century historian to examine their diagrams without reference to evolution would be a foolish restriction.

Circles and cones: Charles Girard's approach to the natural system

ALETA QUINN (University of Pittsburgh, United States)

In this paper I explicate Charles Frederic Girard's theory and method of natural classification. A student of Agassiz, and subsequently (1850-1858) a collaborator with Spencer Baird, Girard claimed that natural classificatory methods do not presuppose either a special creationist or a developmentalist theory of the natural world. The natural system, Girard claimed, comprises three distinct ways in which organisms can be related to each other: affinity, analogy, and height. Girard analyzed these relationships, and justified his classificatory methodology, by appeal to his embryological and physiological work. Girard offers an explicit theoretical answer to the question, what characters are evidence for natural classificatory hypotheses? I show that the challenge of simultaneously depicting the three distinct types of relationship led Girard to add a third dimension to his classificatory diagrams.

ORGANIZED SESSION / STANDARD TALKS

THE CELL AND CONCEPTIONS OF INDIVIDUALITY IN THE 19TH CENTURY

Organizer(s): **MARION THOMAS** (Université de Strasbourg, France); **FRANÇOIS DUCHESNEAU** (Université de Montréal, Canada)

The cell theory is acknowledged as a major conceptual landmark in the history of biology, alongside with the Darwinian evolutionary theory. The aim of the present session is to reconsider one of the key aspect of this theory, namely its emphasize for a renew understanding of biological individuality. Since the late 1830s, the cell was often seen as an elementary unit able to exhibit all the features of the living (first "metabolic" properties, and then, after Remak and Virchow, reproductive capacities). But despite the heuristic power of the cell theory and its growing importance for biological practices and explanations, the concept of individuality it promoted was never unambiguous nor unified. The issue of biological individuality, before being central for Darwinism and afterwards philosophers of biology, was already a major bone of contention for histologists and physiologists during period 1830-1880. The contributions gathered in this session will explore and emphasize the diversity of the concept of individuality from the viewpoints of anatomy, physiology, pathology and evolutionary disciplines, concept which was pivotal in the development of the cell theory. "What counts as an individual?" was answered in several different ways in different contexts, in close connection with empirical, disciplinary and philosophical issues.

Cytoplasmic individuality: The cell as elementary organism

FRANÇOIS DUCHESNEAU (Université de Montréal, Canada)

In the 1860s, a complete revision of Schwann's cell theory took place, which was partly triggered by the demonstration of the new principle that cells formed through endogenic division processes (Remak, Virchow). In the same period, morphological and physiological enquiries about the structural and functional properties of cells defined as "lumps of protoplasm" (Schultze), with or without nuclei, brought to the fore a concept of "elementary organism" (Brücke). Considered as such, cells would represent primordial living units whose various transformations and combinations yielded all higher-level biological individuals. For what reasons would the inner organization of the cell and the functional processes that flowed from it, as they were then analyzed, justify this theoretical postulate and its far-reaching methodological implications?

Inherited individuals and adaptation : Does Ernst Haeckel's theory of development go beyond preformation and epigenesis?

GHYSLAIN BOLDUC (Université de Montréal, Canada)

While Darwin only devoted a few pages to embryology in *The Origin of Species*, Haeckel both foresaw how developmental theories could be deeply reformed by Darwin's theory of descent and how embryological studies could provide empirical support to Darwinism. Achieving a synthesis of the descent theory with the cell theory, Haeckel frames up a notion of genealogical individuality that brings a temporal dimension to the biological individual as it was understood in the German tradition. Grafted to this emerging theory of individuality, the recapitulation law of inheritance provides, according to Haeckel, an explanation of development that supersedes two unsatisfactory alternatives: mechanical preformed development (W. His) on the one hand and teleological epigenetic development (K. von Baer) on the other. Although Haeckel seems to offer a new mechanical and epigenetic developmental theory, commentators are not unanimous on whether Haeckel's theory is preformationist or epigenetist. I will argue that one of the reasons for this disagreement is the existence of a conceptual tension that is internal to Haeckel's system, between the phylogenetic determination of ontogenesis through inheritance and the adaptive nature of all developing individuals. In fact, this tension took form under the conceptual opposition between palingenesis and cenogenesis. Though these concepts are effective tools for integrating anomalies within the system, this growing tension will progressively lead to the implosion of Haeckel's research program.

The fate of cell theory in Strasbourg (1830-1870)

MARION THOMAS (Université de Strasbourg, France)

In contrast to what happened in Paris, the cell theory was well received in Strasbourg. This paper will present factors that might explain this positive reception, focusing on three members of the medical school in Strasbourg (Lereboullet, Küss and Morel), during the period 1830-1870. Based on a study of medical textbooks and

DS M340

09:00 - 10:30

examination of the research work and experimental practices of these scientists, we compare and contrast their interpretations of the cell theory, while emphasizing the fact that they all conceived of the cell as an elementary unit with metabolic properties. We will also examine how these scientists addressed the issue of biological individuality and the more general question of the relationship between parts and whole; did they view the organism as a whole or as the sum of individual and potentially autonomous living units? One striking feature of the scientific landscape in the context of French Strasbourg prior to the annexation of Alsace by Germany was that these men were all followers of Johannes Müller and his disciples. We will also look at whether they broke with the German tradition and developed a specific local approach, or whether they served essentially as a vehicle for introducing the cell theory in France. Finally, we will point out how the physiological concept of the cell promoted by these Strasbourg scientists diverged from alternative views developed in Paris, especially the molecular conception of the organism propounded by Charles Robin, a Professor at the Faculty of Medicine and an outspoken Comtian positivist.

ORGANIZED SESSION / STANDARD TALKS

DS M440

09:00 – 10:30

COSTLY SIGNALING THEORY: EXPERIMENTAL AND THEORETICAL PERSPECTIVES

Organizer(s): **JUSTIN BRUNER** (Australian National University, Australia); **HANNAH RUBIN** (University of California, Irvine, United States)

One of the biggest puzzles in evolutionary theory pertains to how honest communication is possible when the interests of sender and receiver do not completely overlap. Such “partial conflict of interest” settings are commonplace in nature, as it is often the case that an informed sender has reason to conceal information from an ignorant receiver. Yet what ensures signal reliability? In the past few decades the handicap principle has emerged as the dominant explanation. The handicap principle states that honesty is possible if there are significant costs associated with sending a signal. The popularity of the handicap principle is evident by its common use in not just biology, but a variety of related disciplines as well. However, the handicap principle has been called into question on both theoretical and empirical grounds. Modeling work has demonstrated that perfect information transfer is not guaranteed – uninformative arrangements in which little or no information is transferred from sender to receiver are real evolutionary possibilities. On the empirical side, experiments designed to measure the cost of signaling have often been unable to register the high costs stipulated by the handicap principle. For these and other reasons, many have urged that we must look beyond the handicap principle if a defensible explanation of honesty is to be attained. In this symposium we explore a variety of alternatives to the handicap principle that can ensure honesty, or at least partial honesty, in signaling interactions. Additionally, the talks in this symposium showcase both theoretical and empirical approaches to the study of animal communication, and so nicely illustrates how these two perspectives can support and mutually inform each other.

Cheaper than costly signaling in the lab

HANNAH RUBIN (University of California, Irvine, United States); **CAILIN O’CONNOR** (University of California, Irvine, United States); **JUSTIN BRUNER** (Australian National University, Australia); **SIMON HUTTEGGER** (University of California, Irvine, United States)

An alternative “hybrid” equilibrium, in which communication is partially honest, has been shown to be at least as plausible as the “separating” equilibrium described by the handicap principle, in which communication is completely honest. This equilibrium has been known in economics for some time, but the evolutionary significance has only recently been considered (Zollman et. al 2013) We use an experimental approach to evaluate the evolutionary plausibility of the hybrid equilibrium. We use the methods of experimental economics because various learning models which describe the way subjects learn in the laboratory setting are equivalent to a form of the replicator dynamics with perturbations. (Hopkins 2002). We compare an experimental treatment (in which the cost associated with signaling as a low type allows for the hybrid equilibrium) with a control (where the signal cost is high enough that we would expect a separating equilibrium). We also compare the experimental treatment with a null hypothesis of no information transfer. We find that the theoretical predictions are confirmed: populations do evolve toward the hybrid equilibrium.

Cost, expenditure and vulnerability

JUSTIN BRUNER (Australian National University, Australia); **DAVID KALKMAN** (Australian National University, Australia); **CARL BRUSSE** (Australian National University, Australia)

Conventional wisdom holds that signals can only be reliable in conflict of interest settings if there are significant costs associated with signaling. In other words, the act of signaling must decrease some component of fitness of the sender. Yet a number of empirical studies have failed to register the existence of such costs. Moreover, empirical studies of animal communication often do not directly measure cost but merely the expenditure of time or energy associated with signaling. This vital link between expenditure and cost has only recently been explicitly discussed in the literature, and in the course of this paper we consider one natural way of connecting expenditure to cost. In particular, we assume that whether an expenditure is indeed costly is in large part receiver-dependent, and we draw upon a variety of predator-prey signaling systems which appear to have this structure. Namely, the expenditure associated with signaling only counts as a real fitness cost if the receiver (i.e. the predator) gives chase. In this case the expenditure of time and resources associated with signaling increases the vulnerability of the sender, thereby decreasing the probability of survival (conditional on the receiver pursuing them). We formalize this scenario as a signaling game and demonstrate perfect information transfer is no longer possible. Instead, a partially honest equilibrium similar to the so-called hybrid equilibrium is the most likely evolutionary outcome.

Costly signaling in finite populations

ELLIOTT WAGNER (Kansas State University, United States)

Signaling games have been used to explain the evolution of information transfer in systems as diverse as bacterial communication and human language. Almost all signaling games are grounded in the assumption that the interests of the communicators are aligned to such an extent that honest communication constitutes a Nash equilibrium of the game. Here I will demonstrate that this assumption is not necessary. Finite-population evolutionary dynamics will with high-probability lead to honest signaling in a variety of games in which honest signaling is not a Nash equilibrium. This will be demonstrated for three distinct families of games: the persuasion game (Milgrom and Roberts, 1986), the Sir Philip Sidney game (Maynard Smith, 1991), and the Spence's signaling game (Spence, 1973). In each of these games finite-populations can evolve honest communication even when messages are costless. This result casts doubt on Zahavi's (1975) well-known handicap principle, which claims that when the interests of sender and receiver conflict, reliable signaling is only possible if there are significant costs to producing a signal. When costs are added to a signal, so that honest communication is a Nash equilibrium of the game, finite-population evolutionary dynamics only lead to honest communication when it payoff-dominates the non-communicative pooling equilibrium in which the cheaper signal is the only signal sent. This shows that in games with costly signals it is not enough for signaling to be a Nash equilibrium. For communication to be a likely evolutionary outcome it must be both a Nash equilibrium and it must payoff-dominate pooling. This result demonstrates in a dynamic model a common-sense hypothesis that has sometimes been overlooked in the signaling literature: costly signaling should not be expected to evolve if communication leaves both parties worse off than they would be pooling.

ORGANIZED SESSION / STANDARD TALKS

LIFE, THE UNIVERSE AND ALL THAT: TAKING ASTROBIOLOGY SERIOUSLY

Organizer(s): **KELLY SMITH** (Clemson University, United States)

It seems reasonable to suppose that finding extraterrestrial life would likely rank as one of the greatest scientific discoveries of all time. Now that NASA has officially predicted that this will probably happen within the next 20 years, the time is ripe for serious researchers to turn their attentions to the unique problems and perspectives that would be presented by the discovery of extraterrestrial life. How would this cast old scientific and philosophical questions in a new light? What sorts of problems unique to astrobiology might benefit from the efforts of researchers in the humanities? This session will explore some of these issues with an eye to building an ongoing research community within ISHPSSB.

Astrobiology and the nature of the question about minimal chemical life

MARK BEDAU (Reed College, United States)

I assume for the sake of argument that the expected results of astrobiology include convincing evidence for the existence of life forms (animate beings) that arose completely independently of all currently known life forms on Earth. These expected results raise anew and potentially illuminate the notoriously controversial question (Question #1): What is the nature of life (especially minimal chemical life)? The notoriety of Question #1 itself raises a further meta-question (Question #2): What is the nature of Question #1? We can distinguish two broad approaches to answering Question #2: a Cartesian approach that seeks something like necessary and sufficient conditions for being animate (being a life form), and an Aristotelian approach that seeks something like the best overall unified explanation of the full range of phenomena associated with life, including its typical hallmarks, its borderline cases, and any important philosophical and scientific questions it raises. The Cartesian and Aristotelian approaches tend to exclude each other, and most discussion of Questions #1 and #2 are explicitly or tacitly Cartesian. I argue that the expected results of astrobiology fits best with the Aristotelian approach to the question about the nature of life (Question #2).

Finding value outside Earth

DAVID SUAREZ PASCAL (Universidad Nacional Autónoma de México, Mexico)

Some researchers (McLaughlin, 2001, 2002; Bedau, 1992, 1993, 2003) have illustrated the axiological dimension of the biological concept of function and its employment seems to pervade life sciences, specially evolutionary biology (Suarez-Pascal, work in progress). This talk will focus on the perspectives of applying the same value-centered perspective to entities and processes beyond these which earthly biologist are used to, and on its implications for understanding ET-life.

Philosophy through an astrobiological lens

KELLY SMITH (Clemson University, United States)

Astrobiology offers a new perspective through which to view a number of old problems in Philosophy and Theoretical Biology. I will outline a few of the ways adopting a thoroughly astrobiological perspective can enrich ongoing philosophical discussions. First and most obviously, the search for life on other planets elevates questions concerning the nature and extent of life to prominence and frames them in a new light. Second, there are deep epistemic questions about the scientific status of a discipline which, for all its promise, has only a single data point. Finally, there are a series of ethical questions, not merely about how we should treat extraterrestrial life should we find it, but potentially also the metaethical basis of moral value.

DS M460

09:00 - 10:30

DS M540

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

BEYOND MECHANISMSOrganizer(s): **STUART GLENNAN** (Butler University, United States); **HOLLY ANDERSEN** (Simon Fraser University, Canada)

A cursory review of recent literature might lead one to the following characterization of the mechanistic account of biology and the life sciences: Biological discovery is about searching for the mechanisms responsible for some biological phenomena, and biological explanation involves illustrating just how these mechanisms give rise to those phenomena. But while this characterization captures some examples of biological research, it hardly exhausts them. In this session we will consider several ways in which a mechanistic approach to philosophy of biology is compatible with more varied styles of discovery and explanation. **Tudor Baetu** considers the challenges that arise from the fact that much of our supposed knowledge of biological processes arises from the extrapolation from and patching together of data from disparate surrogate models. **Stuart Glennan**, considers the general question of how non-mechanical and non-causal explanations can be squared with mechanistic ontology. **Lane DesAutels** offers an account of the explanatory role of non-actualized possibles in the life sciences.

The big picture: Contextualization and extrapolation in basic research**TUDOR BAETU** (Universidade do Vale do Rio dos Sinos, Brazil)

Not only clinical research, but also basic science systematically relies on the epistemic practice of extrapolation from surrogate models, to the point that explanatory accounts presented in review papers and biology textbooks are in fact composite pictures reconstituted from data gathered in a variety of distinct experimental setups. This raises two new challenges to previously proposed mechanistic-similarity solutions to the problem of extrapolation, one pertaining to the absence of mechanistic knowledge in the early stages of research and the second to the large number of extrapolations underpinning explanatory accounts. An analysis of the strategies deployed in experimental research supports the conclusion that, while results from validated surrogate models are treated as a legitimate line of evidence supporting claims about target systems, the overall structure of research projects also demonstrates that extrapolative inferences are not considered “definitive” or “sufficient” evidence, but only partially justified hypotheses subjected to further testing.

Non-mechanistic and non-causal explanation in a causal-mechanical world**STUART GLENNAN** (Butler University, United States)

Providing one adopts a broad enough conception of mechanisms, there are reasons to believe that we live in a mechanistic world. The world has many parts, with the parts themselves having parts, and the organized (and sometimes disorganized) activities and interactions of these parts collectively are responsible for all the phenomena we find in nature. Mechanisms, in short, are the causal structure of the world. But even if this ontological picture is right, there appear to be many explanatory forms used in biology and across the sciences that do not appeal to mechanisms. Examples include equilibrium explanations, functional explanations, and lineage ex-

planations. In this paper my aim is to give a general account of non-mechanical and non-causal explanation that illustrates how such explanations can be made true by and be informative about a causal-mechanical world.

On the role of unactualized possibilities in biological explanation**LANE DESAUTELS** (University of Notre Dame, United States)

There are many well-known arguments purporting to show that explanation in the sciences should be causal. There are, however, a growing number of philosophers who argue that some of our best scientific explanations are non-causal. In this paper, I draw attention to the role that unactualized possibilities play in our explanations of a few key phenomena in the life sciences: fitness, selection, and (more generally) stochastic mechanisms. Explanations that make indispensable reference to unactualized possibilities, I suggest, don't seem to fit well within a straight-forward causal explanatory framework. Neither, however, do they seem to be instances of the types of non-causal explanations that have received recent attention in the literature. I propose a modified version of Jackson and Pettit's (1990) notion of “program explanation” as a way of understanding these explanations.

DS R510

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

SOCIAL AND EPISTEMIC VALUES IN EVOLUTION (1)Organizer(s): **CARLA FEHR** (University of Waterloo, Canada); **INGO BRIGANDT** (University of Alberta, Canada)

The purpose of this two-part session is to both broaden and deepen philosophical discussions of social and epistemic values in evolutionary biology, with some of the papers specifically discussing evolutionary psychology. With this in mind we consider values in evolutionary biology from a wide range of philosophical perspectives. There are three philosophical themes that run through this session. The first theme looks at social and epistemic values in different stages of scientific knowledge production. Papers engaging this theme include discussions of the positive and negative roles of values in scientific practice ranging from the formation of research questions, to the development and implementation of scientific controls, and ultimately to theory choice. A second theme in this session involves the critical scrutiny of values in science. Papers exemplifying this second theme explore how social and epistemic values can be insulated from critical scrutiny. These accounts urge attention to the social structure of biological research communities and their place in the academy, as well as to differences in the ways that philosophical assumptions and methods pertain to different politically-valenced values. The final theme running through these papers involves analysis of the philosophical practices and methods that we use to characterize and evaluate scientific practice. This theme is exemplified in papers urging philosophers to integrate epistemic and ethical critiques of evolutionary psychology, as well considering strategies for maximizing the impact of philosophical critique on scientific practice. This session offers an exciting variety of perspectives on values in science and a rich depth of understanding of the ways that values are part of evolutionary biology.

Adaptationism in action: The logic of research questions

ELISABETH LLOYD (Indiana University, United States)

I contrast what I have borrowed from recent philosophers, and call a “methodological adaptationist” approach, to what I’ve dubbed the “evolutionary factors” approach. I argue that these different but equally familiar approaches ask significantly different research questions. In the former, the key research question is: “What is the function of this trait?” while in the latter, the guiding research question is: “what evolutionary factors account for the form and distribution of this trait?” I use a variety of case studies, including mine on the evolution of the female orgasm, to illustrate how the methodological adaptationist approach can lead scientists astray. Biases induced by methodological adaptationism have led biologists to fail to see the byproduct explanation as a distinct positive causal hypothesis, and as one that can have evidence in its favor. They therefore fail to compare the byproduct hypothesis against an adaptive one with regard to the evidence. Perhaps, then, it is past time to take Gould and Lewontin’s advice and reevaluate whether methodological adaptationism is truly as benign as it is commonly assumed, by biologists and philosophers alike, to be.

Evolutionary psychology: A positive project for the logic of research questions

EVAN ARNET (Indiana University, United States)

The Logic of Research Questions is an analytic approach being developed by the philosopher Elisabeth Lloyd, which focuses on how the research questions being asked constrain the set of answers that are given serious consideration. Thus far, her focus has been on how an overly restrictive set of research questions a priori screens off answers meriting serious empirical consideration. Extending her project, I emphasize how there is no overarching set of good research questions but rather how appropriate research questions are contingent upon the target of interest and the information already known about it. I focus on evolutionary psychology, maintaining that because of the object of study, namely human behavior, a different set of research questions are motivated than that which guides similar evolutionary behavioral work for non-human animals. This is particularly salient, as if the methods developed for non-human animal behavior are uncritically imported into the human evolutionary behavioral sciences it can lead to a problematic epistemic bias toward adaptive explanations. Drawing from the logic of research questions and the evolutionary psychology literature, I sketch a possible account of what an evolutionary psychology-specific set research of questions might be with the aim of contributing to the development of a rigorous and unbiased evolutionary psychology.

A scientific theory’s purpose: Social values in theory acceptance

INGO BRIGANDT (University of Alberta, Canada)

Philosophical accounts of the role of values in science have clearly acknowledged that values, including social and environmental values, may guide the choice of research projects, the gathering of data, and the eventual application of scientific knowledge. As regards the core of science – the acceptance of theories by evidence

– it has also been argued that social and other values can play a legitimate role, based on either the notion of underdetermination or inductive risk. While both accounts assume that the role of values decreases when the amount of evidence increases, I argue for a stronger role of values in the context of theory acceptance. On this position, social, epistemic, and other values determine a theory’s conditions of adequacy. The latter are standards that can include considerations about what would make a scientific model explanatory, significant, or complete. I illustrate this based on recent theories of human evolution and the social behaviour of primates, arguing that the social value of gender equity informs what counts as a complete theory in this domain, even for a theory of non-human primates. Most philosophical accounts of the role of values, including arguments from underdetermination and from inductive risk, have conceptualized theory acceptance primarily in terms of making inferences from evidence. Beyond this, my approach views a scientific theory as a tool developed for certain intellectual or practical purposes. Such a purpose (in some cases implicating social values) determines not only what investigative methodology is to be used and what kind of data is to be gathered, as prior philosophical accounts on values have recognized. Such a purpose also entails what kind of theory is intended and thus what the theory’s conditions of adequacy are.

DS R515

09:00 – 10:30

ORGANIZED SESSION / DIVERSE FORMAT

AUTHORS MEET CRITICS: “POSTGENOMICS: PERSPECTIVES ON BIOLOGY AFTER THE GENOME” (2015)

Organizer(s): **HALLAM STEVENS** (Nanyang Technological University, Singapore); **SARAH RICHARDSON** (Harvard University, United States)

Participant(s):

MICHAEL DIETRICH (Dartmouth College, United States)

LAURA FRANKLIN-HALL (New York University, United States)

AMY HINTERBERGER (Warwick University, United Kingdom)

MICHEL MORANGE (École Normale Supérieure, Centre Cavallès, France)

SAHOTRA SARKAR (University of Texas at Austin, United States)

At the 2011 ISHPSSB meeting in Salt Lake City, Sarah Richardson convened a panel called “The Genomic Turn.” The session and the subsequent discussions at the ISHPSSB meeting demonstrated significant interest in understanding the phenomenon of “postgenomics” from a multi-disciplinary perspective. This led to an edited volume with contributions from historians, sociologists, philosophers, and biologists: *Postgenomics: Biology After the Genome*, edited by Sarah Richardson and Hallam Stevens, published by Duke University Press in May 2015.

Postgenomics examines developments in biology in the ten years after the Human Genome Project’s completion. Those in the life sciences stand in a moment of uncertainty, transition, and contestation. The contributors

to Postgenomics assess the great changes to the life sciences triggered by the Human Genome Project and place those changes in historical, social, and political context. To make sense of postgenomics—the work done in the life sciences now that the genome is mapped—the contributors examine how electronic data is changing research methodologies and fostering new forms of scientific labor, outline the affective dimensions of studying the genome, and demonstrate how genomic sequencing provides insights into race, gender, and sex. They also show the ways postgenomics is reshaping debates about the environment's role in altering gene expression, and even how postgenomics forces a rethinking of the notion of the genome itself.

The 2015 ISHPSSB meeting provides an ideal opportunity for extending and developing the conversations articulated in this volume. As such, the editors propose a 90-minute roundtable session for discussion and critique of the book's contributions. A diverse panel of influential scholars (to whom we will precirculate the manuscript) have offered to present short and provocative critiques of the volume to serve as starting points for discussion. We also expect that several of the authors who have contributed to the volume will be present at the meeting and will contribute to the discussion. The roundtable session will be structured as follows:

- Brief introduction to the book by the editors (10 minutes)
- Short critiques by respondents (40 minutes)
- Responses by authors and/or editors (10 minutes)
- Audience Q&A and general discussion (30 minutes)

ORGANIZED SESSION / STANDARD TALKS

THE USE AND ABUSE OF FUNCTION CONCEPTS IN GENOMICS

Organizer(s): **STEFAN LINQUIST** (University of Guelph, Canada)

The field of genomics is actively engaged in a philosophical debate over the appropriate use of function concepts. The catalyst for this debate was a widely publicized finding by the ENCODE research consortium. In 2012, ENCODE announced that over 80% of the human genome has a biochemical function. The popular media quickly seized on this finding, claiming that the “myth” of junk DNA had been overturned. Almost immediately, these claims drew fierce criticism from some of the world's leading molecular biologists. They challenged ENCODE's definition of “function” and accused them of exploiting an ambiguity in this term in order to exaggerate the significance of their research. This session will explore three dimensions of this debate. **Dr Gregory** will place the recent ENCODE controversy into historical context, arguing that there is a long tradition of abuse surrounding the function/junk distinction. **Dr Doolittle** will provide an play-by-play account of the ENCODE controversy, identifying what he takes to be at issue in this debate. **Dr Linquist** will discuss some of the philosophical implications of this debate, focusing on whether causal role functions are overly permissive.

Junk and the genome

T. RYAN GREGORY (University of Guelph, Canada)

It has been known for more than 60 years that the amount of DNA in the genome bears no relation to the complexity of the organism in which it is found or the number of protein-coding genes which it contains. Once considered paradoxical, this discrepancy between genome size and gene number is explained by the massive quantity of non-coding DNA in most animal and plant genomes. If media reports, anti-evolutionists, and the authors of many scientific papers are to be believed, this non-coding majority has long been dismissed as useless “junk”, and only now is its potential biological significance being considered. But is this characterization accurate? And what is the current state of knowledge regarding so-called “junk DNA”? In this seminar, I will present historical and conceptual background to this topic and will address the most common misconceptions about the biology of “junk DNA”. In broader terms, this seminar will examine the importance of properly acknowledging the history of scientific research, the dangers of scientific hype, and the standards of evidence necessary for ascribing “function” to biological features.

The ENCODE kerfuffle

W. FORD DOOLITTLE (Dalhousie University, Canada)

The publication in *Nature*, in September 2012, of a flurry of papers describing results from the well-funded ENCODE (Encyclopedia of DNA Elements) megaproject drew much attention in the popular press and scientific/philosophical literature. The upset was caused by ENCODE's claim to have debunked the notion that much of our DNA is “junk” (that is, not expressed in phenotype, or at least not in phenotype within the purview of natural selection.) Two philosophical issues, not often seen as such by practicing molecular and genomic biologists, are at stake. The first is adaptationism – the common belief that every base in DNA is somehow accountable to selection. The second is conflation of causal role and selected effect conceptions of biological “function”. Although the history of debate around these is long and rich, ENCODE investigators seem ignorant of it. Some simple thought experiments involving C-value (DNA content per haploid genome) tell us that unless we humans are very special, not only in the eyes of God but of Natural Selection, our genomes must be very “junky.” An alternative is to regard “function” as diffusible, spreading to engage all of its potential genomic determinants. I will discuss both, and possible reasons for the apparent obtuseness of the ENCODE consortium and *Nature* magazine, a principle supporter.

How best to reform function-talk in genomics?

STEFAN LINQUIST (University of Guelph, Canada)

Until recently, debates about the nature of biological function have transpired primarily across the pages of philosophical journals. The near-consensus in philosophy is a form of pluralism: both selected effect (SE) and causal role (CR) function-concepts are employed in biological explanation. However, the recent controversy surround-

DS R520

09:00 – 10:30

ing the ENCODE project has drawn molecular biologists into the function debate. Interestingly, many of them do not recognize the CR concept as legitimate. The problem is that CR functions are too permissive, allowing for “bizarre outcomes” as one molecular biologist recently put it. This retreat to the perceived legitimacy of SE functions is motivated by ENCODE’s abuse of the CR concept. Does it go too far? This paper will assess three alternative proposals for reforming function-talk in genomics. One option is to abandon CR functions altogether and use “function” exclusively for elements with selected effects. A second strategy limits the kinds of investigator-interests that can legitimately motivate a CR functional analysis. A third strategy (most preferable, I think) is to restrict CR functional analysis to certain types of system. I argue that highly cohesive systems, in which the functional components are proper parts of the systems whose capacities they explain, are most conducive to CR analysis. The further one gets from this ideal, the less useful CR analysis becomes. Recent developments in whole genome biology suggest that the majority of DNA in the genome is indeed far from this ideal.

DS R525

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

WHY IS BEHAVIORAL GENETICS SO CONTROVERSIAL?

Organizer(s): **JAMES TABERY** (University of Utah, United States)

Behavioral genetics has been and continues to be surrounded by controversy. Why? Answering this question requires attending to the history of the discipline, to the social structure of the discipline, and to the philosophical assumptions built in to the discipline. This session is designed to provide such an interdisciplinary approach—drawing on the resources of history, sociology, and philosophy. Historian of science **Nicole Nelson** will assess behavioral genetics’ controversial nature by examining the history of animal behavioral genetic research, paying particular attention to how the environment is conceptualized and controlled in such investigations. Sociologist of science **Aaron Panofsky** examines the controversial nature of behavioral genetics by exploring the way that the discipline structured and then restructured itself in response to external criticism at key moments in the discipline’s history. And philosopher of science **Peter Taylor** evaluates the (lack of) attention given to underlying heterogeneity in attempts to intervene on gender differences.

Accumulating and circulating knowledge about genes and environments in animal behavior genetics

NICOLE NELSON (University of Wisconsin-Madison, United States)

One of the curious features of controversies around behavior genetics is that the field continues to be subject to criticisms that it promotes genetically determinist ideas in spite of practitioners’ recurring assertions to the contrary. This paper approaches this facet of controversy in behavior genetics by examining asymmetries in the distribution and circulation of knowledge about different kinds of factors contributing to behavior. Using ethnographic data from an animal behavior genetics laboratory, I argue that even in cases where practitioners are explicitly seeking out genetic contributions to behavior, they also acquire knowledge about environmental

contributions to behavior through the process of working with animals and creating a controlled experimental setting. Indeed, it could be argued that animal researchers end up accumulating much more knowledge about the effects of environmental factors on behavior than they do about the effects of genes, since so much of their daily practice is devoted to enacting the environmental controls that make the sought after genetic effects visible. This informal knowledge about environmental effects on behaviors, however, is typically neither privileged nor publishable, and I argue that the asymmetric circulation of this knowledge accounts for some of the disconnect between critics’ and practitioners’ views of the field and whether it is genetically determinist. While practitioners may gain an intimate sense of how multiple factors work together to produce behaviors through their daily practice, it is typically only the sought after genetic findings that circulate in published or popular accounts, leaving animal behavior geneticists open to critiques that they are myopically focused on genes.

Controversy in behavior genetics: A structural account

AARON PANOFSKY (UCLA, United States)

Why has behavior genetics been so controversial? Sophisticated accounts, including those of my co-panelists, have focused on the inherent structure of knowledge in this domain, hidden assumptions, and research practices. But why then have behavior geneticists perseverated on topics that draw these critiques? This presentation draws from my book *Misbehaving Science* (2014) to offer a social structural explanation. First, I show that the most inherently controversial topics—surrounding heritability estimation particularly—were denigrated by behavior geneticists themselves at the field’s origins fifty years ago. Second, I show how the IQ and race controversy of the early 1970s put heritability estimation at the field’s intellectual core by splitting and reorganizing the disciplinary composition of the scientists making up the field and by propagating a “bunker mentality” which undermined internal dissent. Finally, I show that provocation—deliberately wielding controversial knowledge to build professional status—became a dominant strategy for scientists in response to the field’s organization and location in scientific status hierarchies. Thus controversy has become inscribed in the field’s professional logic.

His nature, her nurture, or what good are conceptual critiques for tackling practical concerns about the development of gendered individuals?

PETER TAYLOR (University of Massachusetts-Boston, United States)

How difficult is it to change the typical distributions of a trait, such as aggression, substance abuse, suicide attempts, as they differ between males and females? This can be construed as a matter of fixity versus flexibility in the development of traits in individuals over their life course or of the relative degrees of hereditary versus environmental influences on the variation between versus within groups. This paper contrasts the conceptual critiques of research of the two construals with a view to clarifying how they address practical concerns about the development of gendered individuals, as raised especially by feminist scholars. Drawing on my book, *Nature-Nurture? No* (2014), I argue that inattention to heterogeneity has limited critique as well as research under both construals.

10:30 – 11:00

COFFEE BREAK

DS 1520

11:00 – 12:30

ORGANIZED SESSION / DIVERSE FORMAT

RETHINKING REPRODUCTIONOrganizer(s): **MONIKA PIOTROWSKA** (University at Albany, SUNY, United States)

Participant(s):

ELLEN CLARKE (University of Oxford, United Kingdom)**MARION BLUTE** (University of Toronto, Canada)**PIERRICK BOURRAT** (University of Sydney, Australia)

It is standard to suppose that a necessary ingredient for any process of natural selection is reproduction. It is often difficult, however, to determine instances of reproduction. In this session, there will be three presentations followed by a single commentary that examine what it takes to reproduce and what role reproduction plays in natural selection. The following questions will be addressed:

Monika Piotrowska: What type of contribution is sufficient to make something the parent of another thing?

Marion Blute: What does cultural reproduction look like and how might it evolve?

Pierrick Bourrat: Are reproduction and inheritance necessary conditions for, or products of, evolution by natural selection?

Ellen Clarke: Commentator.

The session will consist of three 20-minute presentations, one 15-minute commentary, and 15 minutes of audience discussion.

DS 1525

11:00 – 12:30

ORGANIZED SESSION / DIVERSE FORMAT

FUNCTIONS, TELEOLOGY, AND NORMATIVITY AT VARIOUS LEVELS OF ORGANIZATION (1)Organizer(s): **SOPHIA ROUSSEAU-MERMANS** (IHPST/ Université Paris 1 Panthéon-Sorbonne, Université de Montréal, Canada); **ANTOINE C. DUSSAULT** (Université de Montréal, Canada)

Participant(s):

ETIENNE ROUX (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)**BRANDON CONLEY** (Cornell University, United States)**SOPHIA ROUSSEAU-MERMANS** (IHPST/ Université Paris 1 Panthéon-Sorbonne, Université de Montréal, Canada)**VICTOR LEFÈVRE** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

The notion of function is central to biological theory and has been abundantly discussed in the philosophy of biology (e.g. Huneman 2013 Ariew et al. 2002 Allen et al. 1998). Yet, new directions of investigation have

recently emerged in the literature. A first one explores the conceptual link between the normativity and teleology of functional ascriptions and key notions in theoretical biology like those of organization, self-maintenance and natural kinds (e.g. Krohs 2011 Saborido et al. 2011 Mossio et al. 2009). Another one discusses the applicability of functional language to organizational levels above that of organisms (e.g. Nunes-Neto et al. 2014 Bouchard 2013 Odenbaugh 2010). The main aim of these twin sessions is to gather researchers whose work explores those new directions and discuss some of the conceptual issues that they raise. The twin sessions will include discussions of functional language as applied to physiology, ecosystem ecology, earth systems science and theoretical work on social-ecological systems.

DS 1540

11:00 – 12:30

ORGANIZED SESSION / DIVERSE FORMAT

DIAGNOSTIC ACCURACY: A PRODUCTIVE MEETING POINT FOR SCIENTIFIC PRACTICE AND HUMANITIES RESEARCHOrganizer(s): **NICHOLAS BINNEY** (University of Exter, United Kingdom)

Participant(s):

PAOLA HERNÁNDEZ CHÁVEZ (Centro de Estudios Filosóficos, Políticos y Sociales Vicente Lombardo Toledano, Mexico)**MIKE KELLY** (University of Cambridge, United Kingdom)**NICHOLAS BINNEY** (University of Exter, United Kingdom)**RACHEL ANKENY** (University of Adelaide, Australia)

Disease classification and diagnostic decision making have provided a focus for research in the humanities. However, the methods used by practitioners to evaluate the accuracy of diagnoses have attracted little attention. This is a shame, particularly as researchers in clinical practice have commented that the “theory and methodology of diagnostic research still lags substantially behind that into the effectiveness of treatment”. The purpose of this session is to draw attention to diagnostic accuracy as a topic worthy of close scrutiny, and as a fertile area for the interaction of humanities scholars and researchers from scientific and medical practice.

The session is comprised of three presentations by researchers with close links to scientific and medical practice, followed by a commentary from **Rachel Ankeny**. The first speaker, **Paola Hernández Chávez**, works closely with cognitive neuroscientists, and will highlight areas of potential diagnostic difficulty in brain imaging studies. She will argue that identifying and distinguishing different sources of diagnostic difficulty is valuable to the study of the human brain. The second speaker, **Mike Kelly**, will draw on his experience of producing diagnostic guidelines to argue that philosophical and sociological insights can help illuminate the epistemological status of diagnostic categories and the social process of diagnosis. The final speaker, **Nick Binney**, originally trained as a veterinary surgeon, will argue that the historical development of diagnostic practices is relevant to their evaluation in the present day.

DS 1545

11:00 – 12:30

ORGANIZED SESSION / DIVERSE FORMAT

ECOLOGICAL APPROACHES TO ORGANISMAL DEVELOPMENTOrganizer(s): **THOMAS PRADEU** (Université de Bordeaux, France)

Participant(s):

THOMAS PRADEU (Université de Bordeaux, France)**KARINE PRÉVOT** (Université Paris-Ouest Nanterre La Défense, France)**SCOTT GILBERT** (Swarthmore College, United States)**EHAB ABOUHEIF** (McGill University, Canada)

The development of an organism has traditionally been conceived as the unfolding of internal capacities, in particular through the ideas of developmental “autonomy” and “program”. Recently, however, many phenomena have been described that involve the environment actively regulating development, leading to a new perspective called “ecological developmental biology.” Many specialists consider this a major conceptual and experimental revolution (Gilbert and Epel 2009; Nyholm and McFall-Ngai 2014). Some environmental influences on embryological development have long been known, but they have been largely neglected. Three major changes have occurred in the last decade:

- i) Key technological changes, in particular high throughput DNA sequencing, have made it possible to characterize the genomic structure and function of entire microbial communities;
- ii) Biologists have revealed a whole new continent of symbiotic interactions, through which “influential passengers,” such as bacteria or viruses, are critically involved in the development and the physiology of their host (Gilbert and Epel 2009; Pradeu 2011; Nyholm and McFall-Ngai 2014), including regarding the nervous system and cognitive capacities;
- iii) It is now possible to study ecological influences on development at the evolutionary scale, in particular endocrine signaling, influences due to the social environment, and ecological interactions (Abouheif et al. 2014).

Participants in this session will explore in detail how the environment impacts development, and they will demonstrate that understanding these phenomena requires that developmental biology articulate with other biological fields, including microbiology, ecology and evolution.

Thomas Pradeu An ecosystemic individuality? Host-symbionts interactions in the development of the organism

Karine Prévot Developmental symbiosis: how to understand the spatial and temporal frontiers of the developmental individuals?

Scott F. Gilbert The microbe-gut-brain axis: Symbionts and cognitive individuality

Ehab Abouheif Eco-Evo-Devo: The time has come

DS M240

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

EVOLUTIONARY MODELING IN BIOLOGY AND THE BEHAVIORAL SCIENCES (1): FITNESS AND INCLUSIVE FITNESSOrganizer(s): **CAILIN O’CONNOR** (University of California, Irvine, United States)

Evolutionary modeling is used widely in biology and the social sciences. In recent years, this practice has spread in philosophy, and philosophy of biology in particular. Given the increasing use of evolutionary modeling in philosophy of biology, it is appropriate to ask: what are the limits of this sort of modeling? In what ways does it go wrong? In what ways can evolutionary models be misleading? At the same time, how can this be a useful methodology? How does it provide insight and explanation? This session will explore this methodology focusing on questions related to fitness and inclusive fitness.

Quantitative and population genetics methodologies in the inclusive fitness debate**HANNAH RUBIN** (University of California, Irvine, United States)

The mathematical framework of inclusive fitness has come under intense debate, following an article by Nowak et al. (2010) which launches several criticisms against the generality and usefulness of the framework. Here I will look at two of their criticisms in detail, namely that inclusive fitness calculations require weak selection and are insufficient to completely analyze dynamics. Inclusive fitness calculations can be seen as fundamentally within the tradition of quantitative genetics, a tradition which emphasizes simplicity and measurability (Queller 1992). As such, recent defenses of the framework, and of kin selection results associated with the framework, are often stated within this tradition. The connections to kin selection are also clear within this framework as “relatedness” can be estimated by various methods intuitively connected to kinship, for example by using pedigrees. However, inclusive fitness as a mathematical framework is not limited to use within quantitative genetics. I will look at how inclusive fitness models using replicator dynamics fit in within a unified framework of natural selection (Page and Nowak 2002). I will look at how these models are connected to common inclusive fitness calculations in quantitative genetics, where the need for weak selection may arise, and when the claim of dynamic insufficiency may be appropriate. I will also see whether any intuitive notions of “relatedness” can be recovered from the population genetics models in which the relatedness parameter is not necessarily intuitively connected to kinship.

How game-theoretic models of social behavior (should) track fitness**PATRICK FORBER** (Tufts University, United States)

Evolutionary game theory provides a set of formal tools for exploring the evolution of social behaviors. The biological interpretation of this framework presumes evolutionary fitness is the currency of interactions between behavioral strategies. Based (at least in part) on the payoffs of such interactions, various evolutionary dynamics model how the frequencies of strategies change over time. A crucial challenge for applying these idealized evolutionary models of social behavior to real evolving systems is determining what fitness properties the models

track and how to measure such properties. One standard response to the challenge is to insist that models track the lifetime statistical average effect on fitness of different behavioral strategies (e.g., West and Gardner 2010). This paper will argue that the standard response is problematic, for it must measure fitness consequences over a rigid and too long a time frame (with the exception of a few notable cases, such as sex ratios; see, e.g., Ariew and Lewontin 2004). Based on the critical argument, a set of constraints on how game-theoretic models of social behavior should track fitness will be proposed and defended. Some connections to old puzzles about fitness and concerns about adaptationism will be explored.

Invariance and symmetry in evolutionary dynamics

SIMON HUTTEGGER (University of California, Irvine, United States)

In both evolutionary game theory and population genetics the basic dynamical systems describing evolutionary change are based on quantitative measures of fitness. For instance, the replicator dynamics, the canonical selection equation, or Wright's selection equation assert that evolutionary change is driven by how a type's fitness compares to the average fitness in a population. Because of the role fitness plays in these models, the mathematical form of dynamical equations constrains concepts of fitness in various ways. In this paper I explain how the scale type of a measure of fitness (such as ratio, interval or ordinal scale) is determined by the type of invariance one considers to be important. If the trajectories of a deterministic evolutionary dynamics should be invariant under admissible transformations of the fitness measure, this measure is a ratio scale. However, if only certain topological properties of trajectories should be preserved, fitness may be an interval scale. Finally, for concepts like that of an evolutionarily stable strategy, only the order relations between fitnesses play a role. This paper is an application of the theory of measurement as developed in Krantz et al. (1971) and subsequent volumes to questions in biology. It takes as its point of departure Wagner's measurement theory of fitness introduced in Wagner (2010) and discusses the differences and commonalities of the other concepts of fitness mentioned above to Wagner's measure.

ORGANIZED SESSION / STANDARD TALKS

TOPICS IN THE HISTORY OF GENETICS (1)

Organizer(s): **MARSHA RICHMOND** (Wayne State University, United States)

Genetics witnessed some of the most dramatic advances in knowledge of any of the natural sciences in the twentieth century. From the rise of the Mendelian chromosome theory in the first two decades of "classical genetics," the development of biochemical and structural techniques for unravelling the nature of the genetic material and its functioning, and the rise of population genetics leading to the Evolutionary Synthesis, the discipline witnessed dramatic breakthroughs in knowledge and in practice. These two sessions focus on pivotal

moments in the historical trajectory of the discipline of genetics in the 20th century. The first examines episodes in theory construction and social practice in genetics, while the second highlights human-oriented studies of populations and the rise of the field of human and medical genetics.

Two different ways of doing science: Bateson, Morgan and the chromosome theory (1910-1926)

LILIAN AL-CHUEYR PEREIRA MARTINS (Universidade de São Paulo de Ribeirão Preto, Brazil)

William Bateson (1861-1926) and Thomas Hunt Morgan (1866-1945) who had been previously students of William Keith Brooks (1848-1908), were both interested in evolution and brought contributions to genetics. However, they adopted different attitudes towards the chromosome theory during their scientific careers. Bateson kept an attitude of critical expectation (scientific agnosticism). Before 1910, Morgan's attitude may be regarded as a complete rejection and, after that, of complete commitment. The aim of this communication is to offer an explanation to the conflict between them. It will be defended that Bateson and Morgan had different "styles of scientific thought". Firstly, departing from the analysis made by Harwood (1993) related to the German community of Geneticists in the Inter-War-Years, it will show Bateson had several characteristics similar to the representatives of the Alfred Kuhn's school (comprehensive thought). On the other hand, Morgan had several characteristics similar to Erwin Baur's school (pragmatic thought). Secondly, it will discuss the several domains and aspects of opposition between Bateson and Morgan including methodology, epistemology, scientific work, religion, science and nationalism. The present analysis leads to the conclusion that Bateson and Morgan had different and sometimes conflicting ways of doing science. They adopted different research programs that embodied different methods and purposes. They also represented nature in different ways. The way in which Bateson understood and did science would hinder him to establish chromosome theory or to accept it as a whole contrary to Morgan's one.

Women's work in British genetics (1900-1950): The John Innes Horticultural Institute and the Edinburgh Institute of Animal Genetics

MARSHA RICHMOND (Wayne State University, United States)

Women have been contributors to genetics since the founding of Mendelism in 1900. To date, however, we know very little about the nature of their work. To a large extent, this is because their participation in science—including the problems they studied, their publications, and their role in the broader scientific community—has been hidden from view by a system that accorded primary recognition to the men who directed the laboratories or institutes where they were employed. A continuation of the organization Steven Shapin described in recognizing the "invisible technicians" of the 17th century, this system operated until the 1970s, when social changes, including the rise of feminism and greater opportunities for women to assume leadership roles, emerged and provided greater visibility to women. As part of a broader international comparison of women's work in genetics, this paper examines the work of women at the John Innes Horticultural Center in Britain and at Edinburgh's

DS M320

11:00 - 12:30

Institute of Animal Genetics, 1910 to 1950. By analyzing the nature of the work undertaken by women at these two leading genetics establishments in Britain, it is possible to identify significant changes in the organization of scientific research in the twentieth century—namely, the transition from the pursuit of individual research projects to the development of programs carried out by groups of researchers.

Selfish genes: A tipping point for evolutionary theory?

MYRNA PEREZ SHELDON (Rice University, United States)

During the past century, there have been few evolutionary thinkers with as much public charisma (and who have stoked as much political controversy) as Richard Dawkins. But his most significant contribution to evolutionary theory was perhaps in his first book in 1976, *The Selfish Gene*. In this book, Dawkins championed the notion of gene-centered evolution, helping a generation of science readers to visualize their DNA as the primary objects of evolutionary change. Although widely acknowledged as a watershed moment in the popular understanding of evolution, little has been done to assess the impact of Dawkins's work on the technical science of genetics. Was *The Selfish Gene* simply a more comprehensible distillation of the work of evolutionists such as Robert Trivers and W.D. Hamilton? Or was *The Selfish Gene*, in fact, a crucial catalyst for the theoretical underpinnings of the field of sociobiology and later evolutionary psychology? This paper examines both the popular and technical influences of *The Selfish Gene* with two primary aims: first, to assess the book's role in crucial transformations regarding genetics within evolutionary biology during the 1970s and early 1980s. And second, to consider more generally, the role of semi-popular books in shaping technical developments in evolutionary theory during the last quarter of the twentieth century.

ORGANIZED SESSION / STANDARD TALKS

FROM COMPLEX TO SIMPLE: EVOLUTION BY SIMPLIFICATION, AND ITS PHILOSOPHICAL IMPLICATIONS

Organizer(s): MAUREEN O'MALLEY (University of Sydney, Australia)

Evolution as a historical trend of complexification is usually taken for granted. We will challenge this assumption with several cases that show how major phylogenetic groups have evolved via decomplexification of genomes, intracellular structures and functional capabilities. Most of these cases will be taken from eukaryote evolution, because eukaryotes are standardly understood as comprising the most complex cells and organisms on this planet, and their evolution normally discussed as one of increasing complexification. The examples we will explore in depth are focused on the early evolution of eukaryotes, the evolution of metazoans (particularly the ancestors to metazoans), and the evolution of fungi. We will put these particular eukaryote examples into a larger context of ongoing processes of simplification in eukaryotes across the eukaryotic tree of life, and contextualize further with

regard to prokaryote evolution, in which genome reduction and other simplification processes are very common. What are the philosophical implications of such cases? We will explore what they mean for understanding general trends in evolution, including relationships between simplification and complexification, and how evolutionary simplification can be explained. We will also discuss what simplification means for the standard default to the "most parsimonious" explanation of an evolutionary outcome, when in most cases "parsimony" is consistent with the idea that evolution proceeds via complexification not simplification. Evolution by simplification indicates this time-hallowed epistemic strategy may need revision too. We will conclude with thoughts on why scientists and philosophers have tended to focus on evolutionary complexification rather than simplification.

The early eukaryote garden of Eden and the loss of complexity

MAUREEN O'MALLEY (University of Sydney, Australia)

Eukaryotes contain undeniably complex cells even in their most recent forms, full of specialized compartments, possessing elaborate and often large genomes, and enjoying high-energy metabolisms. But despite these apparently complex extant states, the evolutionary trajectory of eukaryotes cannot be read as a story of increasing complexity from a primitive ancestor. It may be better described as a series of losses as eukaryotes were cast out of their original state of complexity. The five or six major eukaryotic lineages we know today are simplified descendants of a complex ancestor, and the very diversification of those groups was driven at least in part by a variety of decomplexification processes. The secondary simplification of eukaryotes as they diverged is a hugely important finding of recent eukaryote phylogeny. This interpretation suggests that macroevolution in general can be understood as a process of two conflicting dynamics of complexification and simplification: of neutral and adaptive elaboration of structures and functions (at various levels), and the secondary adaptive and neutral pruning of those structures and functions. These dynamic tensions are also at play in prokaryote evolution, which I will outline in order to give further context for the general identification of these processes. I will suggest some important explanatory adjustments evolutionary theorists need to make in light of these macroevolutionary dynamics.

The origin of Metazoa: A genomics and cell biology approach, or why things are never ever so simple

IÑAKI RUIZ-TRILLO (Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra), Spain)

The standard view of animal origins is shaped by decades of accumulated morphological, palentological and genetic data. This view emphasises an explosive origin of animals as shown in the fossil record by the well-known Cambrian fauna. This explosive origin and diversification of animals is seen as a result of competing factors: environmental (increase in oxygen levels), and/or ecological (arms race), and/or genetic reasons (gene regulatory networks). On the other hand, the morphological change from choanoflagellates to sponges that gave rise to animals is seen as a gradual, ladder-like event that proceeds from simple to more complex. These text-book views have been held by researchers for decades. Here I will present new genomic and cell biology data from several unicellular relatives of Metazoa that challenge previous views on animal origins. The data

DS M340

11:00 – 12:30

show that choanoflagellates lost many genes compared to more ancient protists. It also shows that the unicellular ancestor of Metazoa already had many genes and pathways relevant to multicellularity (i.e., genes involved in cell adhesion, cell communication and cell differentiation). All these data suggest a more gradual, although convoluted, acquisition of genes and pathways relevant to multicellularity in the unicellular-to-multicellular transition. On the other hand, the same data suggest a more explosive emergence of the different animal cell types, which was fuelled by a transition from temporal to spatial cell differentiation at the onset of Metazoa. Although the issue remains contentious, the new data tell a cautionary tale about our inherent search for parsimonious simple-to-complex explanations in evolutionary biology.

Learning from our mistakes: Convergent simplification and the kingdom Fungi

JEREMY WIDEMAN (University of Exeter, United Kingdom)

Throughout the history of evolutionary theory, scientists have largely assumed that life evolves from simple to complex but very rarely from complex to simple. Thus, in the past, instances of convergent evolution through simplification have been overlooked in favour of similarity due to common descent. This disregard for simplification has led to a variety of misleading conclusions in the fields of taxonomy and phylogenetics. Recent advances in genome sequencing technology have allowed scientists to distinguish more easily similarity due to common descent from similarity due to convergent evolution, even when convergence is likely the product of secondary simplification. The kingdom Fungi is the best-studied simplifying lineage and contains several instances of simplification that converge with other instances of simplification across the tree of life. I will outline the general cellular simplifications that have occurred in the fungal lineage and show how analogous simplifications across the tree of life have led to confusion and errors in phylogeny and classification. This confusion likely occurred because scientists only ever considered complexification as they sought the most parsimonious explanations of evolutionary relationships. I will argue that the reason scientists and theorists tend to consider complexification as the most parsimonious evolutionary explanation is because of their general focus on plants and animals—lineages in which complexification appears to be the general rule. However, if scientists and philosophers alike take the full diversity of life into account, a more complete picture of evolutionary theory will emerge—a picture that includes mechanisms of simplification and trends toward convergence alongside mechanisms of complexification. This picture suggests a revision of Darwin's famous quote: "From so complex a beginning endless forms most beautiful and simple".

DS M440

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

LINEAGES ACROSS THE LIFE SCIENCES: EPISTEMOLOGICAL AND ONTOLOGICAL ISSUES

Organizer(s): **CELSO ANTONIO ALVES NETO** (Leibniz Universität Hannover, Germany); **THOMAS REYDON** (Leibniz Universität Hannover, Germany)

The lineage concept is central part of the darwinian framework (Sober, 2003). It represents historical relations among biological entities over generations and, therefore, it plays a central role in classificatory methodology and practice (e.g., phylogenetics). The relevance of lineages in classification influence different research areas. For example, under certain conditions phylogenetic hypotheses help in the process of testing homologous traits in Evo-Devo (Ereshefsky, 2009). Another example concerns "lineages tracing", an technique that allows a better understanding of cell replication and fate (Kretzschmar, K. & Watt, M, 2012). The relevance of lineages go beyond classificatory practices. Recently, it was suggested that such a concept takes part in the abstract models of stem cells, playing a role in the conceptual foundations of stem-cell research (Fagan, 2013). Lineages also stand in the background of what is called "lineage explanation", an explanatory pattern that deals with the continuity of change in biological mechanisms across time (Calcott, 2009). Finally, the concept of lineages has been evoked in the context of redefining fitness and natural selection, making selection more sensitive to the evolution of symbionts and ecosystems (Bouchard, 2008). Taking into consideration how widespread the reference to lineages is, a philosophical work consists in clarifying the actual role(s) of this concept across the life sciences. This enterprise can reveal and further explore explanatory patterns, ontological commitments and methodological principles attached to the concept of lineage. In this sense, it is worth asking what this concept does in different biological areas and how it is related to theory and practice in such areas. It is also worth questioning its relation with other pervasive concepts in biology, such as reproduction, populations and biological individuals. The aim of this symposium is to explore such topics, creating an interdisciplinary forum on epistemology and ontology of biological lineages.

The species problem problem and the no solution solution

MATT HABER (University of Utah, United States)

I will be arguing that adopting a Levels of Lineage perspective shifts the species problem to a lineage problem, and that this is a welcome development. It requires that we think of species as multilevel lineages that are studied from a variety of theoretical perspectives. If fragmented fields of biology are tracking overlapping multilevel objects of theoretical interest, then it is an empirical question whether and when these objects align. The patterns of discordance and concordance should be recognized as facts in need of explanation; it is theoretically fruitful to recognize and study when and to what extent these multilevel objects line up. In some cases we should expect discordant groupings, other times consensus. These sorts of research problems encourage understanding how various fields of biology might theoretically and empirically inform each other. To display this final point, I will be considering whether we ought to think of multilevel lineages as heterogeneous individuals,

akin to the heterogeneous organism that Thomas Pradeu argues we ought to adopt as a consequence of the central commitments of immunology. Ultimately, though, the adoption of the levels of lineage perspective gives us a way out of the species problem. It helps reveal a prior problem, namely the species problem problem. Recognizing what this is suggests that the lack of consensus about species is likely to be deeply entrenched, with no straight solution forthcoming. Yet there is hope! Recognizing that this is a consequence of species being multilevel lineages, and considering how biologists deal with this state of affairs in practice suggests that no solution may be needed; rather, I will argue that biologists should adopt a no solution solution. This shifts the focus to lineages from species, and moves past entrenched debates while generating new, more fruitful research questions.

Stem cell lineages: Past, present and future

MELINDA FAGAN (University of Utah, United States)

My talk examines the lineage concept in stem cell biology. The talk is in two parts. In the first, I show that the concept of “cell lineage” is central to stem cell research, both historically and today. Historically, the idea of a stem cell is closely associated with “stem-tree diagrams” expressing 19th century ideas about development and differentiation (Dröscher 2014). These ideas and images are in retained in theoretical discussions of “stem cells and stem lines” by blood cell researchers in the 1960s-70s (e.g., Lajtha 1979). Today, the lineage concept is implicit in the current definition of a stem cell as an undifferentiated cell capable of both self-renewal and differentiation (Fagan 2013). I use this historical survey and present-day characterization to identify features of the cell lineage concept that are robustly associated with the concept of a stem cell, and discuss these features’ significance in light of the entwined therapeutic and epistemic goals of stem cell research today. In the second part of the talk, I consider how the cell lineage concept is transformed in the emerging framework of systems biology. Systems biology is a loosely-affiliated collection of projects unified by emphasis on comprehensive data-sets and a commitment to mathematical modeling of biological processes, including cell development. Though systems approaches have so far made few inroads into stem cell research, this is likely to change in the near future. Traditional and systems concepts of cell development coincide in Waddington’s landscape (1957), a simple model that projects a “stem tree diagram” onto a rugged epigenetic topography. I show how the concept of lineage is reduced, on some prominent systems approaches, to a branchpoint indicating “bistability” (Strogatz 2000). The first part of the talk indicates some cautionary lessons for “reductive” systems accounts of stem cells and cell development.

Lineages as units of evolvability

CELSO ANTONIO ALVES NETO (Leibniz Universität Hannover, Germany)

“Evolvability” is a central concept in contemporary evolutionary thinking that concerns how development influences evolutionary change through biased phenotypic variation supply. This concept implies the existence of

lineages, since the influence of phenotypic variation manifests itself across generations. Furthermore, evolvability is sometimes defined as the disposition of lineages to evolve towards more or less phenotypic diversity (Sterelny, 2007). In other terms, lineages are sometimes taken to be units of evolvability. This paper identifies and analyses some commitments attached to this idea. Evolvability is often attributed to populations, not to lineages (Love, 2003; Wagner, 2008). This is a semantic disagreement, but a quite revealing one. As a dispositional property, evolvability is a property of a thing at a time and also implies identity through time. Ambiguity comes from overlooking these different but interrelated dimensions in defining “populations” and “lineages”. As I demonstrate, bringing this bi-dimensionality – synchronicity and diachronicity – to the foreground helps to understand the ontological commitments of lineage concepts and reveals flaws in Sterelny’s defense of lineages as units of evolvability. Evolvability is also often attributed to homologous traits (Brigandt, 2007). This gives rise to another semantic disagreement, since a different meaning of “units of evolvability” is implied, which I clarify by revisiting the concepts of “units of evolution” and “units of selection”. Sometimes “units of evolvability” is analogous to the former, sometimes to the latter. The semantic disagreement thus reflects an epistemological difference. For instance, the evolvability of homologous traits is related to “lineage explanation”, whereas the evolvability of lineages belongs to evolutionary explanations broadly understood (Brown, 2014). As I show, clarifying semantic disagreements over “units of evolvability” helps to shed light on the nature of biological lineages by revealing ontological and epistemological features of them.

DS M460

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

UNCERTAIN EQUILIBRIUM: IDEAS AND METAPHORS IN 20TH CENTURY ECOLOGICAL STUDIES OF HOST-PARASITE INTERACTIONS

Organizer(s): **PIERRE-OLIVIER MÉTHOT** (Université Laval, Canada); **MARK HONIGSBAUM** (Queen Mary University of London, United Kingdom)

While our current understanding of the nature and cause of disease is clearly informed by ecological thinking, it hasn’t always been so. Yet the historical origins of “disease ecology” remain in need of examination. This interdisciplinary session brings in perspectives from history, philosophy, and immunology on the re-examination of ideas and metaphors such as “equilibrium states”, “immune balance”, or “latent infections”, in addition to changing conceptions of virulence and resistance, underpinning the ecological study of host-parasite interactions in the twentieth century. Historian and philosopher of medicine **Pierre-Olivier Méthot** argues that the work of French microbiologist Charles Nicolle (1866-1936) was neglected by most historians who studied the emerging network of disease ecology around 1900, and offers to re-examine some of its key concepts to medical microbiology as a promising way to gain a better understanding of the origins of our ecological conception of disease. Looking at the work of Swiss-born medical researcher Karl Friedrich Meyer (1884-1974), who attempted to link microbial behaviour to broader bio-ecological, environmental, and social factors that

impact host-pathogen interactions and the mechanisms of disease control, historian of biology **Mark Honigsbaum** proposes that Meyer can be depicted as a pioneer of modern ideas of disease ecology. A theoretician of immunology and historian of biology, **Bartłomiej Swiatczak**, finally, advances that the metaphor of immune balance, which when used in reference to parasite-host interactions, promotes ecologically-based treatment strategies that are better suited than the long-standing self/nonself discrimination to accommodate current experimental data and to address ecological concerns in the present. Rounding out the session, historian and sociologist of biomedicine **Kenton Kroker**, whose current work is on encephalitis lethargica and the twentieth-century trade in emerging diseases, will chair the session and reflect on the papers presented.

Charles Nicolle: A pioneer of “disease ecology” in the early 20th century?

PIERRE-OLIVIER MÉTHOT (Université Laval, Canada)

Born in Rouen, Charles Nicolle (1866-1936) trained in medicine and in bacteriology in Paris before becoming the first director of the Pasteur Institute in Tunis. Mostly known for his work on the transmission of typhus by the louse, which led him to be the recipient of the Nobel Prize (1928), Nicolle also coined the concept of “in-apparent infection”, to account for infections with no visible symptoms, and predicted the emergence of “new” diseases following changes in the environment that upset the ecological balance between interacting species. The relation of Nicolle’s microbiological research to what historian of science Warwick Anderson called “disease ecology” remains unclear, however. Emerging as a “distinct disciplinary network” during the twentieth century, mostly in post-colonial contexts, disease ecology includes key figures such as comparative pathologist Theobald Smith and immunologist Frank MacFarlane Burnet who repeatedly emphasized the need to study the variety of biological interactions between macro and microorganisms and who rejected strict bacteriological determinism to explain the cause and spread of infectious diseases. Although Nicolle’s work correlates with this description, historians have yet to consider how and where his overall contributions fit more precisely within this network. For, while Anglo-American scholars have largely neglected the work of Nicolle that has likely influenced ecologically-minded US bacteriologists such as Hans Zinsser, French-speaking academics have instead tended to view him as the “precursor” of the concept of “emerging disease”, if not as the sole “inventor” of medical ecology. Re-examining the contributions of Nicolle to medical microbiology, I argue, will not only help us to overcome this divide in scholarship and to develop a more balanced view of his legacy but also to gain a better understanding of the origins of our modern, ecological conception of disease.

Karl Friedrich Meyer and the concept of “latent infections”

MARK HONIGSBAUM (Queen Mary University of London, United Kingdom)

The Swiss-born medical researcher Karl Friedrich Meyer (1884-1974) is best known as a microbe hunter whose investigations into animal and arthropod-borne diseases in California in the interwar period did much to break down the barriers between veterinary medicine and clinical pathology. In particular, medical histori-

ans have singled out Meyer’s 1931 Ludwig Hektoen Lecture in which he described the animal kingdom as a reservoir of disease and called for parasites to be studied on a strictly comparative basis as a forerunner of one medicine approaches to emerging infectious diseases. In so doing, however, historians risk overlooking Meyer’s other intellectual contributions. These contributions, ordered around the concept of latent infections, increasingly sought to link microbial behavior to broader bio-ecological, environmental, and social factors that impact host-pathogen interactions and the mechanisms of disease control. In this respect Meyer like the comparative pathologist Theobald Smith and the immunologist Frank Macfarlane Burnet can be seen as a pioneer of modern ideas of disease ecology. However, while Burnet’s and Smith’s contributions to this scientific field have been widely acknowledged, Meyer’s have been largely ignored. This paper aims to correct that lacuna while contributing to a reorientation of the historiography of bacteriological epidemiology by presenting a sketch of Meyer’s intellectual development, his key professional associations, and his studies of zoonotic diseases -such as psittacosis and plague- exemplified his ideas about latent infections and the growing importance of host-parasite interactions and equilibrium states to his research. In particular, the paper argues that at a time when military metaphors dominated the investigation of infectious disease and the relationship between virulence and pathogenesis was being called into question, Meyer’s concept of latent infections provided a means of incorporating more complex bio-ecological ideas into his epidemiological model and for reimagining the relationship between parasites and hosts in less antagonistic terms.

Immunological metaphors and sustainability of microbial ecosystems

BARTŁOMIEJ SWIATCZAK (University of Science and Technology of China, China)

Many historical and philosophical studies emphasize the importance of metaphors in scientific inquiry. These figures of speech have been suggested to differ from descriptive statements in that they structure scientific data, direct research and help to refer to phenomena whose molecular details are not well understood. The focus of this talk is on yet another role of scientific metaphors: that of guiding our interaction with the environment. In particular, an attempt is made to show that in the 20th century immunological metaphors influenced clinical and sanitary conduct thereby affecting microbial ecosystems. Indeed, by appealing to the putative function of the immune system to eliminate all kinds of foreign agents, the metaphor of self/nonself discrimination as well as the preceding concept of own/foreign distinction validated the use of sterilizing agents in the management of human interactions with microbial communities. Despite its provisional curative effect, the widespread use of bactericides led to expansion of antibiotic resistant species and impoverishment of non-pathogenic microflora. Thus, the metaphor of self/nonself discrimination indirectly contributed to the recent increase in the number of infectious diseases, autoimmune diseases and allergies. This should be contrasted with the metaphor of immune balance, which when used in reference to parasite/host interactions, promoted ecologically-based treatment strategies involving use of bacteriophages, probiotics and immune stimulants. We suggest that the latter metaphor is better suited than the one of self/nonself discrimination to accommodate

current experimental data and to address ecological concerns of the day. Overall, the investigation of the link between immunological metaphors and the implicated approach to sanitation and treatment reveals an ethical dimension implicit in the scientific discourse. It suggests that the success of metaphor in science should not only be measured in terms of its epistemic usefulness but also in terms of its far reaching consequences for the environment and society.

DS R340

11:00–12:30

ORGANIZED SESSION / STANDARD TALKS

SLIPPERY CREATURES: ZOOPHYTES, ANIMALCULES, AND SPERMATOOZOA IN THE 19TH CENTURY

Organizer(s): **LYNN NYHART** (University of Wisconsin-Madison, United States)

This session focuses on scientific and literary efforts to make sense of microscopic and other “lower” forms of life in nineteenth-century Europe and Britain, focusing on the use of analogy and metaphor to bring nature’s menagerie of small, slippery creatures under linguistic and scientific control. Scott Lidgard examines scientists’ changing classifications of the “zoophytes” (literally, animal-plants)—a residual category into which a grab-bag of apparently intermediate forms were bundled, sorted and re-sorted according to diverse criteria, which remained contested. Danielle Coriale analyzes the rhetorical strategies that English and American scientists used in the 1830s and 1840s to argue that certain “animalcules” were disease agents, an idea that met with resistance and ridicule until Robert Koch legitimated it with his germ theory later in the century. Lynn Nyhart analyzes the changing analogues of spermatozoa (“sperm-animals”) offered by scientists over the course of the 1830s–50s, as they sought to create general laws of generation that might cover both animals and plants. Collectively, our papers—by a biologist, a literary scholar, and a historian, respectively—demonstrate the varied but essential function of figurative language in efforts to render tiny, unfamiliar creatures comprehensible, yet also how slippery and ambiguous were the results of these efforts. At the same time, we highlight how important these tiny creatures were to the life sciences and their surrounding culture in the nineteenth century.

Zoophytes, analogies, and classifications: A long journey through the order of nature

SCOTT LIDGARD (Field Museum, United States)

Zoophytes, or animal-plants, raised profound questions for natural historians about how different kinds of beings should be organized into a natural system of classification. These questions extended well beyond the well-known 18th century revelations of Trembley’s freshwater polyp, the preformation-epigenesis debate, and the chain of being. Continuing through much of the 19th century, the taxonomic diversity of zoophytes increased and ebbed repeatedly with new discoveries and subsequent removals from this group as different taxonomic classifications representing the order of nature grew and splintered. Until the mid-19th century, classifications

looked downward from more to less complex organisms; from this perspective, the heap of miscellaneous creatures comprising the zoophytes — bacteria, protists, “polypi” and various other invertebrates, algae, lichens, and fungi — were chimera-like beings, ascribed properties linking plant and animal kingdoms. Analogy was used as both heuristic, in determining the nature of newly discovered zoophytes, and justification, in establishing criteria for erecting taxonomic boundaries at different levels of classification. I trace the journeys of different zoophytes through various classifications and their respective criteria. Even as the zoophyte concept waned, its members having been parsed into various other taxa, boundaries remained fuzzy. Strikingly, the positions of many former zoophytes in classifications remained contextual; no clear consensus was reached about which criteria were more important at which level. Analogies did not disappear entirely, at least not when justifying one’s preferred order of nature.

“An animalcule in my blood”: The rhetoric of early germ theory

DANIELLE CORIALE (University of South Carolina, United States)

When Antonie van Leeuwenhoek looked at his own saliva under the microscope in 1683, he described the microbes he saw as “living animalcules, very prettily a-moving.” For the next two hundred years, European scientists would continue to use the word “animalcule” to describe all kinds of motile, microscopic organisms, grouping bacteria together with zoophytes, protozoans, and other tiny creatures. This grouping set the stage for heated disagreements about one question that would percolate over the next 200 years: could animalcules be pathogens, agents of disease? This essay studies the rhetoric that scientific writers used in England and the United States to persuade others of the legitimacy of the “animalcular theory of disease” during the 1830s and 1840s, well before Robert Koch’s provision of definitive scientific proof of germ theory. I argue that while English writers including Henry Holland and Gideon Mantell made measured arguments for the theory’s legitimacy, writers in the United States resorted to more dramatic rhetorical strategies, referring to animalcules a “rioters” or “invaders” overwhelming the human body. In so doing, these writers used the racial and political fears of the public to describe early germ theory. I will use moments of rhetorical excess to consider how risky rhetorical tropes can be in writing about disease, especially when the old idea of contagium animatum was gaining traction as Henle, Klencke, Virchow, and others made vigorous cases for it in Europe from the 1840s to the 1870s.

Spermatic fluidity: The analogical method in the study of generation (1830–1850)

LYNN NYHART (University of Wisconsin-Madison, United States)

What are sperm like? To what might they legitimately be compared—parasites? cells? pollen grains? seeds? From the 1830s to the 1850s, animal and plant physiologists pondered this question of analogy, even as they sought to flesh out empirically their commitment to understanding generation as a fundamental law of life. If the process of generation unified living nature, then how was that unity constituted, and what aspects of generation could vary? Rudolf Wagner, Carl Theodor Ernst von Siebold, Albert von Koelliker, and Rudolf Leuckart came

to form a powerful united front on this matter, collectively setting aside certain characteristics of spermatozoa (e.g., the motility that seemed to characterize them as animals) as less important while assigning other features—their cellular origin—as defining. This, I suggest, then conditioned how they viewed plant reproduction and the search for a yet broader analogical law that would cover both plant and animal generation. The story of the shifting nature assigned to spermatozoa thus illustrates how scientists came to consensus over two questions simultaneously: (1) to what objects a particular (often newly discovered) structure or function should be analogized, and (2) how to use analogy as a legitimate scientific method.

DS R510

11:00–12:30

ORGANIZED SESSION / STANDARD TALKS

SOCIAL AND EPISTEMIC VALUES IN EVOLUTION (2)

Organizer(s): **CARLA FEHR** (University of Waterloo, Canada); **INGO BRIGANDT** (University of Alberta, Canada)

The purpose of this two-part session is to both broaden and deepen philosophical discussions of social and epistemic values in evolutionary biology, with some of the papers specifically discussing evolutionary psychology. With this in mind we consider values in evolutionary biology from a wide range of philosophical perspectives. There are three philosophical themes that run through this session. The first theme looks at social and epistemic values in different stages of scientific knowledge production. Papers engaging this theme include discussions of the positive and negative roles of values in scientific practice ranging from the formation of research questions, to the development and implementation of scientific controls, and ultimately to theory choice. A second theme in this session involves the critical scrutiny of values in science. Papers exemplifying this second theme explore how social and epistemic values can be insulated from critical scrutiny. These accounts urge attention to the social structure of biological research communities and their place in the academy, as well as to differences in the ways that philosophical assumptions and methods pertain to different politically-valenced values. The final theme running through these papers involves analysis of the philosophical practices and methods that we use to characterize and evaluate scientific practice. This theme is exemplified in papers urging philosophers to integrate epistemic and ethical critiques of evolutionary psychology, as well considering strategies for maximizing the impact of philosophical critique on scientific practice. This session offers an exciting variety of perspectives on values in science and a rich depth of understanding of the ways that values are part of evolutionary biology.

Social protection of pernicious values in the biological sciences

CARLA FEHR (University of Waterloo, Canada)

In this paper I explore how the structure of, and relationships among, epistemic communities can hinder the ability of those communities to detect, critically discuss, and negotiate the appropriateness of the roles of

particular social and epistemic values in their own practices. I explore this topic using the example of philosophical critiques of Evolutionary Psychology (EP), a discipline that many philosophers of biology argue harbors pernicious social and epistemic values. I argue that these values in EP are protected by the relatively isolated and local nature of biological research communities in the academy, and by global epistemic and ethical norms such as academic freedom. As a result of these protections, members of the community of EP researchers may have good arguments for ignoring philosophical critiques of their research. However, EP is highly socially relevant and the philosophical critiques are both apt and ethically, politically and epistemically significant. So, it is important to cast a critical eye not only on EP, but also on those protections. Also, the social epistemic features that isolate and protect EP are not only common, but are often prized, in university research environments. As a result, what we learn from this case has the potential to be broadly applicable.

Fixing bad science: Is good science enough?

SARA WEAVER (University of Waterloo, Canada)

This paper looks at how philosophers critically deal with the science of evolutionary psychology (EP), a science infamous for its controversial claims about social categories and human nature. I tease out two distinct approaches. The first approach predominantly criticizes EP for its flawed theory, methods, and data interpretations (TMDs). It proposes that, to fix its program, EP needs to adopt the standards of “good science,” namely, those of evolutionary biology. The second approach also criticizes EP for its flawed TMDs but also rigorously addresses the harmful social values embedded in, and the pernicious social implications which stem from, EP research. Any remedy to fix EP, according to this approach, would also have to contend with its harmful social dimensions. In Part One of this paper, I argue that the first of these approaches, by addressing the social dimensions of EP only minimally, is both injurious to the philosophy of science and inadvertently contributes to the social harms necessitated by EP. In Part Two, I argue that the second approach (1) avoids the ills of the first approach, and (2) contributes to socially responsible science. I conclude more broadly that those who wish to philosophically engage with socially relevant science, ought to model their approach after the second of these approaches.

On the resilience of politically-valenced biases

LETITIA MEYNELL (Dalhousie University, Canada)

It is surely a truism to say that good scientific method should control for bias. When the distorting effects of a type of bias have been revealed through countless case studies, are widely acknowledged, or at least to some extent theoretically understood, it stands to reason that scientific communities should expect researchers to control for them. In this presentation I compare two types of politically-valenced biases that scientists appear to have been reluctant to control—sexist or gender bias and anthropocentric bias. Although the distorting effects of these biases are important in their own domain, due to the centrality of reproduction and evolutionary continuity between species in biological study, these types of bias have implications beyond the considerable

body of research that directly investigates sex differences or uniquely human capacities. Because these biases are politically-valenced one might expect the biases themselves and the disputes around them to have a similar character and similar solutions. However, this is not straightforwardly the case. The criticisms of gender bias have typically been made from an empirical basis, citing various case studies (consider Fausto-Sterling 2000, Lloyd 2005, Jordan-Young 2010, Richardson 2013), while the criticisms of anthropocentric bias have typically been made from a principled basis, citing problematic assumptions, such as the fallacy of anthropomorphism (consider Fisher 1996, Keeley 2004). Suggested remedies have also varied. Moreover, because criticisms of gender bias in the life sciences often involve the cultural contingency of sex differences, while criticisms of anthropocentrism tend to emphasize continuity between nonhuman and human behaviors these critiques tend to function at cross purposes. Through the comparison of these different types of bias we can begin to appreciate the character of each type of bias and politically-valenced biases more generally, and gain insight into the reluctance to control for them despite their clearly distorting effects.

DS R515

11:00 – 12:30

ORGANIZED SESSION / DIVERSE FORMAT

AUTHORS MEET CRITICS: *IN SEARCH OF MECHANISMS* (2013)

Organizer(s): **RUEY-LIN CHEN** (National Chung Cheng University, Taiwan)

Participant(s):

LINDLEY DARDEN (University of Maryland, College Park, United States)

CARL F. CRAVER (Washington University in St. Louis, United States)

LENA KÄSTNER (Humboldt-Universität zu Berlin, Germany)

HOLLY ANDERSEN (Simon Fraser University, Canada)

SHUNKICHI MATSUMOTO (Tokai University, Japan)

HSIAO-FAN YEH (National Chung Cheng University, Taiwan)

Recently, the new mechanical philosophy has ignited numerous discussions about the characterization, structure, and role of mechanisms in scientific explanations, discoveries, causation, experimentation and other related topics. There has been an explosive production of articles on mechanisms across the globe ever since Machamer, Darden and Craver's seminal paper was published in 2000. In their new book, *In Search of Mechanisms*, Carl F. Craver and Lindley Darden present a comprehensive and detailed summary of their views.

We have assembled a cross-national group of experts on this topic. Four panelists will present their commentaries on *In Search of Mechanisms*. **Craver** and **Darden** will respond. **Lena Kästner** questions whether the different mechanisms that produce, maintain, or underlie a phenomenon, according to Craver and Darden's recent new book – go together with the MDC picture of mechanisms. **Ruey-Lin Chen** and **Hsiao-Fan Yeh** focus on the relations between mechanisms and theories on the one hand and between mechanisms and

DS R520

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

THINKING ABOUT CELLS (1): WHAT ARE CELLS AND HOW DO WE KNOW?

Organizer(s): **JANE MAIENSCHNEIN** (Arizona State University, United States); **KARL MATLIN** (University of Chicago, United States)

These two coordinated sessions look at what cells are and how they work, in parallel with consideration of epistemological questions about how we know. The first session examines the evolving understanding of what cells are, including an overview of early concepts and close examination of studies in protozoa and in stem cells. Throughout, we ask about the methods and assumptions involved. The second session turns to questions about how cells work. This includes a look at explorations of cytoplasmic streaming within cells, at the understanding of cell death, and at intersections of form and function through study of mitochondria and oxidative phosphorylation. Here issues of methods, metaphor, and the heuristic use of form in order to inform mechanical explanations of function play important roles. The sessions work together to get at historical, philosophical, and biological questions about cells.

A century of cells

JANE MAIENSCHNEIN (Arizona State University, United States)

Schleiden and Schwann had a very different concept of cells than the team of authors Edmund Cowdry brought together for General Cytology or Special Cytology in the 1920s. The first cell theory saw cells as a structural unit of organisms. It was not the only unit, and organisms did not consist of cells alone. By the end of the 19th century, the cell had become the fundamental structural and functional unit for living systems. In addition, the cell was clearly alive itself, with the capacity to reproduce and differentiate. By the mid-20th century, cells were thought also to go through life cycles and to undergo senescence and death. "The cell" gave way to a diversity of different kinds of cells, each with different properties and behaviors. By a century after Schleiden's and Schwann's initial cell theory, the concept of cells looked very different. This presentation will look more closely at major shifts in our understanding, and what provoked those changes.

Cell heredity, epigenetics, and structural inheritance

JAN SAPP (York University, Canada)

My presentation focuses on discussions and experiments in protozoan genetics beginning in the 1950s concerning two aspects of cell heredity, epigenetics, and structural inheritance, each of which focused on different problems of the cell in development and heredity. Although the term “epigenetics” (though not “epigenetic”) is often traced to Waddington (1942), the term “epigenetics” in the sense of inherited changes resulting from the regulation of genes, as it is used today, is rooted in microbial geneticists’ experiments and discussions of cell heredity in the 1950s, and their attempts to bridge genetics and embryology. Epigenetic inheritance was introduced by microbial geneticists to resolve what is commonly referred to as the paradox of cellular differentiation in the face of nuclear equivalence. A second research program based on ciliated protists, aimed at resolving another long-standing problem of morphogenesis, began in the 1960s based on experimental demonstrations of “structural inheritance” not involving gene regulation. One form of structural inheritance involves the cell cortex acting as scaffolding for the assembly of gene products; the explanation for a second less well known form of structural inheritance (or field heredity) remains uncertain. As we shall see, biologists’ conceptions of the cell are still in the making.

What can we learn from stem cells? Induced pluripotent stem cells as models in cancer research

LUCIE LAPLANE (Institut Gustave Roussy, France); **ALLAN BEKE** (Institut Gustave Roussy, France)

Since the rise of the cell theory in the 19th century, the cell has been considered as a unit of structure, function, and reproduction. Cells are the elementary building block of life. Among cells, stem cells play a particular role and might be “units of development,” “units of regeneration,” and even “units in evolution” (Weissman 2000). What can we learn from those cells? And does stemness make stem cells a unit of particular interest for the explanation of some biological properties? In this presentation, we will focus on the case of induced pluripotent stem cells (iPSC) in oncology. It is now possible to generate pluripotent stem cells from patient cancer cells. Those cancerous iPSC then provide an unlimited resource of cancer cells to study and experiment with. The introduction of iPSC technology in oncology raises the question of whether and how it provides an adequate tool to model, experiment, understand, and cure cancers. We will first highlight the advantages and pitfalls of the introduction of iPSC as a new model in oncology, and then highlight the role of stemness in the ability of iPSC to model cancers.

DS R525

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

DEHUMANIZATION (1): NEW APPROACHES TO UNDERSTANDING THE POLITICS OF HUMAN NATURE

Organizer(s): **MARIA KRONFELDNER** (Central European University, Hungary); **ROBERT A. WILSON** (University of Alberta, Canada)

Debates about human nature in the biological and social sciences as well as in philosophy of science typically consist of a positive proposal of some kind and critical responses to that proposal. Although political considerations often enter into both sides of such debates, there is a sense in which such considerations are secondary. In this double session, we adopt a different approach, drawing on and contributing to the emerging field of dehumanization studies. This approach places the less-than-fully human in the spotlight. On the basis of recent empirical findings on dehumanization, we will discuss how dehumanization, essentialism, eugenics and disability hang together. After a short introduction by **Maria Kronfeldner and Rob Wilson**, we will discuss in the first session: (i) different ways of being an essentialist and the consequences of these different essentialisms for the politics of human nature (**Ron Amundson**); (ii) different kinds of dehumanization processes, some more, some less essentialist (**David Livingstone Smith**); and (iii) consequences of results from empirical dehumanization studies for philosophical theories of the concept of human nature (**Maria Kronfeldner**). In the second session, we will apply the results of the first session to specific political concerns, mainly (iv) ability expectation and ableism (**Gregor Wolbring**), and (v) eugenics and disability (**Rob Wilson**). The five talks are followed by (vi) a round table discussion. As a whole, the session aims to open up some novel possibilities for historians and philosophers of science in analyzing essentialist thinking by taking up a provocative theme, dehumanization, drawing on recent work from the psychological and social sciences.

The contingency of method, or can essentialism be progressive?

RON AMUNDSON (University of Hawaii at Hilo, United States)

The methodological or metaphysical policy labeled “essentialism” has been under serious criticism in recent decades. Much of it is well deserved. This is true when reactionary implications of social or biological theories are derived, not directly from empirical results themselves, but from methodologies that selectively empower the researchers to generalize human characteristics to individuals who are assumed to belong to (essentially defined) groups or classes. Many of the myths of racism, sexism, ableism, and other such ideologies fit this pattern and deserve the disrespect that the critiques of essentialism have given them. Nevertheless, essentialism has been condemned in biological domains other than human social theory, and the implications have been different. Essentialism has been used to label and condemn theories that conflict with mainstream “Modern Synthesis” evolutionary theory. Many progressive social theorists recognize that mainstream evolutionary theory has been used to support politically conservative doctrines. Relatively few have seen that the anti-essentialism of neodarwinism carries much of the conservative load. Essentialism, as it is labeled by mainstream neodarwinians, should not be seen as a regressive methodological position (although the neodarwinians label it as

such) but as a progressive position (notwithstanding the neodarwinian view). Only by recognizing essentialist reasoning can important phenomena like phenotypic plasticity and unity of organic type be properly understood, and these concepts are crucial to a progressive understanding of evolutionary science. In this paper I will first argue that essentialism, under certain conditions, promotes liberatory thought. Secondly, I will try to show the ways in which (anti-Modern Synthesis) essentialism can yield outcomes that are liberatory both for disabled (i.e. non-normal) human beings and for non-human animals.

Metaphysical misfits: Dehumanization reconsidered

DAVID LIVINGSTONE SMITH (University of New England, United States)

On one account of dehumanization, we dehumanize others by denying that they possess a human essence and attributing a subhuman essence to them. However, several critics of this approach have pointed out that dehumanizers implicitly affirm their victims' humanity, even while explicitly denying it. This criticism suggests that the view that dehumanized people are thought to be subhuman animals is either incomplete or false. I propose that dehumanized people are conceived as chimeras possessing both human and sub-human attributes. More specifically, I propose that when we dehumanize others, our mind is pulled in two incompatible directions at once. Because the other appears human, we are inclined to make a similarity-based judgment of humanity. However, in attributing a subhuman essence the other, we categorize them as nonhuman. Dehumanized people are thus felt to belong to two incompatible metaphysical kinds. Because of this, they are felt to be "uncanny" (unheimlich) monsters rather than merely as subhuman animals. Drawing on a range of work by anthropologists, philosophers, and cognitive scientists, I argue that research on monsters, horror, and the uncanny may importantly contribute to our understanding of the phenomenon of dehumanization.

The concept of human nature in light of contemporary dehumanization studies

MARIA KRONFELDNER (Central European University, Hungary)

Within philosophy of science, the concept of human nature has often been criticized because of its political role in demarcating and stigmatizing certain kinds of people, e.g. women or certain ethnic groups. The critique is usually based on well-known historical cases, such as the Nazi's dehumanization of Jews and other outgroups, and on textual evidence from the history of science, e.g. Aristotle's statements on women and slaves. This paper will present evidence on dehumanization as an ubiquitous phenomenon from contemporary social psychology and address what we can learn from it for a philosophical account of the concept of human nature. The claim that will be defended is the following: The evidence from dehumanization seems to entail that the content of the concept of human nature (e.g. that aggression is part of human nature, that altruism is part of human nature, that language is or is not essential for human nature) might well change historically and vary between people and scientific contexts, but without changing its pragmatic political function, namely social demarcation, demarcating in/outgroup, regulating who is "us" and who is "them". That means: the function of the concept

often stays, even if the content varies. A philosophy of science point of view on the concept of human nature should thus not restrict itself to the content of the concept of human nature as such (since it is a historically changing one anyway). It has to acknowledge the function it plays in the social realm. The aim of this talk is thus – in addition to providing evidence – to develop such a functional account of the concept of human nature in light of contemporary dehumanization studies.

12:30 - 15:30

LUNCH BREAK

13:00 - 15:00

EARLY CAREER SCHOLAR MENTORING LUNCH | Room DS-R510

DS 1520

15:30 - 17:00

ORGANIZED SESSION / DIVERSE FORMAT

THE EPISTEMIC AND METHODOLOGICAL UPSHOTS OF HISTORICITY

Organizer(s): **ADRIAN CURRIE** (University of Calgary, Canada)

Participant(s):

CAROL CLELAND (University of Colorado Boulder, United States)

DEREK TURNER (Connecticut College, United States)

ERIC DESJARDINS (University of Western Ontario, Canada)

Scientists investigate many types of systems, from the well-behaved to the chaotic. Many systems of concern to historical scientists exhibit "historicity": they are path-dependent; their dynamics depend necessarily on their past. Although there has been recent discussion of just what historicity amounts to, more needs to be done to understand its consequences for the epistemology and methodology of scientists targeting such systems. Are there qualitative differences between sciences concerned with path-dependent versus more general systems? What epistemic challenges arise from historicity? What methodological responses can (and do) scientists make to those challenges? Answering these kinds of questions will both further our understanding of science's potential to generate knowledge of the past and provide methodological guidance to science in practice.

DS 1525

15:30 – 17:00

ORGANIZED SESSION / DIVERSE FORMAT

BIOLOGICAL COLLECTIVISM, PSYCHOLOGY, AND THE CULTS OF THE GREAT WAROrganizer(s): **SNAIT B. GISSIS** (Tel Aviv University, Israel)

Participant(s):

SNAIT B. GISSIS (Tel Aviv University, Israel)**ROBERT M. BRAIN** (University of British Columbia, Canada)**DEBBIE WEINSTEIN** (Brown University, United States)**CORNELIUS BORCK** (Universität zu Lübeck, Germany)

The session combines three papers that focus on how biological, and in particular evolutionary transformist positions, were entwined with constituting psychological and aesthetic theories in the period from late 19th century until after the first world war. These amalgamations were instrumental in formulating views on individuals and collectivities, and in conceptualizing their relationship within society and in the vicissitudes of war.

Snait B. Gissis: Evolutionizing and Collectivizing**Robert M. Brain:** Art and the Cult of Elementary Life: Henri Bergson vs. Julian Benda on Transformist Aesthetics**Debbie Weinstein:** The Scale of Modern Warfare: Human Nature and the Great War**Cornelius Borck:** Commentary**DS 1540**

15:30 – 17:00

ORGANIZED SESSION / DIVERSE FORMAT

COMPLEXITY AND PROGRESS IN EVOLUTION?Organizer(s): **KELLY SMITH** (Clemson University, United States)

Participant(s):

DAN MCSHEA (Duke University, United States)**CARLOS MARISCAL** (Dalhousie University, Canada)**HUGH DESMOND** (Katholieke Universiteit Leuven, Belgium)

For a very long time, people have been speculating that evolution exhibits a trend or bias in favor of increasing "complexity". The same sort of apparent patterns in the web of life have also long been used to support various notions of progress and meaning. This session aims to explore recent developments that may shed light on these two venerable questions. Each presenter will begin by briefly outlining their take on three central questions in the debate, and then the discussion will be thrown open to all in the room. Three central questions will be discussed:

1) What is complexity and is there good reason to believe in a complexity trend in evolution?

DS M240

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

EVOLUTIONARY MODELING IN BIOLOGY AND THE BEHAVIORAL SCIENCES (2): GAMES AND LIMITING ASSUMPTIONSOrganizer(s): **CAILIN O'CONNOR** (University of California, Irvine, United States)

Evolutionary modeling is used widely in biology and the social sciences. In recent years, this practice has spread in philosophy, and philosophy of biology in particular. Given the increasing use of evolutionary modeling in philosophy of biology, it is appropriate to ask: what are the limits of this sort of modeling? In what ways does it go wrong? In what ways can evolutionary models be misleading? At the same time, how can this be a useful methodology? How does it provide insight and explanation? This session will explore this methodology focusing on limiting assumptions of evolutionary models, including base games in evolutionary game theory.

Studying the real origins of communication and language: Models and experiments**THOM SCOTT-PHILLIPS** (Durham University, United Kingdom)

In proof-of-concept models, verbal theory is expressed in a formal way to establish exactly what conclusions follow (or not) from a given set of assumptions. It is widely appreciated that such models provide explanations only to the extent that the assumptions that go into them are reasonable: poor assumptions make for poor models. What is arguably less appreciated is that a similar point applies also to the explananda of such models: any lack of clarity about what is to be explained will lead to a lack of clarity about what a model can tell us. One clear illustration of this comes from the literature on the evolutionary emergence of communication. Although many models and experiments purport to study this emergence, they often fail to do so because, with few exceptions, they all build some form of communication into their initial specifications. Consequently, they in fact study how communication systems transition from one form to another, rather than how communication itself emerges in the first place. I will present research – both a recent computational model and an older experimental game – that directly addresses this problem (Blythe & Scott-Phillips, 2014; Scott-Phillips et al., 2009). I will explain what this combination of models and experiments can tell us about the origins of human communication, and in so doing I will illustrate why conceptual clarity about explananda is both important and useful, especially in evolutionary modelling.

Social behavior and evolving games

RORY SMEAD (Northeastern University, United States)

Models of the evolution of social behavior typically treat the external environment and the nature of the social interaction as fixed. In evolutionary game theory, most models focus is on how behavior evolves within a fixed game. However, some of the most important and significant evolutionary changes to social interaction involve a change of the game, not simply a change in behavior. Niche construction, for example, involves environmental modifications that may fundamentally alter social interactions (Laland et. al. 2000). Alternatively, signals and recognition ability can introduce previously unavailable strategies and stabilize otherwise disadvantaged behavior (West Gardner 2010). Representing evolving games is necessary for a more complete view of the evolution of social behavior. Although there is relatively little work done on how to formally represent an evolving game, recent work has begun to provide some methods for doing so (e.g., Wordin Levin 2007, Akcay and Roughgarden 2011, Smead 2014). Building on previous work, I will provide a method of representing evolving games that can be largely formulated within traditional evolutionary game theory. I will then explore applications of this framework to the two cases previously mentioned niche construction and the co-evolution of social behavior and type-recognition ability.

Strategic thinking in biology

CAILIN O'CONNOR (University of California, Irvine, United States)

Because game theory was developed to model strategic behavior, “games” are designed to be explicitly strategically interesting. As I plan to argue, however, there are cases in biology that lack strategic interest, and where, as a result, the use of game theory to model them has proved misleading. In this talk I offer two cases of this sort. The stag hunt is a model of cooperation under risk. The payoffs in the stag hunt are restricted so that the cooperative equilibrium is the payoff dominant one, while the non-cooperative equilibrium is what is called “risk dominant”. Without this restriction, the game is not necessarily interesting because it will be expected that actors always choose to cooperate. The stag hunt, restricted this way, evolves to the non-cooperative outcome the majority of the time in standard evolutionary models. Evolutionary game theorists have taken this observation as reason to investigate further mechanisms for the evolution of cooperation in the stag hunt. In real biological scenarios, however, there is absolutely no reason to think that the payoffs for cooperation are restricted as they are in the stag hunt game. This means that the motivating evolutionary puzzle for this work on the stag hunt is a spurious one. A second case relates to conflict of interest signaling in biology. Evolutionary game theorists claim that total conflict of interest signaling will not evolve. While this claim is largely correct when one considers only interactions between two actors in a single scenario, conflict of interest signaling in biology often occurs in the context of a larger strategic interaction. For example, organisms in the process of signaling to potential mates also signal to potential predators. In these two cases strategic limitations of games prevent them from appropriately modeling the biological scenarios they would seem to best represent.

DS M260

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

MODELING REAL PATTERNS IN BIOLOGY

Organizer(s): **COLLIN RICE** (Lycoming College, United States)

The participants of this session agree that abstract and idealized models in biology capture real patterns in the world. The participants also agree that these models can explain those real patterns. What is at issue, then, is the status of the patterns and, accordingly, the form of explanation. According to Rice, appreciating the explanatory role of these idealized models motivates a departure from a causal account of explanation. He develops an account of explanation according to which explanatory relevance amounts to contextually salient counterfactual relevance. **Walsh, Ariew, and Matthen**, drawing on their earlier work, argue that these evolutionary patterns—patterns in natural selection and drift—are statistical in nature. They contrast this view with a causal interpretation of these patterns, which they call the traditional view. Finally, **Potochnik** motivates a view of population biology models that she takes to be intermediate between causal and non-causal construals. In her view, these models represent actual causes, but they do so in a partial and skewed way, due to an emphasis on causal patterns instead of individual causal processes. Thus, in this session, we hope to clarify what is at stake among these alternative interpretations of the explanatory value of models in biology, and of the real patterns those models capture.

Causal patterns and actual causes

ANGELA POTOCHNIK (University of Cincinnati, United States)

The use of optimality models and evolutionary game theory in population biology has been viewed by some as a commitment to adaptationism — to positing natural selection as the only influence, or the most important influence, on evolution. For most philosophers and many biologists, such a commitment is unwelcome. In contrast, some have recently motivated the idea that these modeling approaches succeed in virtue of their distance from representing actual causes at all. These views of how optimality and game theory models relate to biological systems are opposed. The first suggests that these models are intended to represent all causal influences on evolutionary outcomes, or at least all of the most important influences, while the second maintains that these models are not intended to accurately represent anything at all about the actual causal influences on those outcomes. In this talk I introduce an interpretation of the aim of these modeling approaches that is distinct from, and in some regards intermediate to, these two alternatives. In my view, optimality and game theory models are designed to provide a partial and skewed representation of the (actual) causal influences on evolutionary outcomes. The partial and skewed nature of the representation is due to a focus not on the causal influences in individual instances of evolution, but on causal patterns across systems. But this still serves to represent actual causes. I will motivate this interpretation of optimality models and evolutionary game theory by examining how the models tend to be employed, what work is typically done to justify their assumptions, and the direction this research appears to be taking. In my view, this case study illustrates a quite general feature of science: partial and skewed representation that facilitates focus on causal patterns.

Four pillars of statisticalism

ANDRÉ ARIEW (University of Missouri, United States); **DENIS WALSH** (University of Toronto, Canada); **MOHAN MATTHEN** (University of Toronto, Canada)

An evolutionary population dynamics model explains the large-scale patterns of change and stasis in the trait structure of a population. They do so by describing the variation in fitness in the population. When a population varies in its fitness, it is said to be undergoing natural selection. When the outcome of a population differs from that predicted by the variation in fitness, the population is said to be undergoing drift. Over the past fifteen years there has been a considerable amount of debate about what theoretical population dynamic models tell us about biological reality. Two major positions have emerged, the traditional and the statistical. While the debate between the orthodox and statistical factions has been vigorous, it has not always been particularly productive or germane. This may be due, in large measure, to a widespread misapprehension of the statisticalist position. Our objective here is to outline as clearly and simply as possible the fundamental features of the statistical interpretation, in an attempt to forestall some of the more common misunderstandings. As we see it, statisticalism rests on four core commitments (i) evolution is a higher-order effect (as are selection and drift), (ii) trait fitness is a primitive concept in population models, (iii) population dynamics models explicitly represent only the relative growth rates of abstract trait types, and (iv) selection and drift are description dependent, that is to say a population can only be said to be undergoing selection and/or drift relative to a model. Together, these constitute the four pillars on which the statistical interpretation rests. Our objective in this presentation is to expand on these four core commitments and provide reasons for why we remain committed to statisticalism in the face of objections from the traditional perspective.

Biological patterns, idealization, and counterfactuals

COLLIN RICE (Lycoming College, United States)

Biological modelers are often interested in explaining patterns that hold across populations that are extremely heterogeneous. One prominent view of scientific explanation suggests that idealizations can contribute to explanations by distorting only those features that do not make a difference to the explanandum. However, many biological models explain patterns despite their distortion of the difference-making features of their target systems. Moreover, in many cases we are simply unable to “decompose” a scientific model into its accurate and inaccurate parts. That is, we are unable to identify which features are misrepresented and to what degree they are misrepresented. As a result, we need to expand our account of the positive contributions idealizations make to explanations of biological patterns. In this talk, I present an account of explanation that focuses on providing modal information about which contextually salient features are counterfactually relevant and irrelevant to the pattern of interest. On this account, the set of counterfactual information required to explain can be provided in numerous ways—e.g. by a causal model, a statistical model, or an equilibrium model. Moreover, I show that models can provide the counterfactual information required to explain even when they misrepresent

difference-making features of their target systems. This account has several important virtues. First, the account allows us to see how idealized biological models are able to explain patterns even when we cannot decompose them into their accurate and inaccurate parts. Second, the account shows why providing explanations of patterns provides scientific understanding of why those patterns occur across a range of possible systems. Third, the account shows additional ways idealizations can contribute to the explanations of patterns even when they distort difference-making factors. As a result, I contend that we should adopt and continue to develop a counterfactual account of how idealized models explain biological patterns.

DS M320

15:30–17:00

ORGANIZED SESSION / STANDARD TALKS

TOPICS IN THE HISTORY OF GENETICS (2)

Organizer(s): **MARSHA RICHMOND** (Wayne State University, United States)

Genetics witnessed some of the most dramatic advances in knowledge of any of the natural sciences in the twentieth century. From the rise of the Mendelian chromosome theory in the first two decades of “classical genetics,” the development of biochemical and structural techniques for unravelling the nature of the genetic material and its functioning, and the rise of population genetics leading to the Evolutionary Synthesis, the discipline witnessed dramatic breakthroughs in knowledge and in practice. These two sessions focus on pivotal moments in the historical trajectory of the discipline of genetics in the 20th century. The first examines episodes in theory construction and social practice in genetics, while the second highlights human-oriented studies of populations and the rise of the field of human and medical genetics.

Are international networks enough? The genetics of indigenous populations in Mexico in the mid-1960s

EDNA SUÁREZ-DÍAZ (Universidad Nacional Autónoma de México, Mexico)

The history of post-WWI human genetics has increasingly paid attention to actors and locations that did not have a place in previous narratives. A broader understanding of public health practices around the world, the role of international agencies and Cold War concerns have also had an impact on historical studies of this period. Nevertheless, much remains to be done. A thoroughly inclusive view of human population studies must recognize the transnational – but local— character of the field, and how it was composed by different and sometimes contradictory discourses and practices. This paper aims to draw attention, and add needed contrast, to two relevant actors in the study of Mexican populations: Rubén Lisker (director of the Genetics Department at the National Institute of Nutrition), and Alfonso León de Garay (founder of the Genetics and Radiobiology Program at the Mexican National Commission of Nuclear Energy). As post-war international agencies and scientific collaboration established new modes of circulation of practices and knowledge, and public health became a priority in development programs (among fears of communism in the poor regions of Latin America),

physicians and human geneticists sought to contribute to knowledge on “primitive peoples” and to the standard view of human populations as defined by variations in genetic frequencies. Not all of them, however, succeeded in linking their results with the international networks of knowledge. Paradoxically, it was Lisker’s reliance on a heavily local approach (indigenismo) which accounts for the alignment of his results with international accepted knowledge and practices.

The changing face of (medical) geneticists in Canada (1947-1990)

BILL LEEMING (OCAD University, Canada)

This paper explores the close relationship between scientists and physicians in the formation of medical genetics as a medical specialty in Canada. It reviews how the intellectual and specialist movements that supported the use of genetics in clinical settings between 1947 and 1990 were emergent phenomena, created, split, and re-configured numerous times over the course of four decades. Initially, an elite of geneticist-scientists built career paths through their work in newly established clinical settings for “heredity counselling.” These individuals established highly specialized patterns of work by combining hospital work and teaching posts. They drew a clientele of patients on the basis of personal reputations for specialized expertise in science in a manner that recalls Victor Thompson’s early discussion of “personal specialization.” “Task specialization” (à la Thompson) followed between 1960 and 1990 with counselling and laboratory services becoming standardized and more formal occupational roles and work rules becoming institutionalized across networks of regional genetic service centres. In this context, the paper pays special attention to the use of prolepsis (i.e., use of a rhetorical device by which future events are presumed to have already occurred) to cultivate medical interest in applied human genetics. To be historically accurate, the story of prolepsis in medical genetics precedes the establishment of heredity counselling in clinical settings in the 1940s. Early on, chromosomal theories of heredity were promoted as being likely to produce new clinical tools for identifying persons deemed genetically at risk for disease by linking physical signs and hereditary processes. Nonetheless, genetic explanations of disease causality processes remained on shaky ground in medicine until the 1960s when conceptualizations of recurring patterns of disease in families began to shift from “related by kinship and biological relatedness” to “related to chromosomes and genes.”

Human genetics in Mexico during the Cold War

ANA BARAHONA (Universidad Nacional Autónoma de México, Mexico)

After WWII human heredity as a medical field (which included population genetics and medical cytogenetics) developed new techniques and practices intended not only to characterize but also to understand variation differences among populations, and their relation to the presence of certain diseases. Human genetics was transformed from a medical backwater to an appealing medical research frontier between 1955 and 1975. It was precisely during the Cold War that scientists hosted, disseminated and consolidated the emerging model of human genetics in the clinic and the field. This paper explores the origins of medical cytogenetic knowl-

edge and practices in the 1960s and 1970s in Mexico, focusing on the work of the group headed by Salvador Armadares, who spent two years in Oxford, England, with human genetics expert Alan C. Stevenson. Upon Armadares’ return from England in 1966, the first Unit for Research in Human Genetics was created at a medical setting, the Instituto Mexicano del Seguro Social (Mexican Institute of Social Security). Some research projects showed the embeddedness of this unit in both public health policy and medical care, as it tackled the effects of malnutrition on chromosome structure, child mortality, chromosome aberrations and Down syndrome. By posing malnutrition, one of the main concerns of Mexican post-revolutionary governments, as both medical and genetic problem, the unit contributed to positioning cytogenetics as a medical practice and a medical research domain. The focus of this paper will be these set of institutions, physicians, practices and ideas that began to reshape medical genetics in the country. The reconstruction of the early days of cytogenetics in Mexico demonstrates the major roles played by both the clinic and post-revolution public health policies in the origins of medical genetics in Mexico within a global movement to delivering the benefits of scientific knowledge to the general population.

DS M340

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

EXPERIMENTAL DESIGN IN THE LIFE SCIENCES AROUND 1900

Organizer(s): **JUTTA SCHICKORE** (Indiana University, United States); **GARLAND ALLEN** (Washington University, United States)

One of the major topics in the historiography of the life sciences has been scientific experimentation. Historians of experimentation have examined various aspects of experimental practice – research materials, laboratory infrastructure and instrumentation, techniques of visualization, and so forth. In this session, we shift the perspective from materials, practices and instruments to an aspect of experimentation that has received less scholarly attention, namely the methodological concepts and strategies that experimenters were using to support experimental findings and conclusions. We concentrate on the decades around 1900. In this period, new methods of assessing the credibility and significance of experimental research were developed, debated, and – gradually – implemented in a number of different fields, ranging from agriculture to embryology. The papers in this session examine aspects of this process, focusing on key methodological concepts such as randomization, experimental error, and control.

The experimental error of field trials: From conceptualization to computation

GIUDITTA PAROLINI (Technische Universität Berlin, Germany)

Since the beginning of the twentieth century the determination, control and reduction of experimental errors have become an essential part of field and laboratory research in the life sciences. Experimental errors have been advocated as a mark of scientific credibility and strategies for their determination and reduction have been devised based on the design of field and laboratory trials and the type of analysis performed on the result-

ing data. In this process expertise in statistics and computing has proved crucial. Life scientists have forged alliances with statistical and computing consultants or have turned to tools able to facilitate statistical analysis, such as statistical cookbooks or present day software packages. Therefore, the conceptualization and computation of experimental errors are a crucial element to understand how mathematics and number crunching have shaped practical and theoretical developments of the life sciences. The paper will address this issue using as a case study the experimental error of field trials in agricultural science. It will examine the involvement of statistical consultants in the extensive field experimentation performed by a major British agricultural institution, Rothamsted Experimental Station. Concentrating on the first half of the twentieth century, I will discuss how the determination of reliable experimental errors changed field experimentation. In so doing I will examine the statistical tools deployed to tame and control experimental errors, the mutual relationship between accuracy and experimental design, the computing work involved in the process, the presentation of experimental errors in the official publications of the agricultural institution, the relevance of experimental errors for advising farmers on cultivation practices. Despite addressing a specific case study, the paper remains of general interest for all the life sciences due to the success that the statistical methods developed at Rothamsted Experimental Station had in conceptualizing and computing experimental errors across these disciplines.

Randomization? Fisher, “Student”, and the Society for Psychical Research

NANCY HALL (University of Delaware, United States)

In his pivotal 1925 book *Statistical Methods for Research Workers*, Ronald Fisher first published the requirement of randomization in experimental design, to eliminate bias derived from the experimental material or from the researcher, and to make possible a valid test of significance. No where in Fisher’s known correspondence, notes or publications have I found anything directly discussing his development of the concept. But circumstantial evidence suggests two influences: a major one in Fisher’s relations and correspondence with “Student” and a minor one in his advisement to the Society for Psychological Research. In both of these, the concern was mathematics for small samples. “Student” (William Sealy Gosset), a master brewer for Guinness, often had to deal with samples as small as four; the statistics then current were unreliable for samples smaller than about thirty. By 1924, when Fisher was writing the book, he and “Student” had been corresponding for nine years. The Society for Psychical Research, founded in 1882, had the same problem as in many other fields of research: when are results significant and when are they merely due to chance? Fisher did not believe in either telepathy or clairvoyance, but he published three papers discussing the guessing of playing cards, another case of small samples. He analyzed the various probabilities and set up a simple method of scoring. Correspondence makes it clear that Fisher was working on the playing card question in 1923.

“Control(led) experiments” in late 19th-century biomedicine

JUTTA SCHICKORE (Indiana University, United States)

This paper offers an interpretation of experimenters’ views on control(led) experiments in mid- to late 19th century biomedical sciences. There are at least two strands in the discussion about controls, one concerning the comparison of populations, the other the comparison of individual experiments. For methodological thought in 19th-century biomedicine, the second tradition is the more relevant. Focusing on concepts of control in late 19th-century bacteriology, immunology, and experimental embryology, particularly in the works of William Welch, Paul Ehrlich, and Jacques Loeb, I show that in these contexts, the concept of control could mean three things: a practice that “controls for” the impact of specific factors on experimental outcomes, a practice that corrects for unknown variables, and the design of new forms of organic life. The first two practices were by no means novel – but only in the late 19th century, they were called “controls”. I argue that the introduction of the term “control” signals a loss of trust in the practical applicability of John Stuart Mill’s methodology of experimentation. Various experimenters maintained that Mill’s methodology expressed an unattainable ideal and that it could not address the most pressing problems of scientific experimentation in the life sciences – the complexity of living things. Control(led) experiments were seen as a realistic alternative to Mill’s ideal.

DS M440

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

PRESERVATION AND TRANSFORMATION IN CULTURAL EVOLUTION

Organizer(s): **MATHIEU CHARBONNEAU** (Konrad Lorenz Institute for Evolution and Cognition Research, Austria)

Over the last thirty years, cultural evolutionary theory (hereafter: CET) has emerged as a unique perspective on the evolution of culture, distinct from approaches such as sociobiology and Santa-Barbara evolutionary psychology. CET is a rich, interdisciplinary, and increasingly fruitful methodological framework that aims at providing a naturalistic account of the origins of culture, as well as general principles for analysing and describing the evolutionary history of enculturated species. Central to CET are the ways in which individuals learn from one another, and how cultural traits get distributed through the different channels of social transmission. However, CET encompasses different approaches. Some of them hold that cultural transmission is a high-fidelity, preservative, inheritance-like process, closely resembling Darwinian evolution. Domain-general transmission biases explain (in part) how cultural variants become widespread and available for downstream changes, and change of cultural variants is assumed to be gradual and cumulative. Others approaches give more importance to the fact that cultural transmission is a transformative, reconstructive process, and highlight the importance of domain-specific cognitive mechanisms in determining the success of cultural traits. This session will critically appraise these two perspectives to study cultural transmission within CET. It will evaluate concepts central to each, and clarify how they relate to CET modelling practices. Finally, it will assess the compatibility of these two approaches, and clarify when and where each is applicable.

If we are all cultural Darwinian what's the fuss about? Selection versus attraction in cultural evolution

ALBERTO ACERBI (Technische Universiteit Eindhoven, Netherlands); **ALEX MESOUDI** (Durham University, United Kingdom)

Cultural evolution studies are characterized by the notion that culture evolves accordingly to broadly Darwinian principles. However, how far the analogy between cultural and genetic evolution should be pushed is open to debate. I will examine a recent disagreement that concerns the extent to which cultural transmission should be considered a preservative mechanism allowing selection among different variants, or a transformative process in which variants are recreated each time. I argue that there is no real conflict between the two approaches, besides a focus on different aspects of cultural evolution. I will first try to clarify the respective positions, elucidating common ground and genuine disagreements. I propose that considering cultural transmission as a preservative or reconstructive process is ultimately an empirical question, and I examine how both preservative and reconstructive cultural transmission has been studied in recent experimental research in cultural evolution. I will then discuss how the relative importance of preservative and reconstructive processes may depend on the granularity of analysis and on the domain being studied.

Attracting trouble: Disambiguating the concept of cultural attractors in cultural evolution

ANDREW BUSKELL (University of Cambridge, United Kingdom)

There are two main approaches to contemporary cultural evolutionary theory. The "California School", whose members include Peter Richerson, Robert Boyd, Joseph Henrich and others, emphasizes the role of evolved learning strategies and sampling biases. The "Sperber School" on the other hand, takes as central the role of various relational properties between individuals and particular cultural behaviours, or types. In particular, they rely on a notion of cultural attractors. However, the Sperber School has not been consistent in its definition and use of this central concept. In this paper, I analyse three different characterizations of this central concept – what I call attraction as tendency, attraction as force, and attraction as outcome – suggesting that each is aligned with a different approach to modelling. Attraction as tendency is allied with a mechanistic and ethnographic approach; attraction as force with an abstract, aggregative approach; and attraction as outcome to a general, minimal modelling approach. Each of these approaches to cashing out attraction have positive and negative aspects: I here suggest that, however, while the first two approaches have proven their relevance, the third is not yet convincing.

(Re)integrating modification processes to the origins of cumulative culture

MATHIEU CHARBONNEAU (Konrad Lorenz Institute for Evolution and Cognition Research, Austria)

The cumulative open-endedness of human cultures represents a major break with the social traditions of nonhuman species. As traditions are altered and the modifications retained along the cultural lineage, human populations are capable of producing complex traits that no individual could have figured out on its own. A popular explanation for this fact is humans' capacity for high-fidelity social transmission. For cultures to produce

increasingly complex traditions, improvements and modifications must be kept for the next generations to build upon them, and high-fidelity transmission would thus act as a ratchet, retaining modifications and allowing the historical build-up of complex traditions. Mechanisms acting against slippage are important, of course, but cultures also need to move forward for anything important to be retained at all. In this paper, I develop a different albeit complementary line of reasoning about the population-level conditions and evolutionary implications of cumulative culture. I argue that studies of modification-generating processes and the diverse ways they pattern cumulative culture have been overlooked. There are many ways that traditions can be modified and, depending on the structure of the cultural traits and of the design space explored by the population, different kinds of modification mechanisms will lead populations to exhibit different evolutionary patterns. The conclusion I reach is that even if a population is endowed with members capable of innovating and transmitting the improvements with high-fidelity, with the wrong modification processes the structure of the design space will constrain the population to wallow in non-cumulative traditions. I illustrate my claims through the study of technical behaviours, such as tool use and tool manufacture, the very behaviours that are likely the markers of early cumulative culture in the human lineage.

DS M460

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

TYING EXPLANATIONS TO MODELS IN NEUROSCIENCE

Organizer(s): **ERIC HOCHSTEIN** (Washington University in St Louis, United States)

Advances in computer simulations and modeling techniques over the past few decades have provided new tools and avenues of research for neuroscientists to use in the study of the brain (Thagard 1993; Winsberg 1999). These new modeling techniques have brought with them new ways of interpreting and thinking about what the brain is, and what it's doing. This, in turn, has led many to conclude that these new ways of modeling the brain provide new types of scientific explanations, unlike those that came before. These include mechanistic explanations (Craver 2007; Bechtel 2008; Eliasmith 2010), computational explanations (Chirimuuta 2014), dynamical explanations (Van Gelder & Port 1995; Kelso 1995; Chemero 2009), and topological explanations (Huneman 2010). This proliferation of different types of models has resulted in an ongoing debate in philosophy of science regarding the exact relationship between scientific models and scientific explanations within neuroscience. Do different types of models necessarily support different kinds of explanations? If so, on what grounds? Can the same model play a role in fundamentally different types of explanations? Can different kinds of models be part of the same type of explanation? While some stress the epistemic differences between these models and how they impact their explanatory power, others have argued that many of these accounts are not truly distinct and can be integrated into the same broadly mechanistic framework (Piccinini & Craver 2011; Kaplan 2011; Eliasmith 2012). The purpose of this symposium is to further explore this relationship between different types of scientific models and the nature of scientific explanations within a neuroscientific context.

Why no model is ever a mechanistic explanation

ERIC HOCHSTEIN (Washington University in St Louis, United States)

There is a great deal of disagreement within the philosophy of neuroscience regarding which sorts of models provide mechanistic explanations, and which do not (e.g: computational models, dynamical models, network models, etc). These debates often hinge on two commonly adopted, but conflicting, ways of understanding what mechanistic explanations are: what I call the “representation-as” view, and the “representation-of” view. In this paper, I argue that neither account can be used to adequately make sense of neuroscientific practice. In their place, I offer a new alternative that can diffuse some of these disagreements. I propose that individual models never provide mechanistic explanations (regardless of what type of model they are). Mechanistic explanations by necessity span sets of different types of models. To claim that a given model provides us with a mechanistic explanation is in fact to claim that this model, in conjunction with all other pre-existing models and background information we have about the system, allows us to decompose the system into parts and operations for better understanding. Thus the same model counts as both a mechanistic, and a non-mechanistic explanation, depending entirely on what other background information we have available at the time, and whether the model allows us to fill in informational gaps about some mechanism operating in the world.

Perspectives on the brain

MAZVIITA CHIRIMUUTA (University of Pittsburgh, United States)

As has frequently been noted, cognitive neuroscience in the 21st century has been transformed by a proliferation of new technologies for conducting experiments on the brain. These include the numerous modalities of neuroimaging (functional and anatomical, invasive and non-invasive); optogenetics and brain computer interfaces (BCI's). Some philosophers of neuroscience have argued that contemporary neuroscience is also characterized by explanatory pluralism: that different experimental and theoretical research traditions are associated with distinct explanatory styles, such as mechanistic, computational and dynamical ones (Silberstein and Chemero 2013; Chirimuuta 2013, 2014; Ross 2015). The focus of this talk is the relationship between these various research traditions. I first propose that different experimental techniques offer unique and complementary perspectives on neural function, whereby the theories and models associated with one stream of research offer insights not afforded by the others, but at the same time cannot be said to contradict the alternative perspectives (Giere 2006). I discuss the different experimental techniques that are most readily associated with mechanistic vs. dynamical models. I then argue that there is a Levins (1966) style trade-off between the “realism” afforded by mechanistic models and the “generality” made possible by dynamical models.

Graphing the brain's dark energy: Network analysis in the search for neural mechanisms

CARL F. CRAVER (Washington University in St. Louis, United States)

In a recent paper on network analysis, Philippe Hunneman conjectures that topological explanations represent a style of explanation distinct from mechanistic explanation. I discuss these claims in the context of recent work using resting state functional correlations to infer cortical structure. Graph theory and network analysis are central research tools in the Human Connectome Project (Sporns 2011). I argue (in agreement with Hunneman) that network models (often coupled to facts about localization) can be used to describe features of the organization of complex mechanisms that other representational systems are ill-equipped to describe. I catalogue some of the surprising uses of network theory in contemporary connectomics. Network theory can be used to construct accurate, complete, and well-verified mathematical descriptions of both brain activity and brain structure without thereby explaining how brains do anything at all. It would distort contemporary network theory in the connectome project to see it as aiming at a style of explanation distinct from mechanistic explanation. The project is aimed at providing useful information about mechanisms, and the graphical models are a surprisingly indirect means of accessing and representing such information.

DS M540

15:30 - 17:00

ORGANIZED SESSION / DIVERSE FORMAT

FUNCTIONS, TELEOLOGY, AND NORMATIVITY AT VARIOUS LEVELS OF ORGANIZATION (2)

Organizer(s): **ANTOINE C. DUSSAULT** (Université de Montréal, Canada); **SOPHIA ROUSSEAU-MERMANS** (IHPST/ Université Paris 1 Panthéon-Sorbonne, Université de Montréal, Canada)

Participant(s):

ANTOINE C. DUSSAULT (Université de Montréal, Canada)

SEBASTIEN DUTREUIL (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

NEI NUNES-NETO (Universidade Federal da Bahia, Brazil)

ALVARO MORENO (University of the Basque Country, Spain)

The notion of function is central to biological theory and has been abundantly discussed in the philosophy of biology (e.g., Huneman 2013, Ariew et al. 2002, Allen et al. 1998). Yet, new directions of investigation have recently emerged in the literature. A first one explores the conceptual link between the normativity and teleology of functional ascriptions and key notions in theoretical biology like those of organization, self-maintenance and natural kinds (e.g., Krohs 2011, Saborido et al. 2011, Mossio et al. 2009). Another one discusses the applicability of functional language to organizational levels above that of organisms (e.g. Nunes-Neto et al. 2014, Bouchard 2013, Odenbaugh 2010). The main aim of these twin sessions is to gather researchers whose work explores those new directions and discuss some of the conceptual issues that they raise. The twin sessions will include discussions of functional language as applied to physiology, ecosystem ecology, earth systems science and theoretical work on social-ecological systems.

DS R340

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

“ORGANIC PHYSICS”: PHILOSOPHICAL BIOLOGY AND ANTHROPOLOGY IN SCHELLING, TROXLER AND HEGELOrganizer(s): **BARBARA ORLAND** (Universität Basel, Switzerland)

The bio-philosophical debates at the turn of the 19th century laid the foundation to the differentiation and further development of the modern life sciences. An outstanding representative of this period of transition was the Swiss physician, politician and philosopher Ignaz Paul Vitalis Troxler (1780-1866), well known to his contemporaries, but today only seldom commemorated. Troxler had studied medicine and philosophy (with Schelling, also with Hegel) at the University of Jena in 1800. After his return to Switzerland, he became an extremely industrious physician and professor of philosophy at the universities of Basel and Bern, but also one of the intellectual founding fathers of democracy in the emerging Swiss federal state. The session will honour his work by outlining the points of discussion in Schellings and Hegels philosophy of biology and their scientific background. It will trace the path, that led Troxler from philosophical conceptions of organic life towards a new form of philosophical anthropology, called “anthroposophy”. This philosophical enterprise forms one of the many historical roots of and gives a cue to the anthroposophical movement founded by the Austrian philosopher, literary critic and social Reformer Rudolf Steiner (1861-1925).

Periods and rhythm as biological phenomena

BRIGITTE HILMER (Universität Basel, Switzerland)

In classical transcendental philosophy experience of time has been described as a phenomenon of consciousness and cognition. The faculty of imagination in the inscrutable depths of the human soul was supposed, following Kant, to provide schemes of application of categories in space and time. For Schelling and even more for Troxler our organic life has a say if we want to understand our experience of time. It is the periodical and rhythmic structure of biological processes, like respiration, heartbeat, pulse, digestion, sleeping and being awake, menstruation and so on, that make a living organism a scheme of timely experience in itself. Troxler clearly envisages the task of explaining the rhythmic structure of organic processes in its autonomy and as related to the surrounding universe and thus anticipates modern chronobiological research.

Hegel, Schelling and Troxler on sensibility and irritability

CHRISTIAN STEINER (Universität Basel, Switzerland)

Hegel criticizes the theories of irritability of his time in the context of his account of the practical relation between the animal and its anorganic nature. Among the target of his critique are Schelling's and Troxler's theory on sensibility and irritability in their natural philosophies which he blames for being too formalistic. According to Hegel, they understand sensibility and irritability as a merely quantitative relation, rather than as two concrete aspects of the individual organism's relation to its environment. The aim of this contribution is to reconstruct Hegel's critique by drawing on these different conceptions of sensibility and irritability.

Dialectic of the soul: Platonic heritage in Schelling's philosophy of nature

MARIO SCHÄRLI (Universität Basel, Switzerland)

The starting point of any understanding of Troxler's biological and anthropological studies is Schelling's philosophy of nature, in which he deals with the issue of how nature's organic and inorganic phenomena can be given a unified, non-reductive explanation. Schelling first achieves this in his seminal *Von der Weltseele* (1798) by reverting to Plato's conception of a world-soul (*psyche tou pantos*), thereby placing the principle of a “universal organism” at the heart of nature as a whole. By tracing back the development of this crucial idea to Schelling's 1794 commentary of Plato's *Timaeus*, it will be argued that Schelling not only inherits the concept of a world-soul from Plato, but also implements the dialectic of the infinite (*apeiron*) and finite (*peras*) from the *Philebus* in his philosophy of nature. However, as Schelling translates the dialectic into an antagonism of fundamental forces of nature he thereby conceals their Platonic origin. By reference to the commentary it will be shown how Schelling already reads these concepts from the *Philebus* into the *Timaeus* in his 1794 interpretation and thus advocates a profoundly Platonic philosophy of nature. Put in this perspective, Troxler's departure from Schelling's philosophy of nature appears as giving privilege to the organic structure of the world-soul not only in the realm of nature, but also over and above reason.

DS R510

15:30 – 17:00

ORGANIZED SESSION / DIVERSE FORMAT

EXTENDING CHARLES DARWIN'S CONTEXTOrganizer(s): **RICHARD DELISLE** (University of Lethbridge, Canada)

Participant(s):

RICHARD DELISLE (University of Lethbridge, Canada)**RICHARD BELLON** (Michigan State University, United States)**THIERRY HOQUET** (Université Jean Moulin Lyon 3, France)**RICHARD RICHARDS** (University of Alabama, United States)

An attempt is made to expand on the relevant context for understanding Charles Darwin's works: (1) the impact of ideas from the Eighteenth century; (2) the social milieu during Darwin's lifetime; (3) Darwin's interest for variation and inheritance; and (4) principles of classification as compared to approaches in the second half of the Twentieth century.

DS R515

15:30–17:00

ORGANIZED SESSION / DIVERSE FORMAT

SCAFFOLDING WERNER CALLEBAUT'S NATURALISTIC TURN

Organizer(s): **LINNDA CAPORAE** (Rensselaer Polytechnic Institute, United States)

Participant(s):

JOSEPH D. MARTIN (Michigan State University, United States)**WILLIAM C. WIMSATT** (University of Minnesota, United States)**JAMES GRIESEMER** (University of California, Davis, United States)**LINNDA CAPORAE** (Rensselaer Polytechnic Institute, United States)**MASSIMO MAIOCCHI*** (University of Chicago, United States)

Originally, we wanted to propose a round table or symposium on our edited book, *Developing Scaffolds in Evolution, Culture, and Cognition* (2014). However, the untimely loss of our good friend—and scaffolder par excellence — Werner Callebaut — led us to a somewhat different project. We have often been in Werner's orbit beginning with his book, *Taking the Naturalistic Turn, Or How Real Philosophy of Science is Done* (University of Chicago Press, 1993). Bill Wimsatt was an interviewee, Jim Griesemer was a reader for the press, and Linnda Caporael was Werner's sidekick between Manhattan and Lehigh. Twenty years later, Werner scaffolded, from beginning to end, the workshops, KLI visits, and finally, the book that we co-edited. It was the last book that Werner saw published as part of the *Vienna Series in Theoretical Biology* by the MIT Press, and without a doubt, it made that naturalistic turn.

Our goal in this session is to repay his eagerness to build a new interdisciplinary area, his globalizing sensibility, his irrepressible enthusiasm, and most of all, his deep and abiding friendship, with work we feel sure he would have enjoyed and in the spirit of the ISH "tradition of an informal, collegial approach," which he cherished.

Joe Martin is our "discussant with a twist." His grasp of our co-edited book is superb, and we have asked him to begin the session as discussant for that work. **Bill Wimsatt's** evo-devo approach to the analytic-synthetic distinction shows some of the implications of modularity and its consequences for probabilistic changes in evolutionary and cognitive development, all topics of considerable interest to Werner. **Jim Griesemer** reprises a piece of work that always tickled Werner, a counter argument based on scaffolding to Herbert Simon's parable of Hora and Tempus, the two watchmakers purportedly supporting that hierarchy and near decomposability explain the "architecture of complexity." Presupposed in both Simon's and Griesemer's argument is a material body-in-action, which becomes central to the speculative paper by **Linnda Caporael** (a psychologist) and **Massimo Maiocchi** (an Assyriologist), a collaboration in the expansive, interdisciplinary spirit of the KLI under Werner's directorship, and the emphasis on development, evolution, and the importance of grappling with biological and cultural complexity.

DS R520

15:30–17:00

ORGANIZED SESSION / STANDARD TALKS

THINKING ABOUT CELLS (2): HOW DO CELLS WORK?

Organizer(s): **JANE MAIENSCH** (Arizona State University, United States); **KARL MATLIN** (University of Chicago, United States)

These two coordinated sessions look at what cells are and how they work, in parallel with consideration of epistemological questions about how we know. The first session examines the evolving understanding of what cells are, including an overview of early concepts and close examination of studies in protozoa and in stem cells. Throughout, we ask about the methods and assumptions involved. The second session turns to questions about how cells work. This includes a look at explorations of cytoplasmic streaming within cells, at the understanding of cell death, and at intersections of form and function through study of mitochondria and oxidative phosphorylation. Here issues of methods, metaphor, and the heuristic use of form in order to inform mechanical explanations of function play important roles. The sessions work together to get at historical, philosophical, and biological questions about cells.

[Explaining the "pulse of protoplasm": The search for molecular mechanisms of protoplasmic streaming](#)**MICHAEL DIETRICH** (Dartmouth College, United States)

Explanations for protoplasmic streaming began with appeals to contraction in the eighteenth century and ended with appeals to contraction in the twentieth. During the intervening years, biologists proposed a diverse array of mechanisms for streaming motions. This paper focuses on the re-emergence of contraction among the molecular mechanisms proposed for protoplasmic streaming during the twentieth century. The revival of contraction is a result of a broader transition from colloidal chemistry to a macromolecular approach to the chemistry of proteins, the recognition of the phenomena of shuttle streaming and the pulse of protoplasm, and the influential analogy between protoplasmic streaming and muscle contraction.

[Regulating cell death](#)**ANDREW REYNOLDS** (Cape Breton University, Canada)

Since the 1970s cell death has been classified into two chief forms: necrosis, an accidental death due to injury, and apoptosis, a genetically regulated form of cell death associated with normal development and tissue homeostasis. This distinction was based on morphological features of dying cells observed with light and electron microscopy. Apoptosis soon became synonymous with the earlier described phenomenon of programmed cell death, first observed in the context of animal development. Increased attention to cell death led to an expanding catalog of descriptions of novel variations of apoptosis and necrosis with overlapping morphologies. The Nomenclature Committee on Cell Death (NCCD), created in 2005 to provide guidance on the classification and description of cell death, has increasingly recommended eschewing morphological criteria in favor of more precise, quantitative biochemical and genetic criteria associated with causal mechanisms. In its 4th and latest report (published online 19 Sept. 2014) the NCCD recommends a new classification distinguishing "acciden-

tal cell death” and “regulated cell death”, the latter now defined by the ability of researchers to successfully pre-empt cell death through pharmacologic or genetic intervention. This shift away from morphological criteria suggests not only a clinical focus, but also the success of molecular biology at intervening in the regular life of cells. Talk of “rewiring” and “reprogramming” cell “circuits” to alter the outcomes of various “subroutines” of regulated cell death suggests a heavy influence of computer engineering metaphors. Do these metaphors promote the assumption that any regular causal sequence of events (a “mechanism”) in the cell is part of an adaptive and functional “program”?, and should we be asking “How much of the interactions between proteins and other molecules within a cell are more closely analogous to “weather” than to subroutines of a computer program?”

Mitochondrial form and the search for the mechanism of oxidative phosphorylation

KARL MATLIN (University of Chicago, United States)

In the 1950s a group of enzymologists in the United States and Europe proposed and attempted to prove the “chemical hypothesis” of oxidative phosphorylation postulating the existence of mitochondrial high-energy intermediates required for production of ATP. These efforts were, in the end, unsuccessful, and the chemical hypothesis was displaced beginning in 1961 by Peter Mitchell’s “chemiosmotic” hypothesis, shown in subsequent years to be essentially correct. In the same period, cell biologists, led mainly by George Palade, described the intricate structure of mitochondria using electron microscopy. While the controversies surrounding biochemical aspects of the competing chemical and chemiosmotic hypotheses have received significant attention, less historical scholarship has focused on the intersection between biochemical studies and the discovery of mitochondrial structure. This paper explores how mitochondrial form as described by Palade figured in the experiments of these scientists, finding that mitochondrial compartmentalization was adopted by Mitchell as a key element of his chemiosmotic hypothesis, but was overlooked or misunderstood by enzymologists investigating the chemical hypothesis. These historical events are interpreted in terms of a more general approach to explanation of cellular phenomena that utilizes morphology heuristically as a constraint on possible explanatory models.

ORGANIZED SESSION / STANDARD TALKS

DEHUMANIZATION (2): NEW APPROACHES TO UNDERSTANDING THE POLITICS OF HUMAN NATURE

Organizer(s): **MARIA KRONFELDNER** (Central European University, Hungary); **ROBERT A. WILSON** (University of Alberta, Canada)

This is the second part of a double session (see Dehumanization: New approaches to understanding the politics of human nature, Part I). Debates about human nature in the biological and social sciences as well as in philosophy of science typically consist of a positive proposal of some kind and critical responses to that proposal. Although political considerations often enter into both sides of such debates, there is a sense in which

such considerations are secondary. In this double session, we adopt a different approach, drawing on and contributing to the emerging field of dehumanization studies. This approach places the less-than-fully human in the spotlight. On the basis of recent empirical findings on dehumanization, we will discuss how dehumanization, essentialism, eugenics and disability hang together. In this part of the double session, we will apply the results of the first part to specific political concerns, mainly (iv) ability expectation and ableism (**Gregor Wolbring**), and (v) eugenics and disability (**Rob Wilson**). The two talks in this second part are followed by (vi) a round table discussion “Dehumanization: A Dialog”. As a whole, the session aims to open up some novel possibilities for historians and philosophers of science in analyzing essentialist thinking by taking up a provocative theme, dehumanization, drawing on recent work from the psychological and social sciences.

Ability expectations, ability privilege, ability power and ableism: A tool for and against de-humanization

GREGOR WOLBRING (University of Calgary, Canada)

The disabled people rights movements in the United States and Britain coined the term ableism as a cultural concept during the 1960s and 1970s to question and highlight (a) the expectations towards species-typical body abilities (we expect certain abilities from different species; humans are supposed to walk but not to fly, birds are supposed to fly) and (b) the disablement and de-humanization that came with it, the prejudice and negative treatment people experience whose body-linked abilities are seen as sub species-typical and therefore labeled as “impaired”, as deficient. However, the cultural reality of ability expectations (want stage) and ableism (need stage) go far beyond how it is used within disability studies and by disabled activists. Ability expectations are one aspect of culture used by social entities to relate to each other for example, in the case of individuals they lead to an ability-based and ability-justified understanding of oneself, one’s body and one’s relationship with others of one’s species, other species and one’s environment. Ableism does not have to be negative: it simply indicates that one has certain ability expectations one lives out. Yet, ability expectations can and have been used in a negative way to exhibit ability inequity and ability inequality, ability power and ability privilege, not only against disabled people, but also to support negative –isms such as racism and sexism and various other forms of de-humanization.

Subhumanizing the defective: Dehumanization, disability, and eugenics

ROBERT A. WILSON (University of Alberta, Canada)

Work on the history of eugenics has recently shifted from a focus on what might be thought of as the extreme forms of eugenics associated with Nazi Germany and the American eugenics movement to consider eugenic ideas and practices in less familiar cultural contexts and during the post-WWI era. As a part of that shift, in this presentation I will focus on subhumanizing tendencies in the characterization of people with disabilities in science, medicine, and philosophy over the past 100 years. While such tendencies are quite explicit in the first half of the 20th-century, they survive more implicitly in the second-half of that century, and remain with us in

DS R525

15:30 – 17:00

contemporary bioethics and applied ethics. Understanding this subhumanization involves thinking about ideas of human variation, about the expectations of family and kinship relations, and about the role of academics in broader social initiatives. It will also take us into some of the literature on psychological essentialism, and to consider the subhumanization of other putative sorts of people, such as races, ethnicities, and gender.

Dehumanization: A dialog

MARIA KRONFELDNER (Central European University, Hungary); **RON AMUNDSON** (University of Hawaii at Hilo, United States); **DAVID LIVINGSTONE SMITH** (University of New England, United States); **ROBERT A. WILSON** (University of Alberta, Canada); **GREGOR WOLBRING** (University of Calgary, Canada)

In a dialog with all the presenters of the double session on dehumanization involved, we will weave together the different threads of the talks.

17:00 – 17:30

COFFEE BREAK

DS 1420

17:30 – 19:00

INDIVIDUAL PAPERS

GRAPPLING WITH SPECIES

Towards an old-fashioned account of reference for biological species names

JERZY BRZOWSKI** (Universidade Federal da Fronteira Sul, Brazil)

In this paper, I sketch and defend a Frege–Dummettian (FD) account of reference for biological species names. This theory is intended as an alternative to the long-held causal-historical account first defended by Ghiselin and Hull as a consequence of their species-as-individuals thesis. According to the FD account, the reference of a species name is a function of its criterion of application, derived from a code of nomenclature, and a criterion of identity, drawn from a species concept. After presenting the theory, I suggest some lines of inquiry where it can be employed.

De-extinction and the conception of species

LEONARD FINKELMAN (Linfield College, United States)

Charles Darwin asserted in his *Origin of Species* that once a species goes extinct, “the same identical form never reappears.” Geneticists seem to stand on the verge of proving Darwin wrong on that count: with new cloning techniques, we may soon engineer new members of extinct species. This process, popularly dubbed “de-extinction,” promises to resurrect species such as the mammoth, thylacine, and passenger pigeon. Darwin’s claim and the geneticists’ promise both depend on metaphysical commitments regarding the nature of species. I examine this intersection between de-extinction and the species problem. Successful resurrection of

a species through de-extinction requires that the cloned organism be a member of the same species, but not all species concepts accommodate such an idea. I describe two suggested means of de-extinction—somatic cell nuclear transfer of genetic material from an extinct species and re-engineering of genetic material from an extant species—and elaborate the relevant properties of species resurrected through these means. I then compare these properties with the species concepts currently under consideration in the Philosophy of Biology literature. I argue that species concepts accommodating de-extinction are those traditionally considered inconsistent with evolution by natural selection. Without endorsing any of these species concepts, I suggest how research in Philosophy of Biology and de-extinction technologies might influence one another in the future.

Species are probabilistic processes

BECKETT STERNER (University of Michigan, United States)

Nearly every method in phylogenetics today depends on statistical consistency: as we add more character data from contemporary taxa, our estimate of evolutionary history will converge on the true answer. Statistical consistency does not come for free, however. Our ability to know evolutionary history depends on objective facts about how species change over time. The dominant metaphysical accounts of species as individuals or kinds do not address this epistemic demand, and I argue that we need to augment these accounts to capture the probabilistic nature of species. I discuss different ways of interpreting the probabilities involved in phylogenetic models, including deterministic views, and I argue that a strongly subjective interpretation will not suffice. The character of metaphysical argument I give here aims to explicate the full normative commitments that biologists make about the nature of species in the course of their research practices. In this manner, the epistemic constraint of knowing evolutionary history illuminates an under-recognized aspect of the ontology of species.

INDIVIDUAL PAPERS

HUMAN NATURE, LANGUAGE AND CAUSATION IN THE MIND

The evolutionary criterion of human nature

JESSICA LAIMANN (University of Oxford, United Kingdom)

According to Edouard Machery’s evolutionary criterion of human nature, natural human traits are those traits which are common among humans “as the result of organic evolutionary processes.” I discuss two different ways to interpret this criterion. First, a “nature versus learning” approach that contrasts natural traits with learned ones; second, an approach referring to evolved human cognitive architecture. The first approach, I will argue, fails, whereas the second approach either results in an all-inclusive category of the natural that leaves no room to distinguish between natural and non-natural human traits, or results in a distinction that makes significant references to environmental factors, thereby suggesting an altogether different classificatory scheme.

Returning language to biology by the way of culture

TERESA BLASCO MÁÑEZ (Universidad de Oviedo, Spain)

As we advance in our understanding of evolutionary biology and the mechanisms underlying language, the biological plausibility of the standard nativist hypothesis regarding the evolution of a dedicated language faculty becomes more amenable to criticisms. Indeed, cultural and usage-based approaches to language evolution have provided important insights as to how the emergence of particular linguistic features and structures can be delivered through iterated learning. Importantly, cultural transmission studies in songbirds have provided evidence for the emergence of systematically structured communication systems, supporting the view that the capacity for complex vocal control –traditionally regarded as an externalisation device– might actually bear a close relation to syntax. Both positions, however, attempt to explain linguistic structure by black-boxing cognitive development: nativists, on the one hand, by positing the sudden evolution of a syntactic component. On the other hand, cultural, evolutionary approaches tend to focus on external pressures shaping the communication system but abstract away from the organic processes that allow for their emergence. I address these issues by adopting an evolutionary developmental (EvoDevo) perspective on language structure. I argue that EvoDevo provides the conceptual toolkit for tackling –from an “internalist” perspective- the question of the emergence and impact of the capacity for complex vocal control, and the set of interrelated questions concerning language, such as the intersection between speech and grammar. By emphasizing the notion of cognitive development as activity-dependent and grounding it on sensory-motor processes, I show there is no clearcut divide between psychological development and brain development. This perspective allows us to shed new light on means to integrate ontogenetic data from other vocal learning species, and offers means to reframe Darwin’s “Musical Protolanguage” hypothesis for the evolution of language in contemporary terms.

Two-way causation in human mind biological organization

XIMENA GONZALEZ-GRANDON* (Universidad Nacional Autónoma de México, Mexico)

The claim made in this abstract is that there is no current theory of human mind organisation when neural correlates are involved. Traditional theories deny the multi-level nature of biological interactions, with lower level molecular processes just as dependent on higher-level organisation and processes and viceversa when an agent is imagining, thinking or reasoning. I think one of the errors of classical cognitive sciences and philosophy of mind was to assume far too readily that causation is one-way. As Chalmers (2000:31) say, “A neural correlate of consciousness (NCC) is a minimal neural representational system N such that representation of a content in N is sufficient, under conditions C, for representation of that content in consciousness”. In this definition the causal-explanatory relationship is one-way, from internal neural events to conscious experience. I propose a two-way account using the tools of dynamical systems theory based on two enactive propositions: (1) that between neural events and mental activity are reciprocal (two-way) relationships, where relations co-emerge and co-specify because the functional components of the system are inseparable from the relations (the organi-

zation) they take part in, so they are defined by their relational and emergent ones (Bich, 2012, 2013; Longo y Montevil, 2013). And (2) that the mental processes cut across brain–body–world demarcations, rather than being neural events or correlates (Thompson y Varela, 2001, González, 2014; Peruzzi, 2013). According to this, a single descriptive modality express the inadequacy of a one-way causation model, and shows the necessity to move to explanatory models which accounts for both the concept of emergence and how the system is organized in different organization levels and the reciprocity relationship between them.

DS 1540

17:30 – 19:00

INDIVIDUAL PAPERS

ANIMAL SENSING, NEURONAL PLASTICITY AND IMAGINATION IN PRACTICE

Kin selection, multi-level selection, and the truth: Why kin selection may be the better account of the evolution of cooperation despite (sometimes) being false

ARMIN SCHULZ (University of Kansas, United States)

A number of prominent evolutionary biologists have recently argued that, while not strictly speaking wrong, accounting for the evolution of a trait such as social cooperation in terms of multi-level selection (MLS) theory is predictively and explanatorily useless, and might even engender confusions (West et al., 2007, 2008). Instead, they propose appealing to kin selection (KS) theory. In response, defenders of MLS theory note that, while MLS theory and KS theory may indeed often be formally equivalent, it is still true that, in some contexts, only the former gives a correct account of the evolution of social cooperation (Okasha, 2006; Sober & Wilson, 1998; Wilson, 2008). What I want to argue in this paper is that all sides of this dispute may be right in their own ways. In particular, I want to show that it may sometimes be true that (a) only MLS theory gives a completely true account of the evolution of social cooperation, but also that (b) for pragmatic reasons, KS theory remains explanatorily and predictively favored nonetheless.

Early nervous systems and animal sensing

FRED KEIJZER (Rijksuniversiteit Groningen, Netherlands)

Nervous systems are standardly thought to operate as input-output devices that transmit information received by sensors, process it in some way and use the result to regulate effectors. A recent alternative proposal, the Skin Brain Thesis (SBT), challenges this idea for early nervous system organization (Keijzer et al., 2013). The SBT stresses the key role of nervous systems and their epithelial precursors in solving coordination problems faced by multicellular animals that first developed motility through by muscle contraction: Nervous systems arose as a source and coordinator of patterned activity across extensive areas of contractile tissue in a way that was only loosely constrained by sensor activity. However, instead of neglecting sensory aspects, the SBT brings into focus several important issues for the origins of animal sensing. (a) The transition from cell-based

sensitivity to the origins of useful multicellular sensor arrays, in particular given the soft-bodied nature of early metazoans. (b) The transition from a multicellular clusters of cells to integrated animal bodies that can specifically react to extended surface structures. (c) The relevance of self-initiated activity as a prerequisite for animal sensing (e.g. Hurley, 2001; O'Regan & Noë, 2001). (d) The integration of the various sensory modalities into a common framework. In this talk, I will discuss how the SBT bears on these issues and opens up new theoretical options for understanding animal sensing.

Neuronal plasticity, language and free will

BERNARD FELTZ (Université catholique de Louvain, Belgium)

Recent works in neurosciences show that connections between neurons in the brain are marked by a great plasticity. I would like to analyze philosophical consequences of such a phenomenon. I would like first to refer to the works of Eric Kandel and Gerald Edelman to describe different modes of neuronal plasticity. Working on the question of language learning, I afterwards would like to show that specific language logic in relation with the brain conducts to a new conception of a downward influence which can be different from downward causation. Language epiphenomenalism as Wegner's can be avoid.

INDIVIDUAL PAPERS

FROM CELL THEORY TO COMPLEX SYSTEMS: ON METAPHORS AND MECHANISMS

On the relationship between metaphors and mechanistic explanations: Informational concepts in molecular biology

TOMOKO ISHIDA (Keio University, Japan)

Today, there are various informational concepts within the life sciences. In the early days of molecular biology, scientists started to use these concepts intensively. The concept of genetic information had been formed since then and was established once the gene expression mechanism had been clarified. Many biologists and philosophers have discussed the concept of genetic information. Some people consider the concept indispensable, whereas others do not. Sahotra Sarkar is in the latter camp. He characterizes explanations of molecular biology as being mechanistic and argues that informational concepts are not theoretical. According to him, informational concepts are misleading metaphors. At first glance, his argument seems to be plausible. In reductionist explanations of molecular biology, physico-chemical terms are exclusively used as explanantia. Therefore, the role of informational concepts (if any) are educational or heuristic at best. Despite Sarkar's arguments, informational concepts have not disappeared from the life sciences. In fact, new informational concepts like intercellular communication and crosstalk between proteins have been introduced. In this paper, I will reconsider the role of informational concepts as metaphors. I will then clarify the relationship between these metaphors and the mechanistic explanations found in molecular biology.

DS M220

17:30–19:00

Evo-devo mechanisms revisited: A process account

JAN BAEDKE (Ruhr-Universität Bochum, Germany); **FABRIZIO GUERRERO MC MANUS** (Universidad Nacional Autónoma de México, Mexico)

This paper addresses the explanatory and conceptual framework of the mechanistic science of evolutionary developmental biology (evo-devo) which investigates how environmental cues can induce morphological novelties, how developmental mechanisms bias and constrain evolutionary trajectories, and how biological systems generate heritable, adaptive phenotypic variation and thus evolve in evolution. We argue that what recently has been described as genuine explanations in evo-devo – Brett Calcott's so-called lineage explanations – are, if at all, simple developmental explanations. In contrast, evo-devoists, in fact, explain by interrelating two kinds of models: mechanistic models describing relations on a developmental time scale with models tracing homologies and taxonomic distribution of species' traits on an evolutionary time scale. This integration is guided by a theoretical framework which defines the explanatory and methodological standards for both kinds of models. In particular, it provides a special process view of mechanisms which differs significantly from how the new mechanistic philosophy conceptualizes mechanisms. This view guides investigations on the origin and change of levels of organization (i.e. evolvability and evolutionary novelty). Thus, explanatory integration in evo-devo does not occur in a loosely defined "trading zone", as Rasmus Grønfeldt Winther has argued, but within a conceptually and methodologically firm framework. Studies on gene regulatory networks and homology will be reviewed to support these findings.

INDIVIDUAL PAPERS

MODELING, RACE AND CONCEPTION: BIOLOGICAL AND MEDICAL PERSPECTIVES

Concrete biological models and distributed modeling

PIERRE-LUC GERMAIN (Istituto Europeo di Oncologia, Italy)

This contribution examines the nature and functioning of concrete biological models, by which I mean, roughly put, biological systems such as a mouse or tissue culture used to learn about another system. Using examples both from fundamental research and applied biomedical research, I highlight the difficulties in distinguishing modeling from experimentation, and show that, against a dyadic view of modeling, concrete biological models generally do not relate to their target in autonomous ways, but that links between models most often reinforce the models' relationships to their respective targets. This interdependency of models suggests a distributed understanding of modeling spread through a network of concrete systems and practices. I argue that distributed modeling differs in important respects from multiple-model idealization or classical triangulation. Such a form of modeling prompts some questions regarding the nature of models, and more specifically raises to the fore the problem of model individuation, i.e. identifying the boundaries of a model, what is part of it and what is not. I explore two positions on this issue, each related to different research agenda.

DS M240

17:30–19:00

The risks of using, or not using, race concepts in medicine

SEAN VALLES (Michigan State University, United States)

This presentation analyzes the debates over the proper role of race concepts in medicine, placing them into the context of the growing literature on science and values, including inductive risk. There has been a two-pronged debate over the appropriate roles of race and ethnicity concepts in medicine: 1) scholars dispute whether the risks of using race concepts in medicine (e.g. promoting prejudice) disqualify it from use in medical research or practice (Cho, 2006; Graves, 2005). Simultaneously, there is a related debate over whether medical research and practice share an obligation to apply race categories, in spite of their weaknesses, as part of a commitment to equitably attending to the needs of minority populations (Geller, 2011; Cohn, 2006). The debate is thus complicated by the fact that substantial risks and benefits are attached to both using and not using race concepts in medicine. This paper illuminates those debates using the literature on inductive risk (Douglas, 2000) and later expansions of the concept beyond the risks of errors in hypothesis acceptance/rejection to “epistemic risks” due to other aspects of scientific practice (Kukla, 2014; Biddle, forthcoming). This literature, a branch of the philosophy of science literature on values in science, provides a more precise language and structure to the debates over the risks of using race in medicine, illustrating the various roles played by value judgments. Conversely, the race in medicine case illuminates this theoretical framework by exploring how well the framework can account for methodological epistemic risks that take the particular form of choosing which scientific categories to apply in research.

Between natural conception and reproductive medicine

MAYA FISHER (Tel Aviv University, Israel)

This paper examines, using observations and interviews, the meaning of “natural” as perceived by physicians within their daily work at In Vitro Fertilization (IVF) clinics. IVF physicians perceive the concept natural as a non-intervening process similar perhaps to the way J.S Mill sees it: “all the powers existing in either the outer or the inner world... without the voluntary and intentional agency, of man.” (1904). Yet, I found that their relation to nature varies: some see their medical duty to fix/assist nature, some to fight it and others state that IVF tries to imitate nature. One physician said that inquiring about nature is out of place at an IVF clinic. Furthermore, physicians do not see nature as a moral guide, as one stated: “you know, to make nature noble, to make it good, for man is not always right. I mean, nature can be very cruel to humans.” I will show that these relations towards nature and the “natural” affect their decision making at the IVF units; still Nature is not their main concern rather the success of the treatment is. In their opinion medicine always intervenes and interferes with nature – from treating the sick to getting a woman pregnant. As far as they are concerned once a woman enters the clinic, she is out of the natural setting. I show that physicians perceive “natural” in physiological terms, and they regard their work as avoiding doing harm to the patient, and either assisting or “fixing” nature.

DS M320

17:30 – 19:00

ORGANIZED SESSION / STANDARD TALKS

INDUSTRIALIZING REPRODUCTION

Organizer(s): **JESSE OLSZYNKO-GRYN** (University of Cambridge, United Kingdom)

This panel will explore the biomedical industries and commercial markets of human and animal reproduction in postwar America and Britain. By focusing on the relationships between key service industries, technologies and fields of biological knowledge, the panel will chart the establishment, stabilisation and maintenance of new markets for sperm cryopreservation, pregnancy testing, and infertility treatment as they emerged especially in the latter half the 20th century. Building on the sociological approach launched by Adele Clarke's *Disciplining Reproduction* (1998) as well as recent calls by David Edgerton, Jean-Paul Gaudillière and others to follow the money and take seriously the business of science, technology and medicine, the panel will reexamine a crucial period in the making of a distinctively reproductive biomedical industry and interrogate divergences between American and British trajectories. Beyond reproduction, it will also reflect on the more general themes of refrigeration, home diagnostics and the biology of aging.

Cold collaborations: Sperm cryopreservation and refrigeration in the lab, farm, and clinic (1938-1968)

BRIDGET GURTLER (Princeton University, United States)

This paper examines the scientific networks that were integral to the development of the first widely used cryoprotectant substances and refrigeration methods in reproductive medicine. It will investigate how technical problems of cell rupture, death, and storage were solved not only across the human and animal sciences but also across national and industrial divides. Focusing on three key laboratories—the National Institute for Medical Research Laboratory in London, The Rock Reproductive Clinic at Harvard Medical School, and the experimental laboratory of the Linde Division of Union Carbide Company—the paper will show how actors in clinical medicine, experimental biology, and the industrial gas industry cooperated to freeze and store human and animal sperm. Tracing how the initial cryopreservation materials (glycerol, human breast milk, and egg yolk) were tested and attained and how industrial Cold War politics facilitated the transition from dry-ice to liquid nitrogen vapor as cryogenic liquids this paper will reveal that the birth of modern sperm banking (both human and agricultural) could not have emerged without a unique collaboration of resources, knowledge, and personnel across these varied fields.

“As simple as buying a lipstick”? The market for pregnancy testing in Britain (1965-1988)

JESSE OLSZYNKO-GRYN (University of Cambridge, United Kingdom)

Rivalled perhaps only by the thermometer, today's home pregnancy tests are extraordinarily successful retail products. Technologies of fetal testing and imaging have become embroiled in public debates over abortion and designer babies and so attracted much scholarly attention. Yet, although pregnancy tests have transformed

the experience of pregnancy as much as ultrasound or amniocentesis, little is known of their history. Seemingly innocuous devices, pregnancy tests allow us to explore new aspects of big stories in biomedicine, reproduction, and consumerism. In this paper I will examine the transition of pregnancy testing from a commercial laboratory service in the 1960s to a retail product in the 1970s and 1980s. By examining how the British market was cultivated first by Organon's Predictor, Britain's first home pregnancy test, and then by Unipath's Clearblue, the most successful such product to date, I will recover the shifting balance of power over early pregnancy knowledge from doctors and laboratories to pharmacists and consumers.

Buying time: The infertility industry and the biology of reproductive aging (1978-2000)

JENNA HEALEY (Yale University, United States)

When in vitro fertilization (IVF) was first introduced into clinical practice in 1978, patient demand overwhelmed the handful of clinics experimenting with the procedure. In response, clinics enforced strict age limits in order to optimize patient outcomes and shorten waiting lists. Physicians justified these age limits by pointing to clinical observations about the decline of human fertility with age. Potential patients challenged these restrictions, however, even lying about their age in order to gain access. By the end of the 1980s patient pressure, along with the proliferation of the number of clinics offering infertility service, resulted in the extension or elimination of age limits for IVF. In turn, this expansion of the patient population provided physicians with an unprecedented opportunity to study the relationship between aging and fertility. This paper examines the interplay between the emergence of the infertility industry during the 1980s and the development of biological knowledge about aging, fertility, and the human reproductive system. I argue that the expansion of the commercial IVF industry, especially in the United States, provided physicians with both a patient population suitable for studying reproductive aging and the technical means to do so. Technologies such as embryo cryopreservation, human embryo transfer, and oocyte donation allowed researchers to learn more about the mechanisms of reproductive aging than ever before. Although these technologies were not originally developed to combat reproductive aging, the combination of patient demand and the potential for profit led to experimentation within the unregulated industry. By the early 1990s, oocyte donation was being used with success in women up to 50 years old, sparking a debate about the ethics of using reproductive technologies to extend reproductive life.

DS M460

17:30 - 19:00

ORGANIZED SESSION / STANDARD TALKS

PRACTICAL APPROACHES TO INTEGRATING PHILOSOPHY AND ECOLOGICAL RESEARCH

Organizer(s): **GILLIAN CROZIER** (Laurentian University, Canada)

Ecology is branch of biology devoted to the relationships among organisms in the wild, and between organisms and their environments. Ecological scientists work in universities, governments, non-profit organizations, and in industry, and they study a broad range of topics, including the population dynamics of nonhuman organisms, including endangered species; the impact of industrial pollutants on wild populations; and the evolution and dispersal of wildlife diseases, including diseases that are transmissible to humans. Historically, ecological researchers have held considerable scepticism, if not downright animosity, towards ethics because of antagonistic interactions biologists have experienced with animal rights and welfare activist. Indeed, at least historically, ecological researchers have tended to be particularly illiterate regarding ethics since students with ethical concerns about use of animals are often steered to other fields. The need, however, for ethical examinations of ecological research is especially acute since practicing ecologists are at the forefront of important interfaces between humans and nonhuman organisms and natural systems, and ecological research almost inevitably requires manipulation of the ecosystem being studied: sometimes the impact is minimal, but often it is not. This organized session focuses on three distinct approaches to closing this gap between ethics and ecological research. First, evolutionary ecologist **DR. Albrecht Schulte-Hostedde** discusses practical steps he and his colleagues have taken to integrate ecology and philosophical ethics through the activities of a burgeoning interdisciplinary research centre, the Centre for Evolutionary Ecology and Ecology and Ethical Conservation (CEECEC). Second, philosopher of the life sciences **DR. G.K.D. Crozier** presents a decision-theoretic model for identifying the ethical values of practicing ecologists and integrating the results into ethics education modules for graduate students in ecology. Finally, philosopher of physics **DR. Dylan Gault** presents a more theoretical paper exploring how lessons from physics and astronomy can inform ethical decision-making in ecological research.

Integrating ecology and philosophy in an interdisciplinary research centre

ALBRECHT SCHULTE-HOSTEDDE (Laurentian University, Canada)

In 2013, an interdisciplinary (ecology and philosophy) research centre was founded at Laurentian University, in Sudbury, Canada – the Centre for Evolutionary Ecology and Ethical Conservation (CEECEC, pronounced “seek”). This presentation highlights the centre’s objectives and gives a sense of what to expect from it in the near future. Due to the escalating urgency of research regarding the effects of environmental factors such as pollution, climate change, and water management on ecological systems, ecological researchers are under increasing pressure to refine and innovate their methodologies, to adjust the communication of results with policy makers, and to shift the focus of their research. External pressures on researchers due to partisan politics, for example, has become a pressing issue in Canada, where there has been considerable recent controversy concerning the relationship between the Federal Government, the ecological research community, and

conservationists. While it is being increasingly recognized that evolutionary ecologists have a significant role to play in mitigating the loss of biodiversity, support is also growing for the claim that some of the most important challenges presented by applied evolutionary ecology and conservation rest crucially on philosophical and conceptual questions: questions including what values are at stake in environmental ethics, what is meant by “biodiversity,” how are environmental problems formulated, how are ecological models tested, and what is meant by the “extinction” of species and what is its significance for both humans and nonhumans. Additionally, the ethical dimensions of ecological research as a profession have profound implications for the practice of ecology, and therefore for the development and dissemination of knowledge in the domains of evolutionary ecology and conservation. CEEEC’s goal is to add clarity on these issues by promoting interdisciplinary cooperation among researchers on conservation and environmental issues, and by integrating philosophical and evolutionary ecological perspectives in the conservation of biodiversity.

Using decision theoretic software to integrate ethics into the training of ecological researchers

GILLIAN CROZIER (Laurentian University, Canada)

This presentation discusses an ongoing project to initiate an ethics strategy for ecological research to increase the ethical consistency and epistemic soundness of the field. Specifically, we describe a procedure by which ecological researchers can to collectively and iteratively evaluate the ethical dimensions of their research. This procedure will, in turn, provide a solid foundation for the development of practical tools to improve the ethics of ecological research, including an ethics code for professional research ecologists and ethics training for ecology graduate students. More specifically, the decision theoretic software 1000Minds – developed by New Zealand economist and collaborator Dr. Paul Hansen – is used to survey Canadian ecological researchers to determine how they prioritize various ethical factors that are salient to their research, such as the impact of particular field studies on local ecosystems and human communities. 1000Minds offers a ready-made online survey program that is well suited to the task of helping ecological researchers to collectively rank a broad range of alternative scenarios stemming from value-laden decisions. This survey is distributed to the membership of the Canadian Society for Ecology and Evolution (CSEE) – Canada’s main professional organization for ecologists. Through an adaptive series of questions that ask respondents to prioritize certain hypothetical ecological field studies over others, the software produces a weighted list of values, indicating how heavily ecologists, collectively, would prioritize various types of field studies. To validate this finding, a small group of ecologists are brought together at the annual meeting of the CSEE to discuss and analyse the relative weight they believe should be given to hypothetical field studies with a range of characteristics. The result are compared with the product of the 1000Minds survey, validating the survey’s findings regarding how Canadian ecologists weigh a variety of ethical priorities regarding their research.

Uncertainty and ethical decision making in ecological research: Lessons from the physical sciences

DYLAN GAULT (Laurentian University, Canada)

Cost benefit analysis done to consider the licensing of a particular course of ecological research should consider two dimensions of the potential strength of the outcomes of that research: the potential accuracy/specificity of the results taken in themselves and the potential accuracy/specificity of the results when combined with other investigations. This dual consideration is particularly important for ecological research as considering only the accuracy/specificity of individual research projects may unnecessarily favour ecological intervention. Compared to research methods that highly interfere with their subject of study, indirect research methods often produce less accurate/specific results. Because of this difference, it is tempting to see methodologies with direct intervention as a necessary component of ecological research. However, physics and astronomy has done very well without access to methods that directly interfere with many of their subjects of study. A recent example is the work on cosmology to establish the presence of a non-zero cosmological constant; here teams of researchers in independent projects produced restrictions on the possible parameter space of cosmological theory in order to come to very specific and well supported conclusions about what would otherwise be surprising and controversial results. Extending this methodology to ecological research is not without challenge; issues of the unification of ecological claims and theory, issues of the extent to which ecologies present unique objects, and issues of important differences between the physics, biology, and ecological research must be addressed. However, just as physical realities keep astronomers from interfering with their subjects, ethical demands may keep ecological researchers from interfering with their subjects, at least as much as possible. If this is the case, and there is good reason to believe that it is, then carefully considering the possibility of indirect methods to produce valuable research is an ethical imperative.

DS R510

17:30 – 19:00

ORGANIZED SESSION / STANDARD TALKS

RISK PERCEPTION: ISSUES IN PUBLIC HEALTH AND MEDICAL PRACTICE

Organizer(s): **ANNICK OPINEL** (Institut Pasteur, France)

In this session, we will analyse risk perception. We will address several issues linked to risk perception in terms of public health: is risk perception a matter of individuals, of gender, of genetics? In what way social determinants impact this perception? Wouldn’t a broader focus on higher-level social phenomena instead of individual risk factors be more relevant in such a perception analysis? How, in the case of vaccination, real or suspected adverse effects after immunisation modify disease risk perception in general population and therefore health policies?

Risk perception and the individualization social determinants of health

JONATHAN KAPLAN (Oregon State University, United States)

Many researchers argue that, at least in developed countries, the social determinants of health have a greater impact on health outcomes (longevity, morbidity) than do many other risk factors, including variations in the medical systems. Nevertheless, while relatively small associations between genes and particular health outcomes (say) or the availability of a particular treatment option and health outcomes are considered newsworthy, even relatively large differences in the social determinants of health are routinely ignored. The search for genes that might explain some part of the association between relatively poor health outcomes and being “Black” in the U.S. exemplifies this pattern. Part of the reason for this may be that individual risk factors, whether they are under the control of the individuals or not, are easily understood, and fit into our standard narratives about health, well-being, and risks. Broader risk factors associated with higher-level phenomenon, on the other hand, do not fit into our narratives of risks, and are therefore harder for people to take seriously. Attempts to understand the causal pathways by which the social determinants of health have their effects may help by showing how these risks can be understood as impacting on individuals, but the danger is that by doing this, social harms may be reinterpreted as individual harms that can (or should) be responded to by modifying individuals’ risk factors. So, for example, if one way that economic inequality impacts health is through the stresses associated with relative scarcity and deprivation, individual interventions designed to target the stress might be recommended. These would be unlikely to have much of an impact on population-level health outcomes, but fit much better within a system that addresses individual risks. It is therefore important that we resist the individualization of the social determinants of health, and keep the focus on the higher-level social phenomena.

Suspected adverse events after immunisation, subsequent public health policy process and risk perception : The case of hepatitis B in France and MMR in UK (1998-2010)

ANNICK OPINEL (Institut Pasteur, France); **HELEN BEDFORD** (University College London, United Kingdom)

This paper focuses on the development of public health policy following public concerns over suspected adverse events associated with immunisation. Using the examples of hepatitis B vaccine in France and combined measles, mumps and rubella (MMR) vaccine in UK (1998-2010), we compare two events occurring in 1998. In France following several case reports that hepatitis B vaccination may be linked to new cases or relapse of multiple sclerosis (MS), the French Ministry of Health temporarily suspended the school-based adolescent hepatitis B vaccine programme. In UK following publication of a now discredited article in a medical journal which was interpreted as showing a link between MMR vaccine and the development of autism and bowel disorders (Wakefield et al, 1998), the vaccine continued to be offered as part of the routine programme. In comparing the French and British approach to these potential threats to the immunisation programmes we highlight on the one hand how national behaviours differ and the link between public health decision-making and, on the other hand, differences in national risks perception.

“The Future of Humanity”: A critical analysis of gender, risk, and the human microbiome

JESSICA HOUF (University of Utah, United States)

The discourses of science and medicine are powerful, and their influence on what it means to be a woman or a man or something more are seemingly inescapable. This presentation concerns itself with how the body is gendered through science and medicine, and how this gendering functions to constitute bodies and gendered medical practices. Feminist science studies scholars, such as Evelyn Fox Keller, have argued for the recognition of science as a construction project and urged researchers to explore scientific moments of transition to unravel the linkages between humans, nature, and life. This study is a critical analysis of the formation of gender as it is unfolding within human microbiome discourse; specifically, I focus on two gendered discourses of risk coalescing around pregnancy, male circumcision and the human microbiome. I argue that gender’s function within human microbiome discourse is to inscribe very different relations with microbes for men and women, it is not simply a case of finding differing microbiomes. Overall, by tracing this process of scientific construction it allows humanities scholars to intervene in this world making endeavor, which is a difficult task that scientists and physicians must face.

DS R515

17:30 - 19:00

ORGANIZED SESSION / STANDARD TALKS

RETHINKING PHILOSOPHY OF BIOLOGY BEFORE BIOLOGY

Organizer(s): **CHARLES WOLFE** (Universiteit Gent, Belgium)

Biology as a science of the functioning and development of living bodies emerged in the early 19th-century, integrating methodological or empirical advances in various disciplines 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, Bichat, Lamarck, Treviranus) testifies to this epistemic emergence (McLaughlin 2002) of the constitution of a unified framework for investigations of vital phenomena. Philosophy of biology in turn is a fairly recent discipline, developing from the post-positivist tradition in 1960s philosophy of science, with core issues in evolutionary and molecular biology that are also relevant for metaphysics and theoretical biology, e.g. molecular reductionism, adaptationism, units of selection, genetic information. It tends to exclude historical concerns, even though the founders (Ruse, Grene, Hull) devoted real work to the history of biology (Gayon 2009 on philosophy of biology’s gradual self-definition as a discipline). However, philosophers did not wait for the 1960s to address the fact and the nature of life: Aristotle’s telos, Descartes’s animal-machine, Kant’s teleological judgement immediately come to the mind of any contemporary philosopher. More precisely, 18th-century philosophers interested by empirical findings concerning vital phenomena shared the concerns of naturalists with newly observed problem-cases: regeneration of polyps (Diderot on Trembley), chicken embryogenesis (Bonnet reviving Leibnizian preformism), Galvanism, Mesmerism, Kant on

Simmering's theories of nervous diseases. Metaphysical issues such as organization, vital forces or the creativity of nature thus became prominent (Cheung 2000, Wolfe Normandin 2013). This interplay between philosophy and natural science accompanied biology's constitution as a science, forming a configuration we call Philosophy of Biology Before Biology, which, we argue, is relevant to current philosophy of biology, e.g. chemistry-biology relations, the status of development and the ontological nature of biological organization.

Biology and its conceptual foundations: From the distribution of vital functions to transformism

ANDREA GAMBAROTTO (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

The term "biology" has traditionally been traced back to Lamarck and Treviranus in 1802. But if much has been said on Lamarck, almost nothing exists on Treviranus' pioneering attempt at a unified science of life. Interestingly, only twelve years after Kant's prophesized impossibility of a "Newton of the grass blade" Treviranus published the first volume of his *Biologie, oder Philosophie der lebenden Natur für Naturforscher und Ärzte* (1802). What happened between 1790 (the third Critique), and 1802, when Treviranus uses "biology" to describe a scientific treatment of living nature as a whole? A shift in the semantics of organization, from a regulative to a constitutive understanding of natural teleology: biology as a science became possible only once organization was considered as constitutive of living bodies, and as such, requiring scientific explanation. Lamarck also employed "biology" in 1802, in his *Considérations sur l'organisation des corps vivants*. Using a new concept is not a mere philological phenomenon: Lamarck defines biology in contrast to mechanist-materialist methodology, refusing to apply physical and chemical categories to living nature. He thereby expressed the need to define a specifically "biological" field of investigation and started elaborating its theoretical foundation, whose core, it has been claimed, was the laws of evolution (Barsanti 1979). Examining the *Biologie* seems to support this claim (the foundation of biology as autonomous science coincides with the formulation of the first evolutionary research program). However, I stress that this biological research program was the result of an inquiry into the distribution of vital functions in the animal kingdom. Treviranus' *Biologie* allows us to reassess the relationship between German vitalism and Naturphilosophie, as it emphasizes how each contributed to the nineteenth-century formulation of the idea of a general biology, as a result of investigating the self-regulation of nature as all-encompassing organism.

Uncovering the laws of vital organization with chemistry? The case of nutrition in the 19th century

CÉCILIA BOGNON (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

This paper addresses the question of the definition of life and the demarcation between living and non-living through the study of the emergence of organic chemistry. This question is twofold : 1) By the time biology and organic chemistry emerged as separate disciplines, how was the difference between the living and the non-living conceptualized? And to what extent did the results obtained by chemical analysis affect the popular hypothesis of a specific organic matter responsible for the vital phenomena displayed by living beings? 2) In this context, how can one explain the emergence of vital organization out of brute matter and purely physico-chemical processes? To address these issues, rather than focusing on organisms as goal-oriented wholes, this paper will focus on the physico-chemical processes that are responsible for biological organization. This allows to raise questions that have been relatively overlooked: first about the nature of this organization and its types (i.e. how to characterize plants, animals etc.), second about the reasons of this organization, and then about its effects (i.e. to what extent is it responsible for the vital phenomena of interest?). To do so, I will focus on the case-study of nutrition and investigate the conceptual basis of the relationship between nutrition and biological organization in the 19th century. Nutrition will be considered as both an organic synthesis and an organizing synthesis (acting in morphogenesis and conservation) playing a major role in the scenarios of abiogenesis (e.g. in Buffon and Lamarck). I show that nutrition proved fundamental in the distinction between the living and the non-living and contributed to a major shift in focus in the biological sciences from the study of organic matter to the study of the processes of organization

Philosophy of ecology long before ecology: Kant's idea of an organized system of organized beings

GEORG TOEPFER (Zentrum für Literatur- und Kulturforschung Berlin, Germany)

As a distinct biological subdiscipline, ecology did not emerge before the beginning of the twentieth century. But its underlying conceptual framework was developed long before. Important organizing ideas emerged within the physicotheological tradition of the eighteenth century, for example, with Carl Linnaeus' concept of an "economy of nature" or the related idea of an interconnecting "nexus" between the organisms of different species. In the last years of his life, Immanuel Kant elaborated on these ideas and provided concise formulations and conceptual models for them. Kant's underlying idea was to apply his concept of a "natural purpose" (originally introduced by him for the analysis of living beings) to the interaction of organisms of different species, thus arriving at the idea of a second order organization of nature, the "organizing of systems of organized bodies" as he termed it. My contribution will analyze Kant's for the most part completely neglected proto-ecological ideas in their historical context and their reception in German idealist philosophy and early biology of the nineteenth century.

DS R520

17:30 – 19:00

INDIVIDUAL PAPERS

PERSPECTIVES ON THE ENVIRONMENT: POLITICS, ECONOMICS AND PHILOSOPHY**Environment, ethics and politics: The planetary oligarchic caste and its instrumental use of the sustainable development model****DONATO BERGANDI** (Muséum national d'Histoire naturelle, France)

Sustainable development is rooted in the history of two divergent movements – for the preservation of nature, and for the conservation of natural resources – and of their relationship with the natural sciences. Ecology has played a central role in this history. As a societal paradigm that is at once ecological, political, and economic, sustainable development is supposed to embody ideal policy for all societies, and to overcome the opposition between these two diverging views of man nature relationships. An analysis of international texts devoted to sustainable development emphasizes certain fundamental, interdependent principles: true democracy, social sustainability, and respect for the resilience of ecological systems. Despite formal concessions to preservationists with the recognition of the intrinsic value of biodiversity, the sustainable development concept is clearly anthropocentric, and is in direct line of descent from conservationism. As its fundamental principles are not implemented in an integrated way, its ritual evocation fail to hide strong ethical and political contradictions, rendering it merely an impotent utopia. Besides, environmental public policies are suffering the harmful effects of a tacit agreement between political and economical elites. Heedless of philosophical-political references, an international politico-economical oligarchic caste is largely united around dealing with environmental issues based on the sustainable development model, which is an expression of a utilitarian, anthropocentric perspective. Moreover, for this model biodiversity is in the main merely a reservoir of natural resources for human use. A dual transition – both ethical and political – is thus urgently needed to preserve the integrity of natural systems and support the development of human societies.

The levels of selection and the instability of individualism in environmental philosophy**JOHN BASL** (Northeastern University, United States)

Environmental ethicists have defended various views about which beings are morally considerable. Those that think welfare requires consciousness think that the scope of moral considerability, at best, includes only sentient beings. Others, with more permissive notions of welfare, argue that there is a perfectly reasonable sense in which non-sentient organisms such as plants, have a welfare and so are, at least potentially, morally considerable. However, there has emerged a near consensus that Individualism is true; that the scope of entities that have a welfare extends, at most, only as far individual organisms but not to groups, collectives or communities. In this paper, I challenge individualism by arguing that it rests on a false view about the levels of selection. Any defense of individualism requires an argument that non-sentient organisms have a welfare, but that non-individuals such as groups or communities do not have a welfare. The standard argument starts from the idea that organisms, but not non-individuals, are teleologically organized, or goal-directed, entities. In virtue of being teleologically organized, the welfare of organisms can be understood, non-arbitrarily, in terms of what

promotes or frustrates the organisms' ends. Individualists rely on an etiological conception of teleology (similar to the etiological account of function) to ground teleology in non-sentient organisms; it is because organisms are subject to natural selection that it is possible to identify them as teleologically organized, to specify their ends in a naturalistic, and non-arbitrary way. It is then argued, or, most often, just assumed, that since an appeal to selection is required to ground the interests of non-sentient entities, that this notion of welfare only applies to organisms. Since selection only acts at the level of the organism, it is only organisms, and not collectives, that can have a welfare. Despite the near consensus, Individualists are mistaken. Individualism carries with it a concomitant commitment to a view about the levels of selection, but no plausible view about the levels of selection can justify Individualism. In this paper I present a trilemma for the Individualist to argue that Individualism is unstable. The Individualist must endorse either reductionism, anti-realism, or multi-level realism about the levels of selection. Reductionism is both implausible and best supports the view that genes but not individuals are units of selection. Anti-realism both fails to recognize individuals as the sole unit of selection, allowing that non-individuals might be units of selection, and fails to ground a conception of welfare that will be at home in an Individualist view. Finally, multi-level realism, perhaps the most plausible view, fails to discriminate against non-individuals. After developing this objection to the stability of Individualist views, I assess their best prospects going forward, arguing that they are forced to accept multi-level realism and hang the case for Individualism on empirical details about how likely non-individuals are to be units of selection.

The most dismal part of the dismal science: The role of environmental economics in conservation planning**CARLOS SANTANA** (University of Pennsylvania, United States)

Environmental economics has yet to find a paradigm which would allow it to be a satisfactory guide to conservation planning and environmental policy-making. Ecological planning requires methods of comparative valuation, which would allow us to make decisions in the face of value tradeoffs. We need to make decisions in the face of not only tradeoffs between environmental and non-environmental values, but also between the competing values of different groups of individuals. I review the extant methods of systematic environmental decision-making and show how none reliably accomplish comparative valuation. The most popular methods of environmental valuation focus on features, like biodiversity or sustainability, which are endogenous to the system in question. But much of the value of environmental systems comes from exogenous sources: the needs and goals of organisms who benefit from the ecosystem's services. This means that endogenous methods are unlikely to reliably capture comparative value. Unfortunately, extant exogenous methods of valuation do little better. Contingent valuation and revealed preference methods both rely on treating environmental values as isomorphic to market values, but research on the psychology of valuation shows that this assumption is false. And without the data from these exogenous methods, game- and decision-theoretic approaches to decision-making can't get off the ground. Given these facts, I explore two possibilities: (1) a reliable environmental economics is impossible, and we'll have to make do with what we've got, and (2) environmental economics will need to involve tools not traditionally used in economics. I briefly sketc

WEDNESDAY JULY 8

DS 1545

09:00 – 10:30

INDIVIDUAL PAPERS

CULTURE, EVOLUTION, AND ECOLOGY

[Attraction is to culture what adaptation is to biology](#)

THOM SCOTT-PHILLIPS (Durham University, United Kingdom)

There is a large and growing literature on the evolution of culture, much inspired by the successes of evolutionary thinking in biology. Many of these successes are due to Darwin's insight that factors external to organisms themselves (i.e. the wider environment) can be used to explain, in a causal way, why organisms themselves, and their component parts, take the forms that they do. In this talk, I will argue that Dan Sperber's idea of cultural attraction can do the same job for culture. That is to say: it can provide a way by which factors independent of culture itself can be used to explain, in a causal way, why cultural phenomena (kinship systems, language structures, supernatural beliefs, etc) take the forms that they do, and not other forms. Cultural Attraction Theory notes that mechanisms of cultural propagation typically modify cultural items, often as part of their proper functioning. For instance, when communicating information to others, we sometimes cut out parts we deem irrelevant, and add others, and in so doing transform the information itself. Other mechanisms of cultural propagation perform similar modifications. Crucially, these modifications are typically not random, but tend to operate in the direction of a better fit with the goals and dispositions of human minds and human behaviour. Consequently, cultural items are often attracted to particular forms, and away from others. This is attraction in its technical sense, taken from dynamical systems theory, and the specific goals and dispositions that are causally involved in any given case are called "factors of attraction". As outlined above, these factors of attraction play a role in cultural change that is functionally equivalent to the role that selection pressures play in biological change. I will illustrate the explanatory potential of Cultural Attraction Theory with examples drawn from language evolution.

[Zen and the science of cultural evolution](#)

COLIN GARVEY (Rensselaer Polytechnic Institute, United States)

Evolutionary treatments of religion have tended to focus exclusively on the horizontal spread of beliefs within contemporaneous populations, using epidemiological models as guides. Whether "viruses of the mind" or the "epidemiology of representations," most approaches not only pathologize religion but fail to account for the repeated assembly of material forms and practices vertically through time. Consequently, evolutionary theorists

have had little to say about Buddhism, a tradition that has been concerned with accurate transmission of the dharma (or teachings) from one generation to the next, master to disciple, for the last 2500 years. Whenever a novice takes the vows to become a Zen Buddhism monk, they receive a family tree (kechimyaku) tracing this lineage, stretching from the historical Buddha, Siddhartha Gautama, to the present day—in my own case, a descent of 83 generations. “Beliefs” play only a peripheral role in this dharma transmission: instruction by a skilled teacher might include being beaten with a stick, but is nevertheless organized to scaffold the student into a state of “freedom from beliefs” in which Reality is perceived directly. Central to this attainment is the practice of seated meditation (zazen), the diligent enactment of which is said to bring about enlightenment (satori) in the adept, thereby reproducing the self-realization experienced by each and every buddha that has come before. The continued existence of Zen Buddhism relies on the replication of this process in each generation—not on the mere presence of populations of “believers.” Thus Zen has developed, through the centuries, a number of methods and techniques to ensure subjective and objective fidelity in dharma transmission, and these should be of great interest to all students of cultural evolution.

Things Don't Fall Apart: Ecological Selection And Functional Explanation In Social Science

ADRIEN BOUTEL (University of Cambridge, United Kingdom)

One reason functional explanation has become less popular in social science is an argument, associated particularly with Jon Elster, that social phenomena lack a feedback mechanism through which effects can promote their own causes. In biology, feedback is provided by natural selection: a traits' beneficial effects help it to recur in later generations. But, Elster argued, social phenomena are not (with a few exceptions) produced by selection. I argue that the picture of selection underlying this argument is too restrictive. The assumption is, in Mark Risjord's words, that natural selection requires differential survival and reproduction among a population of similar organisms. It is true that societies do not compete by producing offspring societies with differing propensities for further success. But selection comes in other forms. Even ecosystems, which do not reproduce at all, appear to produce adaptive features in response to selection. Frédéric Bouchard has concluded that selection requires only some form of differential persistence, of which reproduction is just one type. Bouchard's moral applies to societies as well. If ecosystems can have adaptations, I argue, so can societies. Ecosystems, like societies, are enormously complex systems of manifold components, which are engaged in internal cooperation and competition (and which do not intentionally plan the systems of production and distribution). Like ecosystems, societies persist differentially: some thrive and spread, others shrink or collapse. Societies and ecosystems also become unstable and undergo radical change, without collapsing but with a similar effect on phenomena associated with the old order. These processes can provide the necessary feedback mechanisms to support functional explanations, both of features of society as a whole and of particular social phenomena.

DS M220

09:00 - 10:30

INDIVIDUAL PAPERS

EXPERIMENTATION AND DOCUMENTATIONS

Animal welfare is subjective welfare

HEATHER BROWNING (Australian National University, Australia)

Animal welfare science is primarily concerned with measuring the welfare of animals under different conditions, using behavioural and physiological indicators to map onto the state of welfare as experienced by the animal. This science therefore requires use of a meaningful welfare concept, describing what it is that we're trying to measure - what comprises the state of welfare itself. Most welfare scientists now accept a tripartite welfare concept, under which welfare consists in feeling good (subjective welfare), functioning well (physical welfare) and living naturally (teleological welfare). In this paper, I argue that subjective welfare is the primary state and is thus the only necessary component of a concept of animal welfare. I will also show how the other two proposed components (physical and teleological) can be collapsed onto subjective welfare. These conditions may then form an important part of the conditions required for the realisation of welfare, but do not themselves comprise the state of welfare.

“Because they tell such an amazing story”: Documentary filmmakers' collaborative relationships with biologists

ELEANOR LOUSON (York University, Canada)

David Kirby's *Lab Coats in Hollywood* (2011) examined the understudied role of science consultants in blockbuster film production. Kirby argued that successful relationships between filmmakers and science consultants occur when scientists' contributions are in service to the film's story. I argue that this also applies within the context of wildlife and environmental documentary films; specifically, that filmmakers carefully manage their collaborative relationships with biologists and environmental scientists in order to enhance their films' storytelling. When successful, the cooperative relationships between biologists and wildlife documentarians result in mutual benefits, including better footage of animal behaviour for filmmakers and greater research publicity for biologists. The filmmaker-science consultant relationship faces tension if scientists' commitment to accuracy undermines filmmakers' effective storytelling. My research into the representation of animal behaviour in wildlife films includes qualitative interviews with Canadian documentary filmmakers, investigating their attitudes and experiences surrounding their complex relationships with biologists. My results suggest that documentary filmmakers involve biologists in 3 main roles: as authoritative sources of information about animal behaviour, as providers of access to wild animals and field sites, and as on-screen experts. Each role offers specific challenges to the filmmaker-biologist relationship. Filmmakers rely on biologists' published work and informal advice to contextualize the animal behaviour they capture on film, but their footage is not necessarily consistent with biologists' accounts. They are required to be sensitive to the biologists' highly constrained time in the field, as well as their unfamiliarity with presenting research to non-expert publics on camera, where a commitment to in-depth scientific accuracy or technical jargon may be inappropriate. Filmmakers emphasized that to be useful, a scientist's contribution

must enhance the film's story. However, each understood that collaborating with consulting biologists offered enormous benefits, emphasizing the positive impact of biologists' research for their films' narrative.

The irreducibility of Piaget

JOHN COLLIER (University of KwaZulu-Natal, South Africa)

The concept of instinct was used extensively by ethologists like Lorenz, Tinbergen and Audrey, but it fell into disfavour with the rise of scientific behaviorism. On the behaviorist account animals have certain behaviors that can be conditioned, and all behavior can be understood in terms of the relation between inputs (stimuli) and outputs (responses) under the control of reward and punishment. However, more recently, instinct has come back into favour, especially with anti-behaviorist work on language, like Steven Pinker's *The Language Instinct*, which develops Chomsky's idea that language capacity cannot be reduced to behaviorist terms. Jean Piaget did much of his early work using a variant of the behaviorist model in which he postulated "circular reactions" that could be martialled and combined to produce more complex behaviours. By the late 1960s, however, he had decided that reflex arcs were not enough to explain behavior and learning, so he introduced instincts into his theory (*Biology and Knowledge*). These instincts are characterized by allowing patterns to be recognized and responded to that cannot be described solely in terms of inputs and outputs and their relations. I will explain Piaget's view of instincts and then use ideas from complexity theory and especially the theory of emergent properties to explain how this might be possible. This approach leads to the possibility that organisms can respond to novel inputs that they are neither preconditioned nor innately structured for. I will then briefly explain how this idea can enhance Piaget's biological theories of the origins of intelligence. I will briefly mention the application to evolutionary moral realism.

INDIVIDUAL PAPERS

CAUSALITY, CONSERVATION AND CITIZEN SCIENCE

Selecting among ontologically different causes: Toward an account of the pragmatics of causal selection

BRIAN HANLEY (University of Calgary, Canada)

Most philosophers are concerned with distinguishing causes from non-causes, where it is supposed that there are no principled ways of distinguishing among causes. The lack of principled distinctions is then taken to imply ontological parity of causes. Without ontological distinctions among causes, any selection of a cause as "the" cause of some effect is understood in terms of purely pragmatic considerations. In opposition, Waters (2007) and Woodward (2010) offer conceptual machinery for making principled ontological distinctions among causes framed within Woodward's (2003) interventionist theory of causation. However, Northcott (2009) objects that Waters' (2007) "actual difference makers" are not strictly ontological due to the pragmatics of causal selection.

Northcott claims that the pragmatic selection of effects fixes the causal claim in such a way that the actual difference making cause is determined by this selection, not just by ontology. Of course pragmatics play a role in causal selection, however, Northcott's argument lacks a clear account of the pragmatics involved in causal selection. Furthermore it is not clear that appeals like Northcott's to the pragmatics of causal selection render Waters or Woodward's concepts not purely ontological. Nor is it convincing that dismissing ontological distinctions of causes is philosophically productive. A detailed account of the pragmatics of causal selection is needed in order to shed light on this aspect of causal reasoning. I suggest that a clear account of the pragmatics of causal selection can be developed using the ontological concepts provided by Waters and Woodward. Detailed in this way, causal selection is understood as selecting among ontologically different causes relative to practical and epistemic interests of scientists. Looking at Waters' (2008 & manuscript) analysis of practice in genetics, I explain how focusing on ontological features of causes helps understand the pragmatics of selecting a cause among other relevant causes.

Were there fishes on the Ark? Re-thinking the ark conservation concept at aquaria

CHRIS ZARPENTINE (Wilkes University, United States); **SAMANTHA MUKA** (University of Pennsylvania, United States)

The ark concept in global species conservation holds that ex situ spaces can be used to maintain and breed endangered species for future reintroduction. While zoos espoused this concept to explain the need for programs focused on the breeding of charismatic megafauna throughout the 20th century, such programs face serious practical obstacles and principled objections. In the face of limited successes, many have reevaluated their commitment to this conservation concept. More recently, however, interest in conserving endangered amphibian and reptile species has revived the concept and linked it more closely with aquariums. Still, discussion of the applicability of the ark concept to exclusively aquatic species has been limited. Historically there are important—though often neglected—differences between zoos and aquariums. This makes it particularly important to consider whether there are important differences in the application of the ark concept to aquatic species. This paper seeks to provide a comparative evaluation of the aquatic ark concept. We identify ethical and practical features relevant to the likely success of an ark. Drawing on historical sources, we evaluate how the aquatic ark concept compares to previous attempts to implement the ark concept. We argue that, while an aquatic ark has the potential to be more successful than similar historical programs for terrestrial organisms, serious concerns remain.

DS M240

09:00 – 10:30

Can you help me fold this? Proteins, computer architecture, and citizen science

SHAWN MILLER (University of California, Davis, United States)

Protein folding science relies heavily on computer simulation because proteins are very small, they transform very rapidly, and they take on myriad shapes, all of which make experimentation of the in vivo or in vitro variety largely unworkable. However, the computational power necessary to simulate the manner in which proteins go from two-dimensional amino-acid strings to three-dimensional structures is extraordinary. Dale L. Bodian et al. noted in the 2011 Pacific Symposium on Biocomputing that simulating the protein collagen for 10 nanoseconds “took approximately 11 months using the CPUs of over a quarter of a million computers.” As a result, protein folding scientists have adopted – and in some cases have helped develop – a variety of different kinds of computers, or computer architectures, in search of ever greater processing power. Different computer types impose different limits and constraints on research scientists. Some, e.g., are simply harder to program than others. Specific computer architectures also necessitate particular collaborations between scientists and non-scientists. The constraints imposed, and possibilities afforded, by these collaborations canalize, or channel, science in particular directions. My paper will look at the Folding@Home distributed computing project, which farms out protein folding simulations to volunteers who make their personal computers available for the purpose. Folding@Home volunteers are very often computing enthusiasts, e.g., video gamers, who own relatively powerful personal computers with characteristic architectures. Attracting and retaining these volunteers has required that scientific researchers acknowledge and adopt the non-scientific values of these individuals in ways that sometimes directly conflict with the aim of efficiently using computer power to understand how proteins fold. Additionally, I will show how the computer architectures of the citizen scientists involved have affected both which proteins researchers study and the statistical methods used on the data.

INDIVIDUAL PAPERS

SELF, EUGENICS, AND ESSENTIALISM

From word to practice: Eugenic language in sterilization legislation (1905-1945)

LUKE KERSTEN (Carleton University, Canada); **LAURA DAVIS** (Queen's University, Canada)

Between 1905 and 1945, 31 states in the United States and 2 provinces in Canada enacted sterilization legislation. Over 70 statutes and amendments were enacted to guide, oversee and regulate sterilization practice, while over 16 distinct conditions were given as grounds for sterilization. Although excellent legal, historical, and philosophical scholarship has investigated the motives, causes and consequences of this legislation (Paul, 1995; Lombardo, 2008), little systematic work has been done analyzing the language of sterilization legislation. The present study attempts to fill this gap in the existing literature. Statistical analysis is conducted using multiple linear regression analysis. Several questions are explored: Is there a relationship between the regulatory

procedures outlined in sterilization legislation and the different kinds of eugenic traits described? Is there a relationship between different categories of traits across legislation? Is there a core set of traits that persists in sterilization through time? In answering these questions, we look to add one more piece to the eugenic puzzle. We argue that part of what lies at the heart of eugenic thought and policy in North America at the beginning of the 20th century is a preoccupation with curbing traits seen as explicitly “mental”, and only secondarily those seen as physical and criminal. We further argue that this study provides support for recent theorizing about the role “mental disability” in eugenic history.

The self in scientific psychiatry

SERIFE TEKIN (Daemen College, United States)

Mental disorders disrupt an individual's relationship to herself, her social environment, and her physical environment, and thereby primarily concern the self – the dynamic, complex, relational, multi-aspectual configuration of capacities, processes, states, and traits that support a degree of agential capacity. However, the concept of the self is not included in the scientific investigations of mental disorders. One example of what I call the problem of the missing self in scientific psychiatry is the concept's limited use in the last three editions of the *Diagnostic and Statistical Manual of Mental Disorders* (i.e., DSM-III, DSM-IV, and DSM-5; henceforth DSM-III+), a classification manual of mental disorders created by the American Psychiatric Association (APA) to be used as a guide for scientific research, and various clinical, forensic, and administrative services. The concept of the self was left out because of the conviction that its use will hinder psychiatry's commitment to be scientific, because the self is neither readily observable nor measurable. This paper takes issue with this conviction and argues the concept of the self can be instrumentalized as a scientific target in psychiatry once it is enriched by contemporary cognitive sciences. In addition, once the traditional approach to objectivity as value neutral body of knowledge is replaced with alternative approaches where science is regarded as a social process, and objectivity, as a community's negotiation of different values, it will be clear that the use of concept of the self is not an impediment to scientific psychiatry. In the first part of the paper, using historical and philosophical analysis, I trace the exclusion of the self as a scientific target in the classification of mental disorders in the DSM. I show that in an attempt to move away from the psychoanalytic framework, with the claim that the individual psyche is not a tractable scientific target, operationalism left out important self-related features of mental disorders from the scientific discussions. More specifically, the historical—narrative features of mental disorders and the phenomenology of the encounter with them have been neglected, presenting obstacles to the progress on the scientific inquiry into and clinical treatment of mental disorders. I then point out some work in cognitive sciences that illustrate how the self is scientifically tractable, thereby challenging the assumption made in DSM-III+. Note that my goal in this paper is not to develop a model of the self to be used in scientific psychiatry, nor to offer strategies as to how this model can be incorporated into the DSM, but rather, to deal with the presuppositions that prevented the use of the concept in scientific psychiatry.

DS M280

09:00 – 10:30

Rejecting sex essentialism: Cases from biology**ELEANOR GILMORE-SZOTT** (University of Utah, United States)

This paper discusses the inappropriate application of essentialism to sex as a biological characteristic, and suggests that essentialism is ultimately unsuitable for biology in general. Sex is an intuitive example of Kripke's application of origin essentialism in biology, however biological cases, such as intersex conditions and tetragametic chimerism, pose problems for both kind and individual essentialism. These biological cases demonstrate that sex is a spectrum with regards to genotype and phenotype, thereby making kind membership difficult to define. Additionally, sex is not necessarily fixed throughout the lifespan of an individual and so too individual essentialism fails. The cases discussed in this paper demonstrate that sex is not an essential characteristic, thus we must question if essentialism fails when more broadly applied to the field of biology.

INDIVIDUAL PAPERS

MORALITY, ALTRUISM AND COMMUNICATION BETWEEN GROUPS**The evolution of morality as a cluster of nonmoral capacities and practices****TOMI KOKKONEN** (University of Helsinki, Finland)

This paper takes a look at some of the recent work on the evolution of morality (empirical work on "evolutionary building blocks" of morality in non-human animals, human moral psychology, and connected philosophical literature) and offers a (somewhat revisionist) philosophical analysis of how morality should be understood as a biologically rooted but probably uniquely human phenomenon. The main thesis is that human morality is a cluster of psychological capacities and tendencies, social practices etc., partly connected to culture and language, that cannot be bundled together as one phenomenon from an evolutionary point of view, nor can the constituent parts be understood from the moral point of view only. This has consequences for both empirical and philosophical study of morality. The cluster of capacities relevant for what we perceive "morality" evolved for various social functions. It is argued that there are four major evolutionary steps in the evolution of morality that all change, in part, the function and interaction of these capacities. The first step involves the evolution of basic pro-social tendencies and simple theory of mind. Second step involves comparative perspective to behavior (rudimentary fairness and normativity) and more advanced theory of mind. The third step has to do with reflection and negotiations on norms, which requires full-blown theory of mind and language and marks the beginning of cultural evolution of norms that perhaps may not yet be considered moral. The fourth step is into full-blown morality, which is a biologically rooted cultural evolutionary step. It will be argued that only after the last step we can talk about true morality in a philosopher's sense, but most of what is actually involved in moral practices is strictly speaking non-moral. This is important for scientific understanding of morality as well as for metaethics, but not for normative ethics or moral practices.

Strong altruism and the egalitarian transitions**JOHANNES MARTENS** (University of Bristol, United Kingdom)

In the biological literature, it is common to distinguish between two kinds of evolutionary transitions from lower levels to higher levels of organization, namely fraternal and egalitarian transitions (Queller 1997). In a fraternal transition, a higher level unit evolves through the operation of kin selection, and emerges on the basis of the altruistic cooperation of the lower level entities (like in an ant colony), while in an egalitarian transition, the cooperation of unrelated entities leads to the emergence of a functional whole (e.g. the physiological integration of a host and his symbionts). Though both of these processes have led to evolution of highly integrated entities (like multicellular organisms and endosymbioses), the fact that both of them are referred to as transitions is problematic. Indeed, a transition typically refers to a process during which the fitnesses of the lower level entities (e.g. unicellular entities) are transferred to the higher level (e.g. the multicellular organism), i.e. during which fitnesses of the lower level entities are progressively decoupled from their phenotypes. But this type of transfer can occur only when some form of division of labor evolved among the parts of the newly emerging collective, which, in turn, presupposes the evolution of strong altruism at the lower level. Therefore, the so-called egalitarian transitions should not be viewed as evolutionary transitions at all, since strong altruism can only evolve between related individuals, i.e. members of the same species (Hamilton 1964). Here, however, I show that such a fitness transfer can occur in cases of endosymbioses, thanks to the evolution of some form of multigenerational altruism. To this end, I demonstrate that strong altruism can evolve between members of different species, provided that behaving altruistically toward an unrelated partner increases the probability that the latter acts positively toward the descendants of the altruist.

Communication between groups and collective entities**SHAWN SIMPSON** (City University of New York, United States)

Signaling arises and is maintained at a number of levels of biological life, occurring not only within organisms but also between them. But what about signaling at a "higher" level, at the level of groups and collective entities? People talk about groups engaging communicating all the time, so there's at least some precedent for thinking communication happens at this level. But how should we interpret such talk? Should it be taken literally? Or is there perhaps some better way of understanding this way of speaking - e.g. as metaphor or pragmatic shorthand? In this talk, I answer these questions by using the sender-receiver model of David Lewis and Brian Skyrms. After introducing the model and the general problem, I first show that groups indeed can play the role of the senders and receivers. I then apply the model to a few real-world cases. I finish the talk with a more speculative discussion on how to understand the relation between the sender-receiver model and the world.

DS M340

09:00 – 10:30

INDIVIDUAL PAPERS

THEORIES AND WORLD VIEWS

The Weltanschauung of Ernst Haeckel vs. the worldview of St. George Mivart and the impact of theory on research**GERALD RAU** (National Chung Cheng University, Taiwan)

Darwin has always had detractors who have questioned the ability of natural selection to explain the whole of evolutionary history, particularly the origin of innovative features, skeptical that the explanations that work very well for changes at the tips of evolutionary branches can be extrapolated to the whole. Nevertheless, Darwinism has not so much repelled all challenges as absorbed them, and seems to have gained strength in each encounter. Philosophers and historians of science may be open to the idea that the Modern Synthesis could eventually be transcended, as have many great theories of the past, but biologists as a whole scoff at this idea. Yet a growing number again are saying Darwinism has a fatal flaw. All scientists agree that there must be a non-random element in evolution, but some are now suggesting that the introduction of variation, long considered to be a random genetic event, may be not only non-random but also more important than selection. Scientists in evo-devo, epigenetics, molecular genetics and symbiosis have challenged the primacy of natural selection, some calling for a turn from the Weltanschauung of Ernst Haeckel to the worldview of St. George Mivart or a new Lamarckianism. Yet non-Darwinian explanations are actively opposed by most biologists, limiting both research funding and the exposure of young scientists to these ideas. This raises a serious social question: how well-supported does an idea need to be before we make the general public aware of it? Why are we willing to produce science documentaries discussing string theory, multiverses, the Higgs boson or potential uses of quantum entanglement, but give no attention to the idea that in stressful times different mechanisms might allow rapid, perhaps even teleological, evolution? Why does theory on the one hand spur new research, on the other restrict it?

Is relational essentialism really essentialism?**ANNA VAUGHN** (University of Utah, United States)

Samir Okasha proposes that essential properties may be relational, or extrinsic, instead of intrinsic. This revision purportedly offers a version of essentialism compatible with evolutionary theory. Michael Devitt and Marc Ereshefsky criticize Okasha's extrinsic essentialism, arguing that merely citing relationships as essential properties is insufficient for answering the two primary questions for essentialism in biology: the trait question and the taxon question. Ultimately, Ereshefsky argues that relational essentialism fails to satisfy one of three requirements of essentialism and, therefore, is not an essentialist view. In this paper, I present an argument to the contrary, and conclude that Okasha's relational essentialism should be considered an essentialist view. However, Okasha's relational essentialism again runs into difficulties with evolutionary theory. Because relational essentialism, despite its best efforts, offers nothing beyond what non-essentialist biological theory already offers and is mired in further difficulties with evolutionary theory, I recommend that relational essentialism be abandoned.

Homology, identity, compositionality, and non-transitivity**JOYCE HAVSTAD** (Field Museum of Natural History, United States); **OLIVIER RIEPPEL** (Field Museum of Natural History, United States); **LEANDRO ASSIS** (Universidade Federal de Minas Gerais, Brazil)

Homology is an evolutionary concept that covers those shared, inherited traits which are “the same but different” (Owen 1843) among those biological individuals expressing said traits. The philosophical trick of analyzing the concept of homology is in capturing both these contrasting elements together: that of sameness with difference. The element of sameness within the concept of homology has primarily been understood as an identity relation rather than as a similarity relation (see Minelli & Fusco 2013). But the view of sameness in homology as an identity relation faces both a general problem of seeming incompatibility between identity and difference (for instance, see the puzzle of personal identity) as well as the particular problem of implied but rejected transitivity among certain homologous traits (from Ghiselin 2005). This paper presents a view of homology, the semaphorontic view, which characterizes the element of sameness within homology as a certain kind of non-numerical identity relation. The view uses Hennig's (1947) concept of the semaphoront (traditionally, among stages in the life of an organism) to capture the element of sameness (among states in the evolution of a homologue) as a relation of compositional identity. This way of characterizing the element of sameness in homology, as a compositional identity relation, avoids both the general (incompatibility) and the particular (transitivity) problems mentioned above. In addition to solving the traditional problems, viewing homological sameness as a form of compositional identity allows for the incorporation of difference, the second required element, into the concept of homology (contra Szucsich & Wirkner 2007, among others). Finally, because it is still an identity-based view, this concept of homology avoids the problem of in principle indiscernibility with homoplasy—a problem that alternative (e.g., Rosenberg & Neander 2009) or agnostic (e.g., Currie 2013) views still face.

INDIVIDUAL PAPERS

BIOMARKERS, INDIVIDUALIZED MEDICINE AND ETIOLOGICAL THEORIES

Multi-modal discordance and the ontology of biomarker research**SPENCER HEY** (McGill University, Canada); **BRIANNA BARSANTI-INNES** (McGill University, Canada)

Research in personalized cancer medicine is centered around the discovery and validation of “biomarkers”—testable properties of a patient specimen that can be assayed to prospectively inform a treatment decision. Successful examples of such biomarkers include HER2 overexpression for treating breast cancer and mutated KRAS for metastatic colorectal cancer. Unfortunately, these examples of successful biomarkers are the exceptions. As many commentators have emphasized, biomarker research is currently plagued by disappointment and difficulty. Some of the difficulty can be explained by social factors. For example, in contrast to drug development, there is no central financial actor that stands to benefit from a biomarker's validation, and therefore, there

is often little financial support for rigorous biomarker diagnostic development. Other difficulties are methodological: Biomarker studies are often retrospective studies of convenience, notorious for their poor reporting and quality. However, the basic ontology of biomarker research also generates a novel set of philosophical challenges. In this presentation, we analyze a case-study in biomarker development in order to illuminate these challenges. The excision repair cross complement group 1 (ERCC1) gene is a biomarker hypothesized to predict patient responses to platinum-based therapies for non-small cell lung cancer. Although this marker has been extensively tested, its clinical utility remains uncertain. We argue that this continuing uncertainty is due to a fundamental confusion about what is the biomarker. In particular, there is discordance among the alternative modalities for assaying ERCC1 - that is, whether the marker is tested at the genetic, transcription, or protein level. We take this to show that "ERCC1" does not refer to a single ontological entity. Rather, it refers to a set of entities and processes in a complex causal system. Therefore, contrary to the assumptions of translational researchers, "What is the predictive value of "ERCC1"?" (without further specification) is not a well-formed scientific question.

Evidence and individualized medicine

MEGAN DELEHANTY (University of Calgary, Canada)

Individualized medicine (IM) combines the molecular subtyping of complex diseases with an understanding of how an individual's genomic, transcriptomic, proteomic, and metabolomic profile affect drug response, with the goal of optimizing treatment regimens for each individual. At the core of individualized medicine is the recognition of the extent to which heterogeneity must be accounted for. This is the case not only at the level of individuals displaying the same phenotype, but genotypically identical individuals who may be heterogeneous at other "-omic" levels, as well as cell heterogeneity that is often present within, for instance, a tumour. Each distinct population may show a different pharmacokinetic/pharmacodynamic response to a given drug. The methods used to accommodate this heterogeneity at multiple levels involve complex models and simulations both to identify potentially relevant variants that might be relevant to drug response, as well as to predict the nature of that drug response. In this paper, I will argue that evidential and explanatory bases of IM contribute a strong additional line of argument against the privileging of randomized controlled trials by evidence based medicine (EBM). In particular, IM demonstrates the severity of the problems EBM encounters due to the recognized difficulties with the exportability of results obtained via randomized controlled trials (e.g. Cartwright 2007, 2010; LaCaze 2008, 2009, 2011), as well as providing a case where evidence from models and simulations together with in vitro assays can be expected to produce higher quality evidence.

Re-evaluating concepts of biological function/dysfunction in clinical medicine: How are etiological theories useful?

BENJAMIN CHIN-YEE (University of Toronto, Canada)

Theories of biological function can be categorized into etiological/historical theories, wherein the function is the causal explanation for the existence of the trait in question, or ahistorical theories, wherein the function is the current consequence the trait produces, irrespective of its cause. The existence of numerous understandings of biological function makes it unclear which concepts best apply to clinical medicine. I propose to re-evaluate the concepts of biological function/dysfunction in medicine to determine which might best inform medical discourse, particularly concerning the definition of disease. Objectivist theories of disease, notably Boorse's Biostatistical Theory (BST) and Wakefield's Harmful-Dysfunction (HD) account, base their definitions in biological dysfunction, assuming that biology provides a straightforward concept applicable to medicine. I begin by clarifying the concepts of function employed by BST and HD analysis, according to the "Taxonomy of Functions" proposed by Walsh and Ariew (1996). Both theories use evolutionary notions of function, either ahistorical function (BST) or historical function (HD account). I highlight problems that these concepts pose in medicine, using the example of Sickle Cell Trait (SCT), which challenges the function/dysfunction distinction offered by these objectivist accounts. The pathological status of SCT is contentious and raises complex ethical issues. The case of SCT also shows how etiological theories may offer a useful heuristic for understanding illness, but alone are insufficient for defining disease. The concept of "Relational Function" proposed by Walsh (1996), which recognizes function as a contextual property, offers a more pluralistic account of function for medicine, which captures useful aspects of both historical and ahistorical function. Relational Function better handles the case of SCT and captures the pertinent medical considerations at issue. Furthermore, this contextual concept of function may be better suited to contemporary medicine, which increasingly considers the roles of physical and social environments in shaping disease.

DS M460

09:00 – 10:30

INDIVIDUAL PAPERS

THEORY AND PRACTICE AND “CHANCE AND NECESSITY” IN BIOLOGY

“Emerging concept” in developmental biology**YOSHINARI YOSHIDA** (Kyoto University, Japan)

Philosophers of science have several frameworks to discuss the dynamics of biological fields such as theory testing or mechanism identification. I argue that, however, a significant aspect of developmental biology cannot be adequately dealt with by those previous approaches. This paper thus formulates the way of research progression that often occurs in developmental biology but has been ignored in philosophy of science. Developmental biologists often express newly found behaviors of, or interactions between, types of molecules, cells, or tissues in a model system in an abstracted proposition, to which they refer as an “emerging concept.” Unlike the philosophical usage of “concept,” here “concept” means a proposition. Offering an “emerging concept” is an important task for them. I point out that proposing such an abstracted proposition about a novel phenomenon stimulates succeeding studies in other model systems, which gradually determine the range of its application. The entire process, to which philosophers have not paid attention, facilitates organizing knowledge about diverse developmental phenomena and gives partial integrity to the biological field that does not have any overarching laws or theories.

Untangling the role of theory and mathematics in biological modeling: An amendment to Giere’s framework**KIMBERLY DEBRULER** (Rice University, United States)

In describing the relationship between models and theories in scientific practice, philosophers confront the fact that modeling occurs both in fields with a rich body of theory and fields with few overarching theories. This raises the question of whether an effective analysis of modeling in a theory-rich field can be productively extended to theory-poor fields without losing descriptive power or internal consistency. This paper analyzes the applicable scope of Giere’s (1988, 2004) framework for modeling, which he drew largely from examples in Newtonian physics. It compares his characterization of models as entities that mediate a specific similarity relationship between theory and world to characterization of models as fictions relatively untethered by theory. This comparison serves to rescue the vital role of theory in Giere’s framework from his implicit assumptions regarding the form of theory. His framework is then evaluated through the lens of the historical development of the first model of the cell membrane, the “sandwich model” developed by Danielli and Davson (1935). I argue that Danielli and Davson drew on a critical set of trends that though not explicated in mathematical form synonymous with theory in physics nevertheless serve the two critical purposes of a theory in Giere’s conception of model building: the identification of a preexisting solution that narrows the scope of a problem, and the imposition of boundary conditions once that solution is adopted. I conclude that mistaking the mathematization of theory, a common feature in physics but a rare one in biology, for the existence of a theory exaggerates the difference in model building between these disciplines. This analysis suggests that the divide between modeling in “theory-rich” and “theory-poor” fields may be bridged at least in part by reevaluating the relationship between the form and the function of theories.

Forty years after “Le hasard et la nécessité” of Jacques Monod**NAOKI SATO** (University of Tokyo, Japan)

The book *Chance and Necessity* (abbreviated as HN according to the French title) was written by a molecular biologist Jacques Monod in 1970. Its principal subject was the theory of genetic code in a broader sense, but the author extends his theory to the evolution of human kind or human society. This raised not only debates and quarrels but also serious confusion. In addition, biological knowledge such as genomics/post-genomics dramatically advanced during the past 40 years. It is time to re-evaluate HN, in the light of various arguments against HN in different countries. In general, HN was not understood in depth and criticized superficially in English-speaking countries or Japan, whereas many thoughtful discussions based on deep understanding of HN were found in Germany and France. Evaluation of HN also depends on different disciplines. Philosophical discussions were abundant in France, while only biological aspect of HN, such as molecular biology and evolution, was discussed elsewhere. In this presentation, I would like to make clear what was chance and what was necessity in HN, which are not as simple as one might think. Then I will show that the most fruitful outcome of the theory of genetic code, which should be understood as the combinatorial flexibility of genetic regulatory system, is actually the synthetic biology and systems biology that flourish in the post-genomic era. The ethics of knowledge that sounded strange at that time was, in fact, realized in the present society which is governed by computers, tools of knowledge with some objectivity. Monod was sometimes criticized as being a strict Darwinist, but his evolutionary arguments in HN were rather obscure in the light of present-day knowledge.

DS R510

09:00 – 10:30

ORGANIZED SESSION / DIVERSE FORMAT

SOCIAL EPIGENETICS (1): SCIENTIFIC EVIDENCEOrganizer(s): **MAURIZIO MELONI** (Institute for Advanced Study, United States); **EVA JABLONKA** (Tel Aviv University, Israel)

Participant(s):

MOSHE SZYF** (McGill University, Canada)**EVA JABLONKA** (Tel Aviv University, Israel)**MICHAEL MEANEY** (McGill University, Canada)**SARAH RICHARDSON** (Harvard University, United States)

Epigenetics has important public implications and the potential to reframe significantly the uses of biological findings in the public sphere. Often in connection with findings from Developmental Origins of Health and Disease (DOHaD), epigenetics is increasingly being hailed as a key mechanism to explain health disparities between the rich and the poor, between and within countries. This session, which is part 1 of a broader double session on social epigenetics and its public implications, aims to bring together biologists, philosophers of biology, and social scientists to start a discussion on the social and political consequences of the changed under-

standing of inheritance that is implied by epigenetic findings. This first session in particular will focus on what we know after a decade of social epigenetics research about the epigenetic correlates of social conditions.

The session will offer a state-of-the-art analysis of the current advancements in social epigenetics and will represent an ideal basis for the following session on the possible sociopolitical implications of these findings.

Moshe Szyf: Social Epigenetics; Scientific Evidence, Questions and Challenges

Eva Jablonka: How can We Study the Epigenetics of War?

Michael Meaney: Parental regulation of the epigenome in the offspring

Sarah Richardson: What Does Epigenetics Explain?

DS R515

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

EXPLAINING A FOUR BILLION YEAR OLD PHENOMENON (1): LIFE AND ITS CHEMICAL ORIGINS

Organizer(s): **CHRISTOPHE MALATERRE** (Université du Québec à Montréal, Canada); **CAROL CLELAND** (University of Colorado Boulder, United States)

Life's originated on Earth around four billion years ago. How do scientists go about explaining this ancient event for which no telling traces remain? Several contemporary theories currently coexist, some favouring metabolism-first approaches, others genes-first approaches. All aim at bridging the gap from non-living matter to living matter. In this session and round-table, three philosophers and two scientists investigate some of the key problems that arise in origins of life research: What considerations ground the distinction between metabolism-first and genes-first theories? Is the origin of life distinct from the origin of evolution? How does chemical evolution relate to biological evolution? What role does thermodynamics play in chemical evolution? How do scientists test hypotheses about the origins of life? And do they?

[A legacy of Aristotle: Metabolism-first vs. genes-first theories of the origins of life](#)

CAROL CLELAND (University of Colorado Boulder, United States)

There is widespread agreement among biologists and philosophers of biology that two characteristics of familiar life are foundational: the capacity to (O) self-organize and maintain self-organization (aka metabolize) for an extended period of time and (R) reproduce and (in light of Darwin's theory) transmit to progeny adaptive characteristics. Precursors of O and R are found in the writings of Aristotle, who identified "nutrition" (O) and "reproduction" (R) as essential to life, debated which was more fundamental, and argued that both involve what

(from a contemporary perspective) amounts to a peculiar form of causation: internally generated, goal-directed causal processes. Contemporary theories of the origins of life echo Aristotle in privileging either metabolism or (genetic-based) reproduction as essential to life. Like Aristotle, they struggle with making sense of the nature of the causation involved. Tacit appeals to causal processes that are self-generating and goal-directed are routine in discussions of the origins of life, e.g., the "spontaneous assembly" of chemically improbable, primordial biomolecules, such as peptides or small RNA molecules, from more basic molecular components, and the "emergence" of proto-organisms from complex autocatalytic, chemical reaction systems. These notions of causation are difficult to make sense of in terms of ordinary, undirected causal processes familiar from the physical sciences. This raises the question as to whether a more fruitful account of the origins of life might be achieved by abandoning the theoretical framework for biology bequeathed to us by Aristotle. Such a move would parallel the abandonment of Aristotle's ideas in chemistry and physics, which were followed by rapid advances in scientific understanding. Indeed, viewed from a historical perspective, it is somewhat surprising that biology is still so closely wedded to Aristotelian ideas.

[The plague of equilibrium in modern origin of life theories](#)

ELIZABETH GRIFFITH (University of Maryland, United States)

One overarching problem plaguing leading origin of life theories is the transition from non-living components to an independent, nominally living, system. Life is known to be a highly out-of-equilibrium system. Our cells maintain gradients through actively pumping material into and out of them on a regular basis, thereby avoiding the tendency to achieve equal concentrations of the material in question on both sides of the barrier. In order to transition from non-life to life, thermodynamic equilibrium must be overcome to ultimately achieve this characteristic disequilibrium. Stemming from their differing levels of analysis, RNA and small molecule (SM) world theories have different problems in this respect. The RNA world stems from a biological level of analysis, originating in the historical discovery of the ribozyme in modern life followed by the extrapolation to the origin of life. Work performed under the premise of the RNA world arguably approaches the transition from non-life to life producing systems that mimic many of the functions of modern life. However, many of these functions still succumb to, or are even dictated by, the principles of thermodynamic equilibrium. In contrast, the SM world stems from a chemical level of analysis and hence concentrates on self-organized and self-propagating chemical systems. Through this concentration on catalysis, SM world studies have focused on the problem of equilibrium, even achieving propagating disequilibrium through time. However, it is difficult to envision an autocatalytic system propagating through time as an example of early life, suggesting that although disequilibrium is a necessary condition for life, it is not sufficient. In these respects, the RNA world and SM world theories face different problems in regards to the transition from non-life to life, which will be discussed in more detail.

Making sense of “chemical evolution”**CHRISTOPHE MALATERRE** (Université du Québec à Montréal, Canada)

The concept of “chemical evolution” aims at explaining how non-living matter has evolved into living matter on the primitive Earth. Endowed with a rich historical legacy, it has come to occupy a central place in scientific debates on the origins of life. It also generates much controversy: for some, it consists in Darwinian evolution applied to chemical systems (Calvin 1961); for others, it is precisely the type of evolution that happened before Darwinian evolution (Joyce 2002, de Duve 2005). Pioneering research in systems chemistry and synthetic biology is fuelling the debate even more by providing radically novel insights into possible prebiotic evolutionary processes like molecular cooperation, the emergence of competition among protocells or the role of simple physical effects in the transition to life (Budin and Szostak 2011). This contribution aims at explicating the concept of “chemical evolution” in the light of such recent advances in origins of life studies. I propose to construe “chemical evolution” as a composite theory that draws upon several evolutionary processes (rather than a single process of natural selection), and I argue that the relative importance of these processes over time helps construing a gradualist transition to biological evolution.

ORGANIZED SESSION / DIVERSE FORMAT

DEBATING DARWINOrganizer(s): **MICHAEL RUSE** (Florida State University, United States); **ROBERT RICHARDS** (University of Chicago, United States)

Participant(s):

MICHAEL RUSE (Florida State University, United States)**ROBERT RICHARDS** (University of Chicago, United States)**DAVID SEPKOSKI** (Max Planck Institute for the History of Science, Germany)**GREGORY RADICK** (University of Leeds, United Kingdom)

Darwin Studies are now moving to a new phase. Date the beginning of professional work on Charles Darwin, his contributions, and his influence, from around 1959, the hundredth anniversary of the *Origin* and about the time that Gavin de Beer was beginning to publish the species notebooks. Since then, we have had fifty years of sustained and valuable work digging through the available material, published and unpublished, and giving basic and insightful accounts of Darwin, his work, and much around him. The time now has come for broader interpretations, less concerned with simply digging out the material and more with making overall sense of what was surely one of the major episodes of Western culture. (One thinks analogously of work now being produced on the First World War and its origins.)

Sensitive to this change of direction and emphasis, **Robert J. Richards** and **Michael Ruse**, both of whom have long been contributors to Darwin Studies, are now offering rival interpretations of the work of Darwin and

DS R520

09:00 – 10:30

its significance. Richards argues that the key to understanding lies in the Romantic Movement in Germany at the end of the eighteenth and beginning of the nineteenth centuries and its influence on Darwin. In total opposition, Ruse argues that Darwin can be understood only as a product of his own home-grown culture, specifically the England and Scotland of the eighteenth and nineteenth centuries. They have a book expressing their disagreements (where they offer rival accounts and responses) in production with the University of Chicago Press. This session will air the Richards-Ruse differences – the rival claims and their putative supports.

Moderating and contributing to the session will be the younger historian of biology **David Sepkoski**, who has written extensively on evolutionary biology, particularly as it applies to the fossil record. He will be concerned less with imposing harmony and more with showing why this debate leads to important new avenues in ongoing discussion of the Darwinian Revolution. Also commenting is the neo-Hodgean historian of biology **Gregory Radick** who has likewise written extensively on evolutionary biology, with special interest in the work by biologists and others in the decades after the *Origin* was published. He too is concerned with how now we should understand the Darwinian Revolution and whether it was truly Darwinian or even genuinely revolutionary.

The session will conclude with responses by the participants to each other and questions and discussions from the floor.

ORGANIZED SESSION / DIVERSE FORMAT

BRINGING RACE/ETHNICITY TO PUBLIC FORAOrganizer(s): **AGELIKI LEFKADITOU** (Universitetet i Oslo, Norway); **PHIL LORING** (Norsk Teknisk Museum, Norway); **EDNA SUÁREZ-DÍAZ** (Universidad Nacional Autónoma de México, Mexico)

Participant(s):

HALLVARD FOSSHEIM (Universitetet i Bergen, Norway)**ADAM HOCHMAN** (Macquarie University, Australia)**JON RØYNE KYLLINGSTAD** (Norsk Teknisk Museum, Norway)**AGELIKI LEFKADITOU** (Universitetet i Oslo, Norway)**PHIL LORING** (Norsk Teknisk Museum, Norway)**EDNA SUÁREZ-DÍAZ** (Universidad Nacional Autónoma de México, Mexico)

In recent years, and at previous ISHPSSB meetings, historians and philosophers of science, social scientists, biological anthropologists, and geneticists have engaged in heated discussions about the reality, reemergence, or even the non-disappearance of race. Research in human genetic variation and genetic ancestry facilitated by the latest technological advances has further fueled these exchanges. Rethinking race and ethnicity among professionals is itself a demanding task. The political relevance and impact of these topics, however, means there is also a responsibility to broaden the field of the scholarly debate to include wider public arenas. Taking

up these issues outside a protected and contained academic environment is fraught with its own types of tension and requires different kinds of nuanced considerations. This roundtable brings together museum curators, historians, and philosophers who share an interest in what happens when questions of race and ethnicity enter contemporary public fora such as museums, newspapers, and social media. Such environments provoke constant renegotiations of representation and misrepresentation, individual and collective identity, inclusion and exclusion. Under these conditions, even seemingly innocuous objects, images, or phrases can become unstable and explosive. The session will include short talks on the race/ethnicity distinction and on public discussions of genetic origins and national ancestry, on the challenges facing university collections and museum exhibitions, as well as on debates over reburial of human remains and representation of ethnic groups. After a brief response from the chairperson, an open discussion will follow.

10:30 – 11:00

COFFEE BREAK

DS 1545

11:00 – 12:30

INDIVIDUAL PAPERS

ON THE BLOOD, FORMATO FOETU AND STEM CELLS**Walter Needham's *Disquisitio Anatomica de Formato Foetu*****ASHLEY INGLEHART** (Indiana University Bloomington, United States)

This paper examines the historical significance and content of Walter Needham's 1666 *Disquisitio anatomica de formato foetu*. *Disquisitio*, an impressive and rich embryological text, has been largely overlooked in the secondary literature. What little attention the treatise has received tends to focus on its resulting controversy with Danish anatomist, Nicolaus Steno. This treatise, however, is a significant contribution to embryology in its own right worthy of closer study. Inspired by the experiments conducted with Robert Boyle and other members of the so-called Oxford circle, *Disquisitio* focuses on the sanguification, respiration, and nutrition of the fetus in-egg or in utero. Because the mechanisms of both respiration and nutrition remained unclear and a subject of contention at the time of Needham's investigations, his experiments on the fetus—itsself a developing animal enveloped in amniotic fluid—are a rather ingenious attempt to understand more fully how these biological processes occur.

Descartes on the heart, blood, and Harvey**JORDAN TAYLOR** (University of Pennsylvania, United States)

The Cartesian human being is a conglomerate organism: a mixture of immaterial, volitional, sentient, and sapient mind-substance, on the one hand; and on the other, extension, manifesting itself as a complicated community of corpuscular particles—that is, material substance. This conception is an innovation on Descartes's part, as it goes hand-in-hand with a novel physical account of the world that departs quite radically from the accepted class of theories of the seventeenth century. With a new understanding of the world's principles and causes comes the burden of explaining the principles governing, and causes underlying, the world's inhabitants. Descartes therefore faces the difficult task of bringing the phenomena of the special sciences in line with the mechanistic corpuscular physics to which he subscribes. This paper focuses on Descartes's theory of human physiology. More specifically, it traces his explanation of the circulatory system responsible for animating the human body. Descartes's account of the motion of the blood is situated within a sophisticated reductionist framework that can account for complex behaviors and bodily functions by appealing, ultimately, to microscopic particles in motion. The paper also explores Descartes's debt to Harvey and the ways in which Descartes's theoretical commitments, as well as his practical outlook, forced him to contradict many of Harvey's own vitalistic interpretations of his experimental observations.

Early conceptualisation of the embryonic stem cell**CHERYL LANCASTER** (Durham University, United Kingdom)

Stem cell history begins with theory, not physical entities. The phrase "stem cell" first appeared in print in 1868, in Ernst Haeckel's *Natürliche Schöpfungsgeschichte*. But what developments had been made in biology to allow Haeckel to reach this milestone? This presentation will consider several aspects of research in the context of late eighteenth and early nineteenth century European (and in particular German) universities, beginning with the identification of cells as the basic units of life, and Schwann and Schleiden's Cell Theory. In the early decades of the nineteenth century, a younger generation of naturalists took-up embryological study, and began by repeating those studies they had learned about as students. Four such researchers were Karl Ernst von Baer, John Evangelista Purkyn, Jean Louis Prévost, and Jean Baptiste Dumas. Purkyn chose chickens as his animal of study, identifying the germinal vesicle in chicken eggs; this was important work, bridging the gap between avian and mammalian embryology. von Baer's work followed that of Dumas and Prévost, dissecting rabbits then a dog. Inside the dog, von Baer claims he observed an egg yolk, and published his observations in January 1828, describing the Graafian vesicle as the true mammalian egg. This egg provided a place for development, and became part of the foetus, possible due to the presence of the egg yolk. The presentation will also consider the practical aspect of embryology and development, from the seventeenth century work made possible due to the technological advances in optics, to the nineteenth century experiments carried out in attempts to prove

or disprove various theories of the era. Such theories created debates over preformation, and whether the sperm or ova were the most influential germ in creation of new life. Eventually, this led to ideas regarding the egg as a cell – an important milestone in conceptualising embryonic stem cells. Foremost in this work was Carl Gegenbaur, a colleague of Ernst Haeckel. From the work describing the unfertilised egg as a cell, the natural conclusion to this was considering what occurred after fertilisation. Possibly the most informative work in this field was carried out in the late 1830s by Scottish physician Martin Barry. In a series of three reports to the Royal Society's Philosophical Transactions, Barry described the maturation of the egg, and the first stages of development. This included identifying that the “vesicles” that arise from division through early embryogenesis are “vesicles” as described by others in the adult. This, I argue, is the first instance in embryology of any individual equating embryonic cells with adult cells. In the 1840s, Barry's observations were confirmed by Carl Bergman (at the time, Wagner's assistant at Göttingen), and Heinrich Rathke. This presentation will then consider how all of these developments led to Haeckel's coining of the term *Stammzelle*, and the contexts it was used in, including the influence of Charles Darwin's “tree diagrams”, and the context of *Stamm*, concluding with how Haeckel's understanding of development led him to identify certain cells as “stem cells”. Inevitably, the term was not used consistently the first years following its conception, however by the early twentieth century, a clear “stem cell concept” was developing. By the end of the nineteenth century, there were more sophisticated tools and techniques available to carry out experimental embryology, and an emerging stem cell concept. The last part of this presentation will consider how these merged to pave the way for the first descriptions of embryonic stem cells. This includes consideration of Wilhelm Roux's “pricking experiments”, Hans Driesch's work with sea urchin embryonic cells, and a short examination of American research (focussing on cell lineage).

ORGANIZED SESSION / STANDARD TALKS

EPISODES OF HISTORY OF BIOLOGY IN SCIENCE EDUCATION

Organizer(s): **MARIA ELICE BRZEZINSKI PRESTES** (Universidade de São Paulo, Brazil)

The inclusion of history of science in all levels of science education is highly evaluated today by the specialists, not only as a critical component of the scientific literacy, as well as a contribution to teach science as a human construction, subject to sociocultural context. This session seeks to discuss specific cases on history of biology, developed from relevant primary sources and updated secondary sources, and chosen from the Brazilian basic school' curriculum guidelines and undergraduate curriculum of courses for pre-service Biology teachers. The historical episodes will be presented as part of teaching learning sequences to be designed, validated, implemented and assessed in different specific school and/or university scenarios. The didactic and methodological approaches adopted seek to engage students actively in the scientific thinking and problem-solving of important historical discoveries.

Charles Darwin and the electric fishes: History and nature of science in teaching young people and adults

GERDA MAISA JENSEN (Universidade de São Paulo, Brazil)

This presentation will discuss the way in which electric fishes were studied by different naturalists, from the seventeenth to the nineteenth century. The main explanations for the phenomenon will be presented, first considered in the mechanical and corpuscular level, and then electric. The historical account will end up with the special difficulty of Charles Darwin in explain electric fish' organs belonging to different taxonomic groups according to the principle of natural selection. Finally, socio-cultural assumptions and guidelines objectives will be appointed for planning, validation and implementation of a teaching learning sequence for students of the Brazilian program of Youth and Adult Education.

Alfred Russel Wallace in the classroom: A historical case to learn botany through discursive interactions

ROSA ANDREA LOPES DE SOUZA (Universidade de São Paulo, Brazil)

The voyage of the English naturalist Alfred Russel Wallace (1823-1913) to Brazil in the mid-nineteenth century, and his studies of the palm trees in the Amazon region were the basis for the development and implementation of a teaching learning sequence in order to promote the teaching and learning of contents related to biological classification and phylogeny of living beings. The teaching learning sequence, composed of eight classes, was applied to high school students from a public school in São Paulo. The aim of this communication is to present the analysis of the construction of meaning in the social plan of some classes through an analytical tool of discursive interactions between teacher and students. It was used the reference system developed by Mortimer and Scott (2002), based on the teaching focus (teacher's intentions and content of speech in the classroom), communicative approach (dialogical or authority; interactive or non-interactive) and actions (patterns of interaction and teacher intervention). The tool has enabled characterization of the “teaching spiral” articulated between the communicative approaches and worked contents (historical, scientific, and metascientific contents).

Charles Bonnet studies on parthenogenesis in a virtual teaching object for undergraduate students

FILIFE FARIA BERÇOT (Universidade de São Paulo, Brazil)

The aim of this work is present preliminary stages of the development of a Virtual Learning Object based on a historical episode of the history of biology, the discovery of parthenogenesis in the 18th century by Charles Bonnet and its implications according the theories of the time (preformism and epigenesis). The Virtual Learning Object, conceived upon inquiry-based learning, will be presented as part of a teaching learning sequence for undergraduate students in biology of a public university of São Paulo, Brazil.

DS M240

11:00–12:30

ORGANIZED SESSION / STANDARD TALKS

PROPAGATING RESEARCH RESULTSOrganizer(s): **ELIHU GERSON** (Tremont Research Institute, United States)

Recent work on the mobility of research results across different settings has extended conceptual work on extrapolation (external validity, Cartwright) to consider the propagation of research results across settings (Morgan, Leonelli). This work also builds on recent scholarship on translation of research, which studies the conditions under which research results can be – and are – used to foster both basic scientific understanding and applications within and beyond techno-science. The approach developed in this emerging literature complements and deepens traditional social science approaches to the diffusion of innovation, which rely heavily on models of contagion in populations (Rogers), but have not paid much attention to the epistemological consequences of the movements of materials, results and concepts across sometimes widely differing environments. This session further extends work on propagation by separately analyzing different aspects of the propagation of data, observation techniques, and models. Our results underscore the importance of examining the different ways in which conventions are created and modified during propagation, and suggest approaches to the analysis of propagation mechanisms.

From the tragedy of the commons to public goods and n-person games**JASON OAKES** (University of California, Davis, United States)

The model in Garret Hardin's 1968 essay *The Tragedy of the Commons* (henceforth Tragedy) described a scenario in which shepherds spoil a common pasture through over-grazing. In Hardin's view, individual choices for personal gain lead to collective ruination, thus requiring a central authority to enforce extraction limits. This study compares the adoption of the model in two of the specialties that took it up, public choice theory and behavioral science/psychology. Researchers in both fields resituated different parts of the model in different ways, and their local contexts meant that they were changed significantly for their new environments. In the public choice work of Elinor and Vincent Ostrom, the commons were characterized as public goods (which later became common pool resources) and institutional failure ensued when "demand begins to exceed supply". The local situation hinged on explaining collective action in the context of rational individual choice. In behavioral science, Robyn Dawes re-situated Hardin's model as an n-person game with the option of cooperating or defecting. This approach leads to multiple possible end states. In both cases the problem addressed by Tragedy's model was left behind. Uncontrolled population growth and the need for coercive authority to restrain it dropped out of the picture, replaced by arguments for markets, and the viability of rational cooperation under particular circumstances. The context of re-situation substantially changed the model, and model propagation entails the emergence of novelty as models address different problems in different local situations.

Data journeys in biology**SABINA LEONELLI** (University of Exeter, United Kingdom)

This paper builds on the notion of data journey, which I define as the movement of scientific data from their production site to many other sites of use within or beyond the same discipline. In previous work, I characterised data journeys as a defining feature of the epistemology of data-centric biology, which marks both its relative novelty as an historical phenomenon and its peculiarity as an approach to scientific inquiry. I now wish to reflect on data journeys as a useful tool to examine the conditions under which scientific data are disseminated and effectively used in biology and beyond, paying particular attention to what "effective use" may involve. I focus in particular on online databases as infrastructures set up to facilitate data dissemination and their multiple re-interpretations as evidence for a variety of claims; and on the wealth and diversity of expertise, resources and conceptual scaffolding used both by database curators and by database users. Through the reconstruction and careful analysis of data journeys, a great deal can be learnt about the multiple roles and valences of data within research, ranging from their essential function as evidence to their importance as currency in trading, tokens of identity and means to foster the legitimacy, accountability and value of scientific research within a variety of contexts. To illustrate these points, I use cases of data journeys from model organism biology and phenomics.

Propagating new data collection and analysis techniques**ELIHU GERSON** (Tremont Research Institute, United States)

Science studies scholars have long thought that new ways of collecting and analyzing data are difficult to transmit effectively, requiring much patience and learning from both producers and users of emerging techniques. When instruments are undergoing development or major refinement, transferring a new technology to a new context and making it work properly can be a very difficult process. Traditional social science approaches to the problem of diffusion are of limited use in understanding this process, since they are typically based on simple contact models of diffusion in populations. The "ladders and bridges" model of propagation developed by Cartwright, Morgan, and others offers a promising approach to analyzing how new observation analysis techniques are desituated, packaged, and resituated. Field observation of a biochemistry laboratory involved with the extension of several important instrument families suggests that these techniques propagate differently than either large datasets or models. For example, propagating observation techniques, especially in the early (i.e., pre-commercial) stages of development, relies more heavily on personal contact and collaboration, and is relatively dependent on the facilities and character of the research sites involved. This appears to be true even when there are published protocols for using techniques, and classes to teach them. I construe these differences as resulting from the relatively high need for effective coordination among the many different activities that go into desituation, packaging, and resituation of instruments.

DS M260

11:00–12:30

ORGANIZED SESSION / STANDARD TALKS

NEW DIMENSIONS IN THE PHILOSOPHY OF PSYCHIATRYOrganizer(s): **NATALIA WASHINGTON** (Purdue University, United States)

In this session we examine some contemporary debates emerging in the philosophy of psychiatry, at the intersection of ethics, metaphysics, and philosophy of science, as philosophers, researchers, and practitioners begin to come to grips with psychiatry's dual nature as a science and an evaluative system. In particular we ask, what is the appropriate ontological framework and methodology for psychiatric research? What kinds of things can psychiatry study and intervene upon? And, what kind of normative standards are the right ones to use in determining what counts as mental illness?

Philosophy of psychiatry after diagnostic kinds**KATHRYN TABB** (Columbia University, United States)

A significant portion of the scholarship in analytic philosophy of psychiatry has been devoted to the problem of whether or not psychiatric disorders are natural kinds, and if they are not, what kind of thing they are. My contention is that this problem is fast growing less relevant to the concerns of practitioners and service-users of psychiatric medicine. Dissatisfaction with what I call the "diagnostic kind model" of psychiatric objects is currently appearing on a variety of fronts. Among clinicians of diverse orientations, it manifests as a dislike of, and in some cases open rebellion against, the hegemonic authority of the American Psychiatric Association (APA)'s *Diagnostic and Statistical Manual of Mental Disorders* (DSM). Among clinically-oriented researchers, it presents as a frustration with the demarcation of nosological boundaries that has so long occupied psychiatry as a science. Among scientifically oriented researchers, it is most obvious in the introduction by the National Institute of Mental Health (NIMH) of an alternative tool for classifying psychiatric research, the Research Domain Criteria project. I argue that by focusing on the problem of kindhood, philosophers have neglected the development of a conceptual account that could explain the sort of scientific progress that the NIMH is envisioning, which could also accommodate the sorts of challenges raised by practitioners about the insufficiency of the DSM to describe their patients or promote their best care. I take as my examples the employment of Richard Boyd's homeostatic property cluster (HPC) kind account by various philosophers, and the "exemplar" account promoted by Dominic Murphy. I demonstrate that these accounts still rely on what I call the "received authority" of diagnostic kinds, the very assumption that the NIMH and others are criticizing.

Let a thousand ontologies bloom**PHOEBE FRIESEN** (Graduate Center, City University of New York, United States)

This project seeks to examine the way in which an overriding focus on the medical model in psychiatric investigations today stands in the way of the dual goals of psychiatric research, to heal and to explain. Like any model of the mind, the medical model contains assumptions regarding ontological priority, by attributing a certain kind

of causal reality to a particular level (neurological), at the expense of others (cultural, psychological, genetic). During scientific investigation, attributions of ontological priority constrain what hypotheses will be tested, what is seen as relevant data, how that data is interpreted, and eventually what explanations and treatments will be developed. This suggests that today's emphasis on the medical model may be leading us to miss out on potential explanations and treatments that could be developed in response to mental disorders. While an abundance of important work is being done focusing on the role of the brain in psychiatric illnesses and developing pharmacological treatments as a result, there are a number of levels or perspectives that are given far less attention, particularly those regarding an individual's cultural and phenomenological experiences. For this reason, I argue that psychiatry would do well to adopt a stance of ontological pluralism, which encourages an exploratory and open-ended approach to ontology within research. Such an approach aims to lessen the impact of restrictive ontological frameworks on our potential for discovering relevant explanations and effective treatments that might not otherwise come into view.

Individualism as a solution to paternalism in psychiatric practice**NATALIA WASHINGTON** (Purdue University, United States)

While ideally a science consilient with the other sciences of the mind/brain, psychiatry also involves normative and evaluative concepts, as one goal of psychiatric practice is to alleviate the suffering caused by mental illness. But what kinds of evaluative standards are the right ones to use in determining what counts as mental illness? Because diagnosing an individual as having a mental disorder can be a way of saying that they have a condition that is bad and ought to be corrected, or that their pattern of behavior is somehow deviant or harmful, the evaluative nature of psychiatric diagnosis has historically been used as a tool of social control (Banaji, 2013; Satcher, 2001). In this paper I argue that, in order to ensure that the concept of mental health will be a useful one for theorizing about human flourishing, it should pick out a real psychological phenomenon in human lives, which has significance to the individuals the theory is about. In short it must have normative authority, "the feature in virtue of which people have a reason to follow the imperatives of a normative theory" (Tiberius & Plakias, 2010). To this end, everyone to whom the theory is supposed to apply should have some motivation to care about what psychiatry recommends, and there should be standards of justification for these recommendations. I examine one contemporary attempt to articulate a normative theory for psychiatry—George Graham's (2010) Rationality-in-Intentionality (RIT) thesis—and argue that it lacks normative authority. The specific norms RIT proposes come apart from what may actually be better for the individual in this case. Finally I argue that in order to solve the problem of paternalism, psychiatry must ground what it means to be mentally ill or mentally healthy in the concerns of individuals.

DS M280

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

DISCUSSIONS ABOUT CONCEPTUAL AND EPISTEMIC ISSUE IN BIOHACKING

Organizer(s): **GUILLAUME BAGNOLINI** (Université Paul Valéry Montpellier III, France); **PASCAL NOUVEL** (Université Paul Valéry Montpellier III, France)

The movement of biohackers and Do-it-Yourself Biology (DIYbio) can be described as the realization of scientific studies in biology outside the traditional scientific institutions. This approach is indeed unrelated to academic and industrial laboratories biology, and mostly developed on DNA experiments and other aspects of genetics. The biohackers defend some values such as sharing, equality, disinterest, and the common good. They inspired from the hackers' movement in computing, and get some of their values from the hacker ethics defended by Stephen Levy and more recently by Turner and Coleman. Is this new science really different and possible? The establishment of participatory and collaborative laboratory "La paillasse" in France proves this can be a reality. On which epistemic foundations is biohacking based? How can it change the relationships between society, research and the economy? The first paper of this session will present the recent history of biohacking and development at throughout the world (**Guillaume Bagnolini**). We will discuss with a philosophical and critical approach to the concept of free sharing defended by biohackers. **Sarah Choukah** will present her concept of "bioethnography" as a potential answer to the analysis of complicated issues. Sarah Choukah became involved as a member of Genspace, NYC's biotech community laboratory and NYC Resistor, a Brooklyn-based hackerspace, in order to know more about biohacking and hacking practices. In doing so she have come across several problems regarding the methodology and epistemology of ethnography in the social sciences. Her concept of "bioethnography" is based on Gilbert Simondon's philosophy of individuation.

The biohacking: A new scientific method?**GUILLAUME BAGNOLINI** (Université Paul Valéry Montpellier III, France)

Citizen sciences are research programs carried out by scientific institutions in order to involve non-professional scientists in scientific studies. The movement of biohackers and Do-it-Yourself Biology (DIYbio) can be described as the realization of scientific study in biology outside traditional scientific institutions. This fairly recent movement emerged in Boston around 2008 from the work of several amateurs and students. Those biohackers inspired from the hackers movement in computing some of the values they defend take their roots in the hacker ethics defended by Stephen Levy and more recently by Garbiella Coleman. The first meeting of DIYbio group gathered 25 people today, the association counts over 2600 members. In this review, I will discuss the philosophy of biohacking based on the history and ethics of biohackers movements. First, I would define and describe the idealistic view of biohackers and its evolution. Indeed, biohacking has grown from a political commitment towards a more playful and artistic vision. The movement induced a number of significant changes in society including the free movement of knowledge. They claim independence from both academic and corporate institutions and therefore rely mostly on open access tools. Morgan Meyer's work concludes that what characterize

the DIYbio network is the creative workarounds of tools and places resulting in the production of more permeable boundaries between professional scientists and amateurs. In a second step, I will consider the free sharing defended by biohackers. What are the motivations leading to this gratuitous act? Is it a need for freedom? Is free biohacking really free? Based on the work of Haraway, I also describe and discuss the free participation of biohackers in this type of projects. I will eventually show the similarities of this movement with the epistemological anarchism developed by Paul Feyrabend in his book *Against Method*.

The biohacker as dislocated self**SARAH CHOUKAH** (Université de Montréal, Canada)

DIYbiology ("DIYbio") and "biohacking" can be approached as forms of collective action that dislocate the sites and practices that were home to the life sciences (away from the world of "big science"). These dislocations are conjugated with several critiques and suggestions for a renewed scientific and political ethos. I focus particularly on sites called "biohackerspaces" and "biomakerspaces", which emerged as embodiments of this renewed ethos. Since the founding of the first biohackerspaces back in 2010, these sites serve as a number of intersections where different disciplines, groups, protocols, people and off-the-shelf equipment converge. In searching for what makes these intersections so amenable to the kinds of projects they foster, I made an intersection of my own self as a researcher. Even before I became involved as a member of Genspace, NYC's biotech community laboratory and NYC Resistor, a Brooklyn-based hackerspace, I realized the best way for me to know about biohacking and hacking practices was to become my own lab monkey, so to speak. In doing so I've come across several problems regarding the methodology and epistemology of ethnography in the social sciences. My answer to these problems found its way in a methodology and epistemology I am tentatively calling "bioethnography". I borrowed its conceptual precursors from Gilbert Simondon's philosophy of individuation. This one cryptic sentence he wrote launched me into it: "Beings may be known by the subject's knowledge, but the individuation of beings can only be grasped by the individuation of the subject's knowledge". I propose we dwell on that intersecting thought together.

DS M320

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

OF FROGS, MICE, AND MEN: A COMPARATIVE LOOK AT THE PUBLIC PERCEPTION OF CLONING, GENETIC ENGINEERING, AND TRANSGENESIS IN THE UNITED STATES AND EUROPEOrganizer(s): **NATHAN CROWE** (University of North Carolina at Wilmington, United States)

The creation of new biological forms in the 1970s and 1980s, both potential and actual, were thoroughly debated within the public sphere. While these discussions had many precedents, their scale, level of media coverage, range of stakeholders and the engagement of scientists with these discussions during these decades were unprecedented in the 20th century. Despite the high profile, the mediation of new life forms took diverse trajectories, as multiple actors worked to differentiate between the realities and fictions of the promises, both dire and optimistic. Some innovations, like recombinant DNA or cloning, were met with an outcry, while others were received with much more optimism. This panel will explore the communication of two technologies centered around nonhuman embryos: cloning and transgenesis (a form of genetic modification). With a tight chronological focus, we will explore what made a biological intervention controversial in this period, with a focus on how earlier public debates affected later ones, on the strategies that scientists employed to avoid or mitigate the fallout, and from comparative experiences in the United States and Germany.

Controversies about cloning in the 1970s: Futures, fraud, and facts surrounding nuclear transplantation in the United States**NATHAN CROWE** (University of North Carolina at Wilmington, United States)

This paper focuses on the 1970s and the issues surrounding nuclear transplantation and its public understanding as a technique that could lead to the cloning of humans. Beginning in the late 1960s, and increasingly throughout the 1970s, depictions of cloning became more widespread in the American public through a series of bioethical debates, popular science fiction books, and movies. This trend peaked in 1978 when David Jorvik published *In His Image: The Cloning of Man*, which supposedly documented the cloning of a wealthy businessman. Rorvik's book led to intense public discussion concerning the veracity of his claims and the ethics of cloning, which culminated in a congressional hearing on the subject that included many of the leading scientists who worked with nuclear transplantation techniques. For the history of cloning, this decade shows how closely connected cloning became to concepts like genetic engineering and in vitro fertilization. I argue that these terms became inexorably linked in many ways, with the terms used interchangeably to articulate the potentials, both good and bad, of science during this period. These incidents also show how precarious the line was for scientists who had to sometime promise that revolutionary breakthroughs were soon to be realized to garner funding and support, but other times had to be pessimistic and downplay the near-term possibilities of their work.

Contingencies, risks and anticipation: How cloning and genetic engineering changed the public reception of science and technologies in the 1970s and early 1980s**CHRISTINA BRANDT** (Ruhr-Universität Bochum, Germany)

This paper analyzes public debates on cloning and genetic engineering in the context of main discursive shifts that took shape during the 1970s and early 1980s. I will argue that the controversies about cloning - as a symbol for the new biotechnologies more general - contributed to major changes in the public view of the social consequences of science and technologies. These debates are analyzed in the context of other developments that deeply affected the public view of technological outcomes at that time, such as the "future studies" or the increasing awareness of an environmental crisis since the early 1970s. In these 1970s debates, ideas of "progress", but also the way of how the "future" of technologically driven societies was perceived, changed drastically. It was a period of transition in which a futuristic discourse on techno-scientific optimism and technological utopia (that had been typical for the 1950s and 1960s), turned into a discourse of risks, crisis and the needs of prevention, leading to ideas of an "anticipation" of future scientific developments as a main political task for present societies. The first part of the paper briefly traces how media, science fiction, bioethicists and philosophers turned the vision of cloning man into a near-by scenario, focusing on how the controversy, which emerged primarily in the US, was received in Germany. The second part interprets the 1970s changes in the popular discourses in a long term, by discussing the concept of a temporal and social "regime of anticipation" (Adams, Murphy, Clarke 2009) as a kind of management of the future, or a "moral economy" of Western societies to react against contingencies and uncertainties related to science and technology.

DS M340

11:00 – 12:30

INDIVIDUAL PAPERS

PERSPECTIVES ON HUMAN EVOLUTION**Beyond standard body?****PEGGY TESSIER** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

New body reconstruction techniques, i.e., technologies such as implantation of high-tech prostheses or surgical face transplant, require a shift from homeostasis to allostasis. In the context of classical biology, homeostasis is basically the return to "normal" conditions (Claude Bernard, 1865), while allostasis has been defined as "remaining stable by being variable" (Sterling & Eyer, 1988). It is probably the whole history of disability that hangs in the balance with this transition. Historically, logic of "compensation" has provided opportunities to people with disabilities in order for them to do what "everyone" can do (and, as a result, to restore homeostasis). The development of prosthetic devices has been part of such a process of "standardization", whose purpose was to gradually phase out the difference between disabled and non-disabled persons. However, this logic of "compensation" has driven these opportunities to a point where the classical definition of "disability"

necessarily changes. In this presentation, I will present the allostatic model that emerged in the 1970s, which relies on new social practices concerning Nature and Biomedical Sciences (Arminjon, 2014). I will then show that, today, the new prosthesis, even more sophisticated, not merely enable to compensate (to provide a return to normal), but enable to offer another *allure de la vie*, “pace of life” (Canguilhem, 1966). Finally, I will try to clarify how the concept of “standard body” has changed through this shift.

Niche construction and neoteny: The evolution of language within an updated evolutionary research program

FRANCESCO SUMAN (Università degli Studi di Padova, Italy)

In the evolution of language debate some scholars rely on the primacy of natural selection as the only factor shaping traits (selection as a designer), others rely on the role played by phenotypic and developmental constraints in the evolvability of structural and functional traits (evolutionary tinkering). In order to enrich this too much radicalized debate, we should have a look at the overall status of evolutionary theory (Pievani, 2015); today, two different conceptions seems to be in place: one which argues that a rethinking of the theory is necessary and the other arguing it is not necessary (Laland et al., 2014). The former emphasizes the fact that four phenomena in particular should gain more importance within the evolutionary research program: phenotypic plasticity, niche construction, inclusive inheritance, developmental bias. With recent data coming from brain evolution and development (molecular level) and data coming from hominin anatomy and behavior seen through the lens of niche construction theory (ecological level), it is possible to gain an integrated view of the selective pressures which might have acted during hominin evolution (with particular attention to relaxed selective pressures and their effects on neotenic traits), in order to understand the interplay between biological and cultural evolution and its effects on the evolution of complex traits such as human language.

Human self-domestication hypothesis: Developmental considerations

BERNARDO YAÑEZ (Centro de Estudios Filosóficos, Políticos y Sociales Vicente Lombardo Toledano, Mexico);

VERA JOSÉ LUIS (Escuela Nacional de Antropología e Historia, Mexico)

Domestication syndrome characterizes a set of features from animals and plants that had been exposed to artificial selection through time. In this sense, several academic references had established that the domesticated species share a suite of morphological and behavioral traits which had been interpreted as byproducts of the domestication process. In the case of humans there are some particular morphological and behavioral traits that seem to be related to a self-domestication process (Wrangham et al. 2014). Furthermore, in the primatological literature there is also an interesting proposal in this sense which is used to explain the differences between common chimpanzees and bonobos (Hare et al. 2012). In this paper we would like to highlight two particular claims: I) that Hare and colleagues (2012) show a strong intent to incorporate a developmental perspective in this approximation. However, we have not been able to discern precisely which is the notion of “develop-

ment” that these authors are taking into account. This clarification is not a minor aspect; rather we believe it is crucial in terms of the epistemological accuracy that can be established with some perspectives of evo-devo approaches. II) Our impression is that there is still a significant reminiscence of the adaptationist program. For instance, they propose a hypothesis in which selection against aggression is at the heart of the conundrum; however, what is surprising is that they propose that selection in favor of aggression is the principal alternative hypothesis. Our contention is that we think there is sufficient theoretical background to try to work out a different explanation in which adaptation plays an important role but not necessarily the most fundamental. Rather, a multifactorial set of events, particularly in the developmental pathways of primates in this case, could be a more explanatory perspective.

DS M440

11:00 - 12:30

INDIVIDUAL PAPERS

EVOLUTIONARY PSYCHOLOGY: SEX DIFFERENCE, LANGUAGE AND INTENTIONALITY

Reconceptualizing transgenerational stability and change in the context of evolutionary psychology of sex differences

EWELINA SOKOLOWSKA (Uppsala universitet, Sweden)

Evolutionary psychology has been gaining increased attention in the social sciences over the last years. The topic of sex differences in human behavior is one of the more intensively examined through the lens of the evolutionary perspective, and seems to be socially and politically most controversial. The arguments that certain differences between men and women are evolutionarily-based and should thus be regarded as “natural” or the assertions that the institution of patriarchy is something to be “expected” from the evolutionary point of view strike a chord not only with feminists but also beyond. In this paper, I want to draw attention to one particular assumption that underlies the project of Evolutionary Psychology, namely, the assumption of stability of psychological adaptations. It is the assumption that the psychological mechanisms that we possess today are adaptations to the environment of the Pleistocene and have not changed since then. This assumption is commonly taken for granted and rarely problematized - with a customary statement, cutting off any further discussions, that evolution is just “a very slow process”, taking into consideration the sheer time it takes for thousands of small random mutations to accumulate, and so, for evolutionary change to occur. In this paper, I want to explore this assumption in the context of the recent and increasing recognition in contemporary biology of the need to extend the concept of heredity beyond its exclusively genetic terms, in order to include other potential inheritance mechanisms (epigenetic, behavioral, cultural, ecological). As such an extended concept of inheritance, in turn, gives rise to the need for a reformulation of the orthodox gene-centered view of evolution, it also points to a possibility that the way evolutionary stability and the speed of evolutionary change are typically thought about needs to be re-conceptualized as well. This shows that the assumption of stability of psychological adaptations

should be far from being taken for granted, and that a great deal of dynamics may in fact be possible in this area. I conclude this paper by exploring the implications that this alternative unorthodox view may have for the way sex differences in human behavior are being studied from the evolutionary perspective.

Saltationism and over-simplification: Biolinguistics and the evolution of the faculty of language

ERIC MUSZYNSKI (Université du Québec à Montréal, Canada)

In recent years Noam Chomsky has come forward with explicit ideas regarding the evolution of the faculty of language, which he has long claimed ought to be studied as a biological organ. Using the theoretical framework and the findings of “biolinguistics” and the Minimalist Program, Chomsky (2010) and Berwick & Chomsky (2011) propose a saltationist and non-adaptationist scenario for the evolution of the faculty of language. According to them, at the core of the faculty of language is recursive combinatorial algorithm which is so simple it cannot be broken down into sub-routines. Accordingly, it could only have evolved in a single step, allowing no intermediate stages. This further implies that it did not appear as an adaptation (not even for communication) since it appeared fully-formed. I begin by pointing out various problems with this account, namely regarding their use of concepts in evolutionary biology. I further argue that Chomsky and Berwick’s approach is problematic because it does not take into account the evolution of lexical units and lexical features that they themselves use in linguistics more generally. I contend that this is not a mere gap that can be filled later, but radically changes their account of the evolution of the language faculty. I propose a hypothetical chronology of language evolution taking into account these points to demonstrate that the saltationist approach is far from being the most likely scenario.

Evolutionary psychology, normativity, and dynamic ecologies: An exapted theory of intentionality

JOHN ATYTALLA (University of Ottawa, Canada)

I propose a model of intentionality, which, through an interdisciplinary approach to the study of the mind, seeks to reconcile evolutionary accounts of its organization with theories that focus on the socio-historical and normative determinations of thought. My investigations take empirical science to be a dialectical starting point from which our philosophical investigations must proceed. This is in contrast with the approach taken by John McDowell, which seeks to articulate thought as normatively governed “all the way down”. His approach entails that our understanding of the operations of thought will not benefit from empirical investigations and that the problem of intentionality can be solved by embracing the idea that thought emerges from the manner in which social inculcation makes us sensitive to normative demands. He calls this sensitivity to normative demands “second nature” while calling the biological aspects of human nature “first nature”. I agree with the terms of the debate while nonetheless regarding McDowell’s version to be incomplete. It is clear that the terms “nature” and “nurture” and the terms “phylogenetic” and “ontogenetic” afford us with similar distinctions, despite coming from distinct fields. I will propose a solution to the problem of intentionality that depends on my distinction be-

tween “aboutness” and “directedness” which are oftentimes used interchangeably to describe the relevant phenomena. This theory suggests that the contents to which our thoughts and volitions are directed issue from our evolved phylogenetic traits; whereas the contents that an agent is thinking about depend upon ontogenetically acquired behaviours in a socio-historical environment. By describing the socio-historical properties of human life in terms of a dynamic array of ecological niches I aim to preserve the intuition that some elements of thought are socio-historically contingent without regarding them as free of biologically necessary determinations.

DS M460

11:00 – 12:30

INDIVIDUAL PAPERS

PRACTICE AND ASSESSMENT IN ENVIRONMENT AND EVOLUTION

The fallacy of accident and the case of adaptationism

CATHERINE HUNDLEBY (University of Windsor, Canada)

The fallacies approach to argument evaluation helps to explain and explore the significance of adaptationist tendencies in evolutionary biology identified by Elisabeth Lloyd (2006): the unjustified assumption that all characteristics result from a distinct evolutionary adaptation. I argue this presumption qualifies the error as an example of the fallacy of accident. Mistaking an accidental feature for an essential one can account for the mistaking of a non-adaptive trait for an adaptive one. Fallacy diagnosis reveals how this confusion is not unique to evolutionary thinking, and at the same time that it may be reasonable to assume that a trait is adaptive. The most advanced account of fallacies, Douglas Walton’s (1995; Tindale 1997) pragmatic approach, does not dismiss any type of argument associated with a fallacy but demands that it be systematically open to question. Likewise, appeals to popularity and authority may be reasonable, but only insofar as the particular employments withstand critical questions associated with those presumptions. Lloyd identifies a list of considerations necessary for accepting a trait as an adaptation. Treating adaptationism specifically as a case of accident has advantages over other possibilities, such as fallacies of generalization or causal fallacies. Accident relates adaptationism to a metaphysics of essences and natural kinds, a diagnosis that accounts for the complicating political resonances of adaptationism. The fallacies approach allows that sometimes such assumptions may be reasonable, yet in raising the possibility of accident does not assume the correctness of such a metaphysics. It merely helps reasoners to address how that ontology and hierarchies of traits might be justified, and support the demand that without such justification the assumption must be abandoned. Accident tends to be left out of contemporary lists of fallacies specifically because of its metaphysical baggage, but the engagement of metaphysics also indicates its singular potential to address adaptationism.

Sticky matters of fact: On the production of “material” knowledge

JULIA HEUNEMANN (Bauhaus-Universität Weimar, Germany)

In 1857 a sticky substance was hauled up from the bottom of the Atlantic Ocean. In its first examination it apparently did not prove particularly exciting for Thomas Henry Huxley as he afterwards shelved the specimen for ten years. Upon re-examination a decade later, the British biologist realized tiny objects had developed within the sample and concluded that the substance had the potential to produce life. (Huxley 1868) He considered it an organismic matter embodying biological vitality in its most simple form. Recognizing that it exhibited attributes of Monera, a taxonomic group Ernst Haeckel just recently had claimed to exist (1866), Huxley named the new species *Bathybius haeckelii*. However, seven years later, the organism was proven not to be alive at all, but a product of its conservation in spirits (Rehbock 1975). It was not even “natural”. During the years of its “biological existence”, *Bathybius* literally served as substantial proof to theories on evolution, the origin of life, and lines of demarcation between organic and inorganic material. My paper investigates the conditions of possibility that made the slimy matter become a matter of fact. It traces transformations the substance went through between the sea bottom and its becoming biological evidence. Considering that the technical prerequisites of its finding (sounding apparatuses, microscopes, conservation) intermingled with epistemological conditions of its employment for materializing theory (“material” empiricism), historical knowledge production in biology is at stake. How did investigation techniques and epistemologies produce *Bathybius* in the first place? And, in this particular case: how did biology participate in producing bios as its very own study subject? For answers to these questions, the history of *Bathybius* is particularly suitable: it initiates in the depths of the ocean, a medial space par excellence, the knowledge about which necessarily is a technically produced one.

What physics needs to learn from biology

MARTIN BREMER (Florida State University, United States)

This paper looks at the historical and cultural development of Biology and Physics. Specifically, it focuses on the continually segregated nature of Physics - a discipline fraught with gender and ethnic disparity - and Biology, a discipline which has been able to develop to become much more inclusive. Included with the historical/cultural analysis of the disciplines, this paper includes data collected from interviews of current physics majors. The interviews shed light on the current cultural status of Physics as seen through those attempting to become part of the physics community. These interviews lead to insights on the issues surrounding the lack of cultural development within physics which leads to lack of diversity within the community.

DS R510

11:00 - 12:30

ORGANIZED SESSION / DIVERSE FORMAT

SOCIAL EPIGENETICS (2): SOCIAL AND POLITICAL IMPLICATIONS

Organizer(s): **MAURIZIO MELONI** (Institute for Advanced Study, United States); **EVA JABLONKA** (Tel Aviv University, Israel)

Participant(s):

FRANCES CHAMPAGNE (Columbia University, United States)

BECKY MANSFIELD (Ohio State University, United States)

MARGARET LOCK (McGill University, Canada)

MAURIZIO MELONI (Institute for Advanced Study, United States)

GIUSEPPE TESTA (IEO and University of Milan (Fondazione Semm), Italy)

Epigenetics has important public implications and the potential to reframe significantly the uses of biological findings in the public sphere. This session, the second part of a broader double session on social epigenetics and its public implications, will focus on the following key-questions about the social circulation of epigenetic findings:

- 1) Will epigenetics be seen as positive factor of change and improvement because of its potential reversibility, or as the signature of a persistent disadvantage that characterizes certain social groups because of their repeated exposure to poor environments?
- 2) What are the concerns that epigenetic findings will be used to fuel a new rhetoric that targets pregnant women as a site of interventionist strategies?
- 3) What are the implications of epigenetics for the notion of race?
- 4) Will epigenetics findings result in an expanded notion of responsibility and in a moralization of specific behaviours (e.g. smoking, eating, and physical exercise)?
- 5) How will public policy initiatives based on epigenetic findings relate to (or differ significantly from) previous initiatives of social intervention based on genetic knowledge?
- 6) What is the historical legacy in public policy of notions of neo-Lamarckian inheritance?

Frances Champagne: Epigenetic interplay between mothers, fathers, and offspring: Implications of the legacy of parental experiences

Becky Mansfield: Epigenetic abnormality biological plasticity and new configurations of race and reproduction

Margaret Lock: Should Epigenetics be Politicized?

Maurizio Meloni: The trouble with Lamarck: Anti-Lamarckian arguments from Kroeber’s anthropology to Soviet eugenics and their significance for today

Giuseppe Testa: From ants’ colonies to working classes: molecular epigenomics and the digitization of social status

DS R515

11:00–12:30

ORGANIZED SESSION / DIVERSE FORMAT

EXPLAINING A FOUR BILLION YEAR OLD PHENOMENON (2): PARADOXES AND THEORIES ON THE ORIGINS OF LIFEOrganizer(s): **CHRISTOPHE MALATERRE** (Université du Québec à Montréal, Canada); **CAROL CLELAND** (University of Colorado Boulder, United States)

Participant(s):

ELIZABETH GRIFFITH (University of Maryland, United States)**STEVEN BENNER** (Foundation for Applied Molecular Evolution, United States)**CAROL CLELAND** (University of Colorado Boulder, United States)**CHRISTOPHE MALATERRE** (Université du Québec à Montréal, Canada)

Life's originated on Earth around four billion years ago. How do scientists go about explaining this ancient event for which no telling traces remain? Several contemporary theories currently coexist, some favouring metabolism-first approaches, others genes-first approaches. All aim at bridging the gap from non-living matter to living matter. In this session and round-table, three philosophers and two scientists investigate some of the key problems that arise in origins of life research: What considerations ground the distinction between metabolism-first and genes-first theories? Is the origin of life distinct from the origin of evolution? How does chemical evolution relate to biological evolution? What role does thermodynamics play in chemical evolution? How do scientists test hypotheses about the origins of life? And do they? After an introductory talk by **Steven Benner** and commentaries by **Carol Cleland**, **Elizabeth Griffith** and **Christophe Malaterre**, an open discussion will follow.

Paradoxes and theories on the origins of life**STEVEN BENNER**

The question: "How did life originate?" is phrased as a historical query. To answer it would require the recounting a sequence of events that occurred perhaps four billion years ago, and most likely in an isolated environment that occupied a geographically negligible portion of the geosphere. Accordingly, most scientists rephrase the question to ask: "How might life have originated?" Here, the origin of life is tied closely to the origin of Darwinian evolution, as neither theory nor experience has so far identified another way in which matter might self-organize to create systems that behave as we expect life to behave. The "RNA first" model has the virtue of providing a clear path connecting non-Darwinian precursors to Darwinian outcomes. Unfortunately, numerous efforts to reconstruct in the laboratory key intermediates along that path have failed. Those advocating a "metabolism first" model point to the ability of prebiotic Earth to generate small molecules. However, they have not provided, even conjecturally, any path from pre-Darwinism to Darwinism. This talk will concentrate on the research strategy problems that these facts create, in a field where "hypotheses" that might be followed are few and fragmentary.

DS R520

11:00–12:30

ORGANIZED SESSION / DIVERSE FORMAT

PROCESS AND METABOLISMOrganizer(s): **JOHN DUPRE** (University of Exeter, United Kingdom)

Participant(s):

DANIEL NICHOLSON (University of Exeter, United Kingdom)**STEPHAN GUTTINGER** (University of Exeter, United Kingdom)

Anne Sophie Spann (University of Exeter, United Kingdom) This session will explore the importance and role of concepts of metabolism from the perspective of a process-centred view of living systems. After a general introduction to the Process Ontology project (**Dupré**), the next paper (**Nicholson**) will discuss the advantages and limits of reconceptualising living systems as dynamic flows of circulating matter, in contrast to the more standard conceptions of them as complex machines. The single most important feature captured by this processual perspective is metabolism. The next paper (**Guttinger**) will address problems in defining the boundaries of metabolic systems, with reference to the complexly intertwined metabolic interactions within microbial consortia, and the metabolic relations between organelles (e.g. mitochondria) and the environment of the eukaryotic cell. The third paper (**Spann**) will explore the centrality of metabolism to more general metaphysical issues, specifically the distinction between living and non-living entities, and the problems in developing a concept of diachronic identity for biological entities. This discussion will demonstrate the necessity of deploying a process ontology to address these questions in a biological context.

ORGANIZED SESSION / DIVERSE FORMAT

HEREDITY AND TRANSMISSION: DISCUSSION ACROSS THE DISCIPLINES (LABEX "WHO AM I?")Organizer(s): **ANTONINE NICOGLOU** (LabEx "Who am I?", France); **JEAN GAYON** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France); **FRANÇOIS VILLA** (Université Paris Diderot - Paris 7, France); **JONATHAN WEITZMAN** (Université Paris Diderot - Paris 7, France)

Participant(s):

JEAN GAYON (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)**FRANÇOIS VILLA** (Université Paris Diderot - Paris 7, France)**JONATHAN WEITZMAN** (Université Paris Diderot - Paris 7, France)

Current discoveries regarding "non-Mendelian" effects and epigenetic mechanisms have opened debate among biologists about the nature of extended inheritance, its prominence in biological systems and its impact on evolution. In light of these issues, it is timely to explore anew the concept of transmission, while acknowledging that heredity must go beyond the genetic perspective. This project should draw on an integrated dialogue between the

disciplines studying biological systems. The purpose of this round table is to generate discussion between team leaders in different fields (i.e., cellular biology, evolutionary and developmental genetics, psychology & psychoanalysis, philosophy of biology), who are all interested in the same question: how are complex factors – be they psychological or behavioral traits, based on a “cultural” and/or “parental” environments – transmitted, if not through the genes? More broadly, one of the purposes of the session will be to investigate the “nature/culture” distinction and how the contours of the “nature-nurture debate” could be defined. Each of the team leaders from different disciplines will begin by addressing the question: “What does “transmission” mean to you?” This discussion will highlight similarities and differences between the disciplines and define a common ground to open the debate.

12:30 – 15:30

LUNCH BREAK

13:00 – 14:00

GRADUATE STUDENT MEMBERS GENERAL MEETING | Room DS-R510

14:00 – 15:00

MEMBERSHIP DIVERSITY MEETING | Room DS-R515

DS 1525

15:30 – 17:00

INDIVIDUAL PAPERS

DISUNITY, CULTURE AND EVOLUTION**The disunity of cultural group selection****OLIVIER MORIN** (Central European University, Hungary)

Cultural Group Selection (CGS) is touted as a solution to the problem of explaining the rise of large-scale cooperation among humans. I will argue that CGS is not a coherent theory, but a collection of models with discrepant assumptions and objectives. Two objectives can be distinguished. One is to justify the claim that evolutionarily altruistic behaviors (reducing the agent's fitness at the expense of a group) are frequent and matter to the evolution of cooperation. The other objective is to provide a mechanism for equilibrium selection, the process by which sub-optimal forms of cooperation are replaced by stable ones. Equilibrium selection may occur without evolutionary or behavioral altruism. “Altruistic” models face a difficulty that Equilibrium Selection models do not face: individuals are not purely selfless or irrational. They would rather join coalitions, or adopt institutions, that do not demand uncompensated sacrifices. Historically, CGS was able to counter this objection by assuming that cultural evolution is mostly driven by group-level demographic dynamics (birth rates, wars, etc.), which decide the outcomes of competition between coalitions. Such forces are arguably beyond the power of individual decisions to control, which is what made CGS attractive to social scientists since Hayek. Yet, this assumption is arguably too demanding. Equilibrium selection models can function without it: in recent

theorizing (e.g. the work of Peter Richerson), the mere diffusion of mutually beneficial institutional practices (e.g. using insurances, or adopting majority voting) qualifies as CGS, because it promotes mutually beneficial cooperation. Selection between competing coalitions is no longer crucial. Such forms of CGS are morphing into a variety of functionalism, the twentieth-century doctrine that stressed the contribution of culture to social cohesion. This disunity is a sign of dynamism, but we run the risk of buying into CGS' most controversial claims inadvertently, when we endorse its milder versions.

The “final wave” model for the evolution of cognitively modern humans: A multi-level approach**ANDREA PARRAVICINI** (Università degli Studi di Padova, Italy); **TELMO PIEVANI** (Università degli Studi di Padova, Italy)

Growing evidence corroborates the hypothesis of multiple waves undertaken by Homo sapiens populations out of Africa. Recent data show that the emergence of symbolic behaviors coincides with the final third wave. New southern African dating and chronological reconstructions of Still Bay and Howieson's Poort industries (about 75-60Kya) seem to confirm the occurrence of punctuated bursts of technological and behavioral innovation, which may be strictly linked to climate changes and demographic fluctuations in southern Africa. We propose the Final Wave model stating that one of these bursts of innovation have been particularly successful in contributing to bring a small population of H. sapiens (carrying L3 mt-DNA haplogroup) out of Africa, together with the symbolic capacities showed by the members of this group in Europe and in South East Asia. This model exemplifies, on the one hand, how we could integrate archaeological, paleoclimatological, molecular and demographic data in order to explain the biological and cultural evolution of cognitively modern humans. On the other, it is an ideal example of the the way a hierarchical framework works within the evolutionary processes, as the model reveals the presence of a complex interplay among patterns and processes belonging to different hierarchical levels (ecological and genealogical).

Normative cognition and the disunification of moral judgment: Ontogenetic and phylogenetic perspectives**IVAN GONZALEZ-CABRERA**** (Australian National University, Australia)

Moral judgments are neither a unified domain (Sinnott-Armstrong & Wheatley, 2012, 2013) nor a natural kind (Kelly & Stich, 2008; Kelly, Stich, Haley, Eng, & Fessler, 2007; Nado, Kelly, & Stich, 2009; Sripada & Stich, 2007). This suggests that the class of moral judgments is determined by the speakers' intentions, with members of that class sharing a form of family resemblance. Empirical sciences such as evolutionary biology and cognitive science should then focus on broader categories of normative judgments along the lines of Nichol's (2002, 2004) approach of norms with feelings or Sripada and Stich's (2007) psychology of norms, and/or more specific varieties of moral judgments (see for instance Mameli, 2013). In this paper will sketch how this enterprise can be carried out by looking at some findings in developmental and comparative psychology. I will explain how a basic capacity of normative judgment can produce some varieties of moral judgments, and how this capacity emerges during ontogeny. Finally, I will suggest some evolutionary hypotheses about the evolutionary trajectory of this multi-dimensional capacity for moral judgments.

DS 1540

15:30 – 17:00

INDIVIDUAL PAPERS

BIOCHEMISTRY BETWEEN DISCIPLINES

Portraying the immune self: Between “Panama-blot” and protein microarrays**MARIA STRECHT ALMEIDA** (Universidade do Porto, Portugal)

The present paper is focused on imaging practices in the life sciences and explores, in particular, research conducted around the immune self. Proposed within the context of the cognitive paradigm of immunity, the entity referred to as the immunological homunculus is described as an immune system’s internal representation of the body. Useful for the understanding of the immune response in that context, this epistemic object refers to a somehow delocalized entity, distributed throughout the body, and proteinaceous in nature. This presentation will explore how pioneering experimental work conducted in the 1990s and resorting to an adapted and rather complex immunoblot method played an important role in providing visual (and material) evidence for the existence of such an entity. It will look at the development of the later called “Panama” immunoblotting; mapping antibody repertoires, the procedure is a quantitative assay requiring extensive processing and computational analysis of the obtained profiles of immunoreactivities. The results revealed defined patterns of reactivity, were described as evidence for the existence of an immunological homunculus and acknowledged as such. The analysis will address the visualization dimension of that work and particularly the interplay between the visual and the computational both contributing to the evidential strength of the reported data. “Panama-blot” are somehow portraits of the immune self. They represented a novel strategy in research for considering antibody reactivities to several hundreds of antigens simultaneously. Initial tools of immunomics, one can argue, they preceded current protein microarrays. A number of advantages of the latter are clear, although expressing the same idea. This similitude is worth emphasizing. How these two ways of portraying the immune self might illustrate different roles of concepts, design and technological advancement in the dynamics of research will be discussed.

Pharmaceutical biochemistry: The research program of George Hitchings and Gertrude Elion (1940s-1950s)**THIBAUT SERVIANT-FINE** (Université Claude Bernard Lyon 1, France)

This paper concerns the early career of George Hitchings and Gertrude Elion, co-recipients of the 1988 Nobel Prize in Physiology or Medicine. Hitchings was hired in the early 1940s by the Burroughs Wellcome company as head of a new biochemistry department where he was joined by Elion. Together, they developed a research program of drug design based on the principle of antimetabolites, recently established by Donald D. Woods and Paul Fildes. Attracted by this new “rational approach to chemotherapy”, Hitchings sought to combine its promising theoretical hints with his personal expertise in nucleic acids in order to develop innovative drugs that could specifically act on nucleic acids synthesis. This venture is often hailed as the beginning of what is today known as rational drug design. Based on the first comprehensive historical study on Hitchings and Elion, this episode allows us to shed new light on the history of biochemistry along several lines. First, whereas the

historiography of biochemistry and molecular biology tends to focus on genetics, this episode allows us to look at biochemistry from a different angle, putting macromolecules and genes to one side to look more closely at vitamins and other small organic compounds. Second, this work on nucleic acids gives us the opportunity of looking at the expansion of a research program in a field that was neglected at the time. This allows us to re-examine the general shift in interest from proteins to nucleic acids in the 1940s and 1950s. Third, the focus on a pharmaceutical laboratory allows us to reflect on the production of biological knowledge in an industrial setting, and thus to consider the blurred frontiers between “fundamental” and “applied” research in this field. Indeed, for the actors themselves, the ultimate goal of drug discovery did not preclude acquiring significant biological knowledge in the process.

Interfield research on plant growth hormones**CATERINA SCHÜRCH** (Ludwig-Maximilians-Universität München, Germany)

In the early 1930s, groups in Utrecht and Pasadena set out to study the plant growth hormone. In both cases, chemists and botanists were convinced that this research had to be carried out interdisciplinary – a belief, which endured the following years of intensive research unchallenged. This early bio-chemical project was perceived as excessively successful. Furthermore, the analysis contributes to the philosophical debate on strategies in the search of mechanisms. This study integrates the historical perspective with a philosophical analysis. The first of these involves careful examination of publications, lectures and correspondence, as well as retrospective accounts. The second employs Machamer, Darden, and Craver’s (2000) concept of mechanisms, and ideas from Darden and Maull’s (1977) work on interfield theories and Deutsch’s (2006) theory of cooperation and competition. The sought after hormone is analysed as a chemical entity, identified by its physiological activity; the biologist’s modelling of mechanisms is constructed as an exemplary of forward/back-ward chaining (Darden 2002) based on the hormone’s and the plant cell wall’s chemical structure. The cooperation is explained as a consequence of the positive goal interdependence of the chemists and physiologists involved: On the one hand, the biological Avena-test is used as a bioassay to isolate the growth hormone; on the other, samples of auxin are supplied for biological experiments, and knowledge about its chemical structure is used in modelling the mechanism of growth in plants. This analysis elucidates the fact that explaining a phenomenon by advancing an account of the mechanism responsible for it often involves interfield theorizing, as Bechtel and Abrahamsen (2007, p. 28) have proposed. Conclusions arrived at can be employed both in arguments concerning historical dynamics, as well as the philosophical relation between interdisciplinarity and other concepts such as reductionism, level of explanation or causal relevance.

DS 1545

15:30 – 17:00

INDIVIDUAL PAPERS

MECHANISMS AND DESIGN IN PRACTICE**The flat vs. the dimensioned view of constitutive mechanisms****BEATE KRICKEL** (Ruhr-Universität Bochum, Germany)

In the new mechanistic literature, authors usually distinguish between two different types of mechanisms: etiological mechanisms, which consist of the preceding causes of a phenomenon-to-be-explained, and constitutive mechanisms, which underlie or constitute a phenomenon (Salmon 1984; Craver 2007a). While the notion of causation is extensively discussed in philosophy of science as well as metaphysics, the way in which mechanisms “underlie” phenomena remains unclear (for analyses of this notion see Craver 2007a, 2007b; Harbecke 2010; Kistler 2010; Couch 2011; Fagan 2012, Kaiser and Krickel under review). In this paper, I will present two different general views on constitutive mechanisms, the flat and the dimensioned view of constitutive mechanisms. I will argue that the flat view is problematic in ways in which the dimensioned view is not. More specifically, this paper proceeds as follows: in Section 2, I will present the general idea behind the notion of a constitutive mechanism. In doing so I will explicate the central characteristics of the relation involved (“mechanistic constitution”) and of the relata of this relation (the mechanism and the phenomenon). I will argue that there are two different ways of interpreting the general idea of a constitutive mechanism. In Section 3, I will introduce the first way of interpreting the general idea, which I will call the flat view. Most authors, for example Craver (2007a), seem to endorse this view. In Section 3, I will present four problems for the flat view. In Section 4, I will introduce an alternative view of constitutive mechanisms, which I will call the dimensioned view. I will argue that this view avoids the problems that arise for the flat view.

Design and variation in synthetic biology**TERO IJÄS** (University of Helsinki, Finland)

Synthetic biology is a novel biological research field which aims to construct artificial biological components and systems by applying engineering-inspired design methods and principles in biotechnological research. This paper aims to clarify the conceptual questions of different design approaches in synthetic biology and the role of variation in these stances. According to rational design approach, synthetic biology should aim to decrease biological complexity and create well-defined standardized synthetic components and devices. Ideally, rational design aims to generate a library of characterized components and modules that can be assembled to more complex devices with predictable outcomes. In turn, evolutionary approach uses “semi-rational” design methods like “directed evolution” to tune or explore device functionality. These methods induce variation and perturbations with unknown impacts to target devices (e.g. gene circuit) to generate a library of mutants that could be screened for desired phenotypes. Both rational design and evolutionary approaches are treated as complimentary rather than opposing methods in synthetic biologists’ toolbox. However, in philosophical and methodological literature these approaches are seen to take different views of biological variation and natural

evolution. For rational design, natural evolution is considered as a destructive force that leads to a loss of function, and therefore random variation is seen as something to be suppressed. On the other hand, evolutionary methods consider biological variation to be an important part of biological function and development. In this paper, I will give a closer analysis of role of variation in synthetic biology’s design approaches. I distinguish between different types of random variations and fluctuations, like mutational and functional variation, or cellular noise. Furthermore, I analyze how these different types of variation relate to system design and engineering in synthetic biology.

Reconstructing concepts: A new approach to the problem of referential stability**CORINNE BLOCH** (Marquette University, United States)

Debates between realists and non-realists have often centered on the question of referential stability throughout theoretical shifts. One obstacle to settlement of the debate has been the difficulty of differentiating between cases of referential change and cases in which theoretical changes have taken place alongside referential stability. If we acknowledge that, throughout the history of science, some theoretical changes have resulted in referential change, yet we wish to avoid the implication that any change in theory must result in a change in a concept’s referents, then we must provide criteria for distinguishing the reference-grounding elements from additional theoretical commitments that scientists hold about the referents of the concept. I address this challenge, and propose a solution through analysis of the concept “synapse” throughout dramatic theoretical shifts with respect to the function and structure of synapses. I argue that reference across different theories can be established through the reconstruction of the conceptual hierarchy (i.e., the relations of generality and inclusion between the categories) within each theoretical framework. This reconstruction, I suggest, can be achieved by analysis of the causally fundamental distinguishing characteristics featured in scientific definitions, within their original context. I also consider the implications of this proposal for questions of incommensurability.

INDIVIDUAL PAPERS

ETHICS, EXPERIMENT AND CONFIRMATION IN ENVIRONMENTAL STUDIES**Generalizing and confirming multi-proxy reconstructions: A case study in data-laden simulations, uncertainty, and methodology****KIMBERLY BRUMBLE** (Indiana University Bloomington, United States)

Recently, philosophers have debated whether simulations present novel challenges for the philosophy of science and, in particular, for replication. Ensuring that a simulation replicates its target system requires the ability to observe each one independently. However, a class of simulations exists that cannot be evaluated independently from the target system because the simulations themselves provide the only means of access to

DS M220

15:30 – 17:00

the target system. Simulations based on paleoclimate proxy data are one such case. Paleoclimate proxies are biological and geological phenomena such as ancient tree rings, ice bores containing pollen records, sedimentary deposits, and coral reef growth patterns. Data are collected from these natural instruments and used to study the past states and behavior of historically remote ecological and geological systems such as regional and global climate patterns (e.g., precipitation averages and temperature patterns) as well as ecological systems such as forest density and composition. The historical remoteness of the target system and the reliance on proxy data make paleoclimate reconstructions the only means to observe these past systems and conditions. Additionally, proxy data suites require a considerable amount of data handling and adopt considerable uncertainty from multiple aspects of the reconstruction process. These aspects mean that replication attempts of individual reconstructions can only check methods for errors and thus cannot lead to any strong inferences about the target system. Rather than appealing to replications for generalization of results, paleoclimate reconstructions are typically evaluated for robustness across sufficiently different suites of proxy data and statistical methods. While similar kinds of methodological challenges may exist in using more traditional proximate systems, the degree to which data-laden constructions like paleoclimate reconstructions must rely on inferences across sufficiently different reconstructions make them methodologically novel.

A duty to cognitively enhance animals

YASHA ROHWER (Oregon Institute of Technology, United States)

In this paper I argue that sometimes humans have a duty to cognitively enhance other animals or at least research the technology to do so. In this paper I will use as a case study a particular set of animals: smaller Australian marsupials. Many of these animals were nearly driven to extinction after the introduction of the fox and the domestic cat to the continent of Australia. Ecologists conjecture that these marsupials do not have the behavioral flexibility to cope with these novel predators. Humans have wronged these animals in the past and are still doing so, and many argue that we can have duties of restitution or restoration to nonhuman animals and other species, which have been wronged (e.g. Taylor 1986, Wenz 1988). Traditional means of conservation simply cannot fulfill our duties to these animals; therefore, there is a potential duty to cognitively enhance them.

The very idea of a natural laboratory: A philosophical assessment

STEPHEN FRIESEN (Indiana University Bloomington, United States)

There are special places on earth that command public and scientific interest; places such as Yellowstone National Park and Galápagos National Park. Such places are frequently referred to as natural laboratories, in a variety of different contexts including scholarly writing. This ascription is rarely explained or defended. The purpose of my presentation is to bring this idea under critical examination: to understand whether and how philosophical sense can be made of this notion of a natural laboratory, and what implications or consequences follow from such an ascription. The very concept of a natural laboratory is deeply problematic insofar as it con-

joins two contexts, or ideas, that are usually juxtaposed by scientists and philosophers of science: nature, and the natural processes we wish to understand, and the laboratory; an artificial, highly controlled environment in which we hope to better understand nature. In ecology, especially, there is a perennial concern about whether the results of highly controlled laboratory experiments can be generalized “in nature” or in natural systems. From the standpoint of experimentation, then, there is an intrinsic problem with the very idea of a natural laboratory. What does the metaphor of the natural laboratory signify, other than the scientific and educational value of some place, such as Yellowstone National Park, and the Park Service’s commitment to science-based decision making? Is it largely rhetorical, functioning like a grant-writing trope, or a normative assertion about jurisdictional power/reform? Is it a substantive description of a special place that provides information about causal, ecological structure in these domains? My paper explores these questions and offers perspectives for moving forward with the idea of the natural laboratory.

DS M240

15:30 – 17:00

INDIVIDUAL PAPERS

EVOLUTIONARY EXPLANATIONS: TREE DIAGRAMS, EVO-DEVO AND PLURALISM

Neo-Darwinism and evo-devo: An argument for theoretical pluralism in evolutionary biology

LINDSAY CRAIG** (Temple University, United States)

There is an ongoing debate over the relationship between so-called neo-Darwinism and evolutionary developmental biology (evo-devo) that is motivated in part by the possibility of a theoretical synthesis of the two (e.g., Amundson 2005; Brigandt and Love 2010; Laubichler 2010; Minelli 2010; Pigliucci and Müller 2010). Through analysis of the terms and arguments employed in this debate, I argue that an alternative line of argument has been missed. Specifically, I use the terms of this debate to argue that a relative significance issue (Beatty 1995, 1997) exists and reflects a theoretical pluralism that is likely to remain.

Darwin’s tree diagram and its relation to his argumentative strategy and the doctrine of chance

JUAN L. BOUZAT (Bowling Green State University, United States)

Since the publication of the *Origin of Species*, there have been numerous debates about the specific nature of what Darwin called “My theory” and its relation to Special Creation as the main alternative explanation for the diversity of life. On the assumption that Darwin’s Diagram of Divergence of Taxa represents a conceptual model of his theory, illustrating the causal efficacy of natural selection in producing well-defined varieties and ultimately species, I review Darwin’s argumentative strategy and scientific methodology. Although Darwin claimed that his research followed “true Baconian [inductive] principles,” he emphasized the importance of making observations in relation to supporting or rejecting particular ideas (hypotheses), what we now consider as the core element of the hypothetico-deductive method. I argue that the original representation of Darwin’s Tree Diagram in his “Big

Species Book" demonstrates that Darwin followed a hypothetico-deductive strategy, framing his theory as an alternative to the doctrine of chance rather than Special Creation. Darwin's allusion to Special Creation in the *Origin of Species* may be in part related to concerns regarding the reception of his theory by the Victorian society rather than to his argumentative strategy, since he assigned no explanatory power to the idea of Special Creation.

What evolutionary explanations can't do

SUBRENA SMITH (University of New Hampshire, United States)

Evolutionary theory is taken by some to provide the explanatory platform upon which accounts of biological systems rest. If nothing in biology makes sense except in light of evolution, then explanations about organisms need to be consistent with or be framed in evolutionary terms. The idea is that the theory sets the options for what one can say about organisms. One can understand the theoretical and intellectual impulse for this idea, but it has been overextended. Evolutionary theory and explanations of biological phenomena framed in evolutionary terms are general-purpose origin accounts: they tell us (when they do) that traits of organisms and varieties of organisms came about through blind unintentional organic physical processes. That is all. Such explanations are not concerned with particular mechanisms (selection is not a mechanism in this sense). In this paper, I will argue that evolutionary explanations are unable to deliver on their promises of being informative. Such explanations can tell us no more than that features of organisms are the result of blind processes that produce certain effects—selection (although in some cases the questions are about whether a trait evolved or whether it is the result of non-evolutionary biological processes). My view is that important questions about features of organisms require proximal treatments, since knowing that a certain trait has a function (that it has historically performed that function) does not also show what causal factors made that function possible. I am therefore claiming that evolutionary explanations are often not informative and that the appearance of content in evolutionary explanations arises from the difficulty of keeping separate the distinction between functional explanations and mechanistic ones. This kind of fudging is especially salient in attempts to offer evolutionary accounts of human social behavior.

INDIVIDUAL PAPERS

STRATEGIES AND LIMITS OF MODELS AND THEORIES IN BIOLOGY

Evolutionary models in a post-theory-centric philosophy of cancer biology

MATTHEW SLAYTON (University of Chicago, United States)

This paper explores evolution as a model in cancer biology. Cancer evolution, which has received increasing attention in the field, considers tumors to be a population of rapidly mutating cells that compete for space and resources. Lineages that acquire increasingly malignant mutations are successful in the environment of the human

body. This process gives rise to tumor growth and progression. Evolution is an unusually theoretical approach in a molecularly-oriented science, and has begun to see attention in the philosophical literature. I will address Germain's 2013 argument that cancer is, at best, a trivially evolutionary phenomenon that is better explained by cellular mechanisms. Following Fagan, I take issue with the idea that a theory or model can be isolated from its use in experimental science and be manipulated by philosophical methods alone. Germain evaluates cancer evolution in terms of its explanatory capacity. I will argue that his criteria are too narrow to capture how models operate within an interdisciplinary, experimental, and applied field like cancer biology. I will offer an alternative view of models in the biomedical sciences by examining evolution's multiple functions in cancer biology (whether applied explicitly in quantitative modeling or in unifying conceptual statements, or implicitly when used as a metaphor.) A biomedical science may use a model that is not uniformly and consistently applied, and this does not affect the value of this model in producing knowledge for that discipline. I close with an argument for why we should not dismiss the role of evolution in cancer biology simply because it fails to satisfy one set of standards elaborated by philosophers: there is good reason to expect that cancer evolution will grow in scope and sophistication, and become a theoretical and investigative foundation for the field.

Affective management strategies: Emotion, care and control in the construction of beagles as biological models

EVA GIRAUD (Keele University, United Kingdom); **GREGORY HOLLIN** (University of Nottingham, United Kingdom)

Through an analysis of the consolidation of beagles as the standard experimental dog, this paper contributes to broader debates about the role of affective labour within the biosciences. Focusing on the first experimental beagle colony (at University of California, Davis, 1951-1986), the paper explores the role of affective human-dog relations in standardizing beagles as biological models. Throughout the first half of the twentieth century dogs were increasingly used in laboratory work due to their amenable temperament (Lederer, 1992) and the ease with which their body language could be "read" (Degeling, 2008). Beagles, more specifically, became the breed of choice due to their "merry disposition" and "gay personality" (Anderson, 1970). In addition to breed-personality being part of the rationale for selecting beagles, the management of canine emotion – via care-taking practices and living arrangements – was seen to be not just of ethical but also epistemic importance. Stress-free animals were perceived as vital in ensuring consistency within both physiological (Dror, 1999) and psychological (Kirk, 2004) research. This paper explores the processes through which affect was regulated during the consolidation of beagles as standard laboratory dogs and, in so doing, complicates two specific strands of theoretical work. Beagles, firstly, problematize work that has valorised the epistemic and ethical role of emotion within the biosciences, illustrating the vulnerability of affect to instrumentalization. Beagle research also contributes to ethical debates about tensions between the push to standardize animals, and the need to foster affective relations with individual animals in order to manage their emotions effectively. These strands of argument are then synthesised within the broader claim that a historical examination of laboratory animals is important in contextualising contemporary ethical debates about affective human-animal relations within the biosciences.

DS M320

15:30–17:00

DS M340

15:30 – 17:00

INDIVIDUAL PAPERS

NEGATIVE RESULTS, MEDICAL PROGRESS AND ADVERSE EVENTS: INTERDISCIPLINARY INSIGHTS ON BIOMEDICINE**Negative results in biomedicine: The biomedical community's response to the Paxil scandal****LAURA SEGER** (Indiana University Bloomington, United States)

The label “negative” is often applied to experimental results that do not support an investigator’s initial hypothesis – although any undesired result may be termed “negative” – and these results rarely appear in published form outside the field of biomedicine. Biomedical scientists now recognize more than anyone else the importance of negative results because they are driven not just by the epistemic goal to get at the truth. As a community of inquirers according to Helen Longino’s social epistemology, they also share the practical value of preventing harm to patients, and there’s a growing awareness in biomedicine of a direct relationship between the nonpublication of negative results and potential harm. This awareness is due, in part, to community-wide reaction to scandals involving publication bias against, or the outright suppression of, negative biomedical results. In this paper, I describe how certain aspects of the physician-biomedical industry dynamic changed following the Paxil scandal of the early 2000s. Most importantly, major organizations (e.g. U.S. Food & Drug Administration, American Medical Association, European Medicines Agency, World Health Organization, World Medical Association, and the International Committee of Medical Journal Editors) began requiring public registration of all clinical trials, trial results, and adverse events once it came to light that Paxil trial results demonstrating both inefficacy and an increased risk of suicide in adolescents had been purposely suppressed. As a result of this and other similar scandals, which exposed physicians and the biomedical industry to new levels of financial and criminal risk, physicians no longer trust the industry to be honest about the true effect of pharmaceuticals on patients, thus physicians and clinical researchers are beginning to demand access to all results – including negative results – to properly evaluate their prescribed treatments.

The ideal of scientific progress and the DSM**STEEVES DEMAZEUX** (Université Bordeaux Montaigne, France)

In this presentation, I explore the ways in which the *Diagnostic and Statistical Manual of Mental Disorders* has been informed by the ideal of scientific progress since the 1980s. My aim is not to evaluate the arguments for or against the scientific nature of the DSM as they have been brought forward and discussed in the public debate for purely promotional or polemical purposes. It is rather to highlight the kind of scientific optimism that has been a driving force in the recent history of the DSM. I argue that while the nature of the scientific ideal of the DSM through its three last editions has remained the same, its effects and its rationale have dramatically changed. Whereas scientific progress required that the DSM-III firmly espouse what I call here a “permanent innovation principle”, it would later paradoxically motivate, in the DSM-IV and especially in the DSM-5, an opposed principle that I call the principle of “prudential conservatism”. I conclude that, while in the past decades

the DSM has made an important effort to improve the scientific quality of its revision process, development from the DSM-III to the DSM-5 can hardly be said to have been scientifically progressive.

Suspected adverse events after immunisation, subsequent public health policy process and risk perception : The case of hepatitis B in France and MMR in UK (1998-2010)**ANNICK OPINEL** (Institut Pasteur, France); **HELEN BEDFORD** (University College London, United Kingdom)

This paper focuses on the development of public health policy following public concerns over suspected adverse events associated with immunisation. Using the examples of hepatitis B vaccine in France and combined measles, mumps and rubella (MMR) vaccine in UK (1998-2010), we compare two events occurring in 1998. In France following several case reports that hepatitis B vaccination may be linked to new cases or relapse of multiple sclerosis (MS), the French Ministry of Health temporarily suspended the school-based adolescent hepatitis B vaccine programme. In UK following publication of a now discredited article in a medical journal which was interpreted as showing a link between MMR vaccine and the development of autism and bowel disorders (Wakefield et al, 1998), the vaccine continued to be offered as part of the routine programme. In comparing the French and British approach to these potential threats to the immunisation programmes we highlight on the one hand how national behaviours differ and the link between public health decision-making and, on the other hand, differences in national risks perception.

DS M440

15:30 – 17:00

INDIVIDUAL PAPERS

MAKING BIOLOGY PUBLIC AND MAKING PUBLIC BIOLOGY**Speaking on “large subjects”: Philosophy, democracy, and the American biologist as public intellectual in the early 20th century****JUDY JOHNS SCHLOEGEL** (Independent Scholar, United States)

This paper examines the historical circumstances contributing to the emergence of American biologists William Emerson Ritter (1856-1944) and Herbert Spencer Jennings (1868-1947) as public intellectuals in the early decades of the twentieth century. While Ritter’s career at the University of California was significantly shaped by his close relationship with the wealthy newspaper publisher, E. W. Scripps, and his sister, Ellen Browning Scripps, Jennings’ east-coast laboratory career was largely informed by more conventional academic contacts, including early philosophical study with John Dewey and considerable subsequent contact with pragmatists and pragmatism. Receiving their PhDs under E. L. Mark at Harvard’s Museum of Comparative Zoology in 1893 and 1896, respectively, Ritter and Jennings were associated by an extensive network of Mark’s students who collectively had far-reaching impact on the development of biological research in the United States in the late nineteenth and early twentieth centuries. Like many in Mark’s network, Jennings and Ritter were close colleagues: Jennings served as an advisor to Ritter in plans to expand his newly established Scripps Institu-

tion; and while they were among each other's sharpest critics, they encouraged each other in their respective philosophical and public discourse. At the same time, both developed their philosophical postures and public persona from notably different institutional and professional environments. This paper examines the institutional, professional, political, and cultural conditions that promoted Ritter's and Jennings' philosophical and public discourse on biology and society during the first three decades of the twentieth century. Both leveraged the capaciousness of philosophical and public discourse in a common effort to defend and promulgate democratic principles against countervailing movements in biological science and the public sphere.

François Magendie: From dogmatic empiricism to the practice of experimental reasoning

JOSÉ LUIS GONZÁLEZ RECIO (Universidad Complutense de Madrid, Spain); **RUTH GARCÍA** (Universidad Complutense de Madrid, Spain)

The historiographical studies focused on French nineteenth-century physiology have eventually enshrined the thesis that the need to resort to hypotheses was assumed and proclaimed for the first time within the works and scientific practice of Claude Bernard (1813-1888). His teacher, François Magendie (1783-1855), is presented as a figure that fights against vitalism and that, devoted to an absolute empiricism, only admits the bare facts as constitutive elements of science. For the mature physiology he wanted to build, he discarded -it is often said- any support based on the formulation of hypotheses. According to Bernard, while he worked with him, he heard every day his mentor's impassioned justification of a militant and radical empiricism. Magendie -Bernard claims- advocated and practiced an uncompromising empiricism, opposed to any theoretical systematization whether it was the prompter or the result of observation. He admitted generalizations -as long as they were not premature- from what he called materials collected within experience, but rejected that ideas or hypotheses could lead the scientific path. The facts should speak for themselves, without being associated to any preconceived notion, as the truth would eventually show itself in them. Although this image of Magendie is widely shared -and was even prompted by some of his statements- this paper aims to show precisely that it is an image that does not correspond to reality. Magendie did know the crucial role of hypotheses within physiological research. Not only that: he used them extensively in his scientific work and in his activity as a researcher committed to the implementation of experimental physiology. And what is more, he did this using those hypotheses with the same goals that Bernard later reserved for them: to guide observation, to serve as a basis for the explanation of the facts and to be susceptible of verification. As we shall see, you only need to read Magendie's texts and to examine his scientific activity to confirm this beyond any doubt. Experimental physiology, equipped with all the necessary methodological resources, began its journey in nineteenth century France through the works carried out by François Magendie.

Hatching standards of Gallus gallus: Creating pathogen-free birds for research

MIGUEL LOPEZ-PALETA (Universidad Nacional Autónoma de México, Mexico)

Gallus gallus (domestic fowl), a well-known character in biological research, is not standardized in the same way than other model organisms used in experimental biology. Instead of being part of a standardized strain created by researchers, and distributed by centralized institutions, chickens used in experimental biology are commonly obtained from different sources: from local farms to Specific-Pathogen Free birds (SPF) specialized companies. In this paper, I claim Gallus gallus standardization has been developed by diverse groups of people which were not specifically interested in biomedical research and which had different aims when they standardized chicken. I highlight a particular context where this standardization had occurred: immunology (particularly that related to avian diseases). This field gave rise to a particular standardized group of birds (SPF) which became commercialized by companies established by agricultural researchers/entrepreneurs. Although these birds became frequently used in fields such as developmental biology, this was not the only context where chicken was standardized. SPF birds were developed using a previously developed chicken breed (i.e. White Leghorn) as a basis. This breed was established by fanciers and commercial breeders at the beginning of the 20th century, and it was later employed for conducting experiments in biology laboratories. Consequently, the chickens nowadays used in experimental biology were standardized diversely and they have different characteristics insofar as they belong to different breeds and varieties. The Gallus gallus model provides, thus, a door to discuss scientific and model organisms' standardization from a historical, highly contextual perspective.

DS M460

15:30 - 17:00

INDIVIDUAL PAPERS

EXPERIMENTATION, ETHICS AND SOCIAL ENGINEERING

Reflections on harm/benefit analysis in research involving nonhuman animal subjects: Can sympathy and dissent guide a refinement of Bateson's Cube?

GILLIAN CROZIER (Laurentian University, Canada); **GILLY GRIFFIN** (Canadian Council on Animal Care, Canada)

We advocate refining Bateson's Cube – a visual heuristic device designed to help determine whether particular scientific research projects ought to proceed, depending on the importance of the research, the likelihood of medical benefits, and the suffering of animal test subjects. Specifically, we introduce a fourth dimension – a plane within the cube representing the “degree of valid dissent” of the animal research subject. One fulcrum of this plane is determined by “sympathy,” which we ground in the position that empathy, compassion, and caring ought to underwrite any ethical evaluation of research methods involving live animals; sympathy is required on behalf of the researcher or technician to identify the preferences of particular animals, including preferences to not participate. The other fulcrum is determined by “moral status”, which we ground in the position that the moral status of an animal subject must be based on the best scientific knowledge about the species' sentience,

according to what is known about its cognitive, affective, and social traits. Thus, researchers working with animals at the high end of the moral status scale might need to respect the potential preference these animals may have to refuse to participate in an experiment. Together, “sympathy” and “moral status” provide an estimate of the “degree of valid dissent” – a plane within a Bateson’s Cube representing the threshold or boundary condition separating experiments that, on the one side should be endorsed, and on the other side should be prohibited. Taking into account the degree of valid dissent would involve pushing that plane to be closer to one of the “extreme case” vertices or the other. Insofar as an in-principle, long-term goal for animal research would be to eliminate harms to animals, the flexibility of this four-dimensional cube permits the scientific community to iterate towards that ideal.

From social engineering to bioethics: Human genetics and society in Denmark and Germany in the 2nd half of the 20th century

DIRK THOMASCHKE (Carl von Ossietzky Universität Oldenburg, Germany)

For most European countries, the cultural history of human genetics between the end of the Second World War and the present has hardly been examined in historical studies so far. The proposed paper compares the development of human genetics and eugenics in two European countries, Denmark and Germany, in a discourse analysis from c. 1950 to 1990. The focus lies on the changing relations of the field to society and politics and on the correspondingly changing subjectivity of human genetics experts. The paper draws on partly unexplored archival sources from Germany and Denmark: personal papers of leading scholars and research institutes in the field of human genetics as well as documents from research trusts and governmental agencies. In the 1950s and 1960s, human genetic experts in Germany and Denmark initiated various efforts to “follow and control” the “rate of mutations” in human populations. The Danish national registry on genetic diseases in Copenhagen for instance was a well known institution for that purpose. These efforts were fueled by the anxiety of an irreparable rise of the rate of mutations due to nuclear irradiation during the 1950s and an unknown amount of potentially mutagenic chemical substances in the human environment during the 1960s. This paradigm shifted significantly in the 1970s in both countries. The freedom of the individual to prevent hereditary diseases of its own offspring became the central concept accompanying the establishment of prenatal diagnosis in Germany and Denmark. At the same time, genetic diagnostics turned into the main source of research material for scientists. The relationship of human genetics experts to society was re-modeled according to a pattern of individual demand and public supply. An international competition about the comprehensive provision of “medical products” arose. In the late 1970s a new phase set in. Human genetics research gained hitherto unknown social, ethical and psychological dimensions. With the expansion of molecular genetics and genetic engineering in the background the Danish and German society seemed to be increasingly burdened by the genetic knowledge offered to it. New types of expertise like bioethics came into existence in both countries in the 1980s.

From informed to informing materials: Drugs as tools for exploring cancer mechanisms and pathways

ETIENNE VIGNOLA-GAGNÉ (McGill University, Canada); **ALBERTO CAMBROSIO** (McGill University, Canada);

PETER KEATING (Université du Québec à Montréal, Canada)

Our group has previously argued that anticancer drugs are “informed material”, i.e. that they undergo an informational enrichment process situating them in a dense relational web of qualifications and measurements. Such informational enrichment has typically been pursued through clinical experiments, including clinical trials, that articulate histologically defined tumors and drugs in a matrix of correlations. Recently, genomics platforms – in particular: next generation sequencing – have been used to characterize individual patients’ tumors on the basis of their mutational landscapes. We argue that, as part of this new approach, drugs targeting specific mutations, instead of being merely the object of informational enrichment have become tools for informing their targets or, in other words, tools to explore cancer pathways and mechanisms. This evolution is exemplified, for instance, by the establishment of centers for “mechanistic-based therapy” within leading cancer research institutions. While numerous studies in the philosophy and history of biology have called attention to the heuristic relevance and experimental deployment of mechanisms, few have explored how mechanisms are investigated and deployed in the clinic, which has today arguably become a central site of knowledge production in a field such as oncology. This presentation will track some of the reconfigurations taking place in the informational enrichment of anticancer drugs in the post-genomic era, with a focus on their transformation from informed to informing material, i.e. as instruments for the generation of new biological, pathological, and therapeutic insights into the modalities underlying the etiology and evolution of cancer.

DS R510

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

IS THE BRAIN A PREDICTION MACHINE? EXPLORING THE BAYESIAN REVOLUTION IN NEUROSCIENCE

Organizer(s): **MADELEINE RANSOM** (University of British Columbia, Canada)

While philosophers of science and epistemologists are well acquainted with Bayesian methods of belief updating, there is a new Bayesian revolution sweeping neuroscience and perceptual psychology. First proposed by Helmholtz, predictive coding is the view that the human brain is fundamentally a hypothesis generator. On this view, the processes by which the brain tests its self-generated hypotheses against sensory evidence are seen as conforming to a hierarchical Bayesian operation; each level of the hierarchy involves a hypothesis space, with higher levels entertaining hypotheses about more complex and slower regularities as compared to the lower levels. The higher-level hypothesis spaces serve to generate and constrain the lower-level hypothesis spaces, thus enabling the lower-levels to predict the evidence. When there is a mismatch between the predicted and actual evidence, a prediction error is produced and is relayed up the hierarchy, where it is used to revise the hypothesis. Through the iterative interaction between top-down signals (which encode predictions) and

bottom-up signals (which encode prediction error) the generative models that can predict the evidence most accurately are selected. Given the crucial role of sensory evidence in supervising the hypothesis testing process, it is no surprise that the view has garnered the most significant empirical support as a theory of perception. Nonetheless, increasing numbers of neuroscientists are also adopting the predictive coding framework in some capacity in order to elucidate attention, decision making, dreaming, hallucinations, felt agency, interoception and the emotions. Not since dynamical systems theory has there been a theoretical framework as popular. However, it is unclear that the success of the predictive coding theory of perception will extend to these other areas. This session will critically examine and explore the prospects of predictive coding theories of attention, dreaming and the emotions.

Three problems for the predictive coding theory of attention

MADELEINE RANSOM (University of British Columbia, Canada)

Attention has been a central topic of study in neuroscience and psychology due to its pivotal role in guiding perception and thought. It has also recently garnered significant interest in philosophy due in part to the close link between attention and consciousness and the lack of a coherent theory of attention. While predictive coding has most prominently offered a theory of perception, the Bayesian framework also promises to deliver a comprehensive theory of attention that falls out of the perceptual theory without the need for positing additional machinery. On this account, attention is optimization of the precision of prediction errors. In perceptual inference, prediction errors are measurements of the difference between predicted and actual sensory data. Expected precisions are a measure of how reliable, or precise, we expect the prediction error signal to be in a given context: how likely is it in a given situation that the incongruent data constitutes legitimate prediction error as opposed to noise? Optimizing expected precisions is the process of guiding perceptual inference by directing processing resources towards the prediction errors with the higher expected precisions – we attend to what is expected to be the most informative, and use this information to preferentially revise our perceptual hypotheses. I argue here that this theory of attention faces significant challenges on three counts. First, while the theory may provide a successful account of endogenous spatial attention, it fails to model feature-based attention – a central aspect of attention that any theory must explain. Second, it does not accommodate non-perceptual forms of attention such as attention to one's thoughts. Third, it fails to accommodate the influence of affectively salient objects or high cost situations in guiding and capturing attention.

Evaluating the predictive coding model of dreaming

SINA FAZELPOUR (University of British Columbia, Canada)

The predictive coding framework promises the potential of a grand unifying theory in which any cognitive function can be understood on the basis of the brain's overarching function of hypothesis testing, carried out at various levels of the cortical hierarchy by a single kind of computational process with the shape of a Bayesian

inferential operation. Within the hierarchically structured hypothesis space, the brain's generative model makes predictions whose probabilities are updated in proportion to how well they explain away the current sensory evidence. While the framework has proved successful in dealing with cognitive functions constrained by sensory input, it is difficult to see how it can be extended to prominent cognitive phenomena, such as dreaming, that proceed in a largely decoupled fashion from environmental stimuli, given the crucial supervisory role played by sensory input within the framework. Nonetheless, Friston and Hobson have recently proposed a predictive coding model of dreaming has been assigned the functional role of optimizing the statistical efficiency of the brain's generative model by minimizing the model's redundancy and complexity. Furthermore, the function of complexity minimization is carried out by Bayesian inferential processes aimed at explaining unpredicted oculomotor input the only sort of input available to the system during REM sleep. My aim here is to critically examine three foundational issues facing the model, with a view towards developing constructive guidelines for future research. First, at the phenomenological level, what empirically testable implications does this functional role, assuming its correctness, have for the sort of content within a dream episode? Second, with regards to the processing level, are Bayesian inferential processes in general suited to the task of reducing a model's complexity? Third, is the Bayesian operation in light of oculomotor input in particular capable of delivering the assigned functional role?

Predicting emotions, emotional predicting

MARK MILLER (University of Edinburgh, United Kingdom)

While predictive coding frameworks have primarily been applied to exteroceptive signals and the ways in which we model the outside world, there is a growing interest in how same functional models may be used to describe the processing of interoceptive signals. Anil Seth (2013) has recently proposed a predictive coding theory of emotion. According to the model cascading top-down predictions about the source of interoceptive signals counterflow with bottom-up interoceptive prediction errors. The integration of the various predictive representations results in the felt aspect of an emotion. The model is intended to extend traditional cognitive appraisal theories of emotion by filling out the neurocomputational mechanisms underlying the interaction between the affective (eg. neural and physiological arousal) and appraisal (eg. memories, evaluations, predictions, etc.) elements commonly considered to make up an emotional experiences (Schachter & Singer, 1962). I will argue that such an account of emotion ends up being embodied in ways that refute the cognitivist assumptions of existing appraisal theories. My argument will be based on affective neuroscience descriptions of the anterior insula (AI). Seth's account of processing in the AI lends substantial support to recent network models of the brain (Pessoa 2014) that aim at dissolving the boundaries between emotion and cognition, and also between notions of a thinking brain and a feeling body. The aim of the paper will be to highlight the ways in which predictive coding can contribute to live debates in emotion theory, as well as suggest how affective neuroscience can in turn facilitate a better understand predictive coding theories of mind. The hope is to contribute support for a theoretical framework that bridges predictive coding and embodied cognitive science.

DS R515

15:30 – 17:00

ORGANIZED SESSION / DIVERSE FORMAT

STUDIES IN THE HISTORY OF THE MODERN SYNTHESIS: MOLECULARIZATION AND UNIFICATION

Organizer(s): **DAVID DEPEW** (University of Iowa, United States); **RICHARD BURIAN** (Virginia Tech Philosophy and Science Studies (Emeritus), United States)

Participant(s):

VASSILIKI BETTY Smocovitis (University of Florida, United States)**MICHEL MORANGE** (École Normale Supérieure, Centre Cavaillès, France)**GUNTER WAGNER** (Yale University, United States)**JEAN GAYON** (IHPST/ Université Paris 1 Panthéon-Sorbonne, France)

This session deals with an important issue within a larger research program on the history of the Evolutionary Synthesis (ES) in which the participants and about twenty others are engaged. The issue is the effect of molecularization on the ideal of synthesis, integration, and unification imparted to the ES by its founders. By the 1950s the ES achieved a dominant position in evolutionary inquiry by integrating systematics, speciation, and paleontology. In a forthcoming issue of *Journal of the History of Biology*, members of our group examine extensions and revisions of the ES resulting from its interactions with a larger array of disciplines, e.g., ecology and ethology. Molecular genetic tools and techniques played a major role in these extensions. The session asks whether and how the overtly reductionist aims of early molecular genetics affected and remolded the ES's aspirations to achieve the full unification of biology. Some ES adherents found reductionist ideals attractive as a way of casting evolutionary biology as mature science. But most of its founders disagreed; some sought help from philosophers to blunt reductionist claims in order to protect and consolidate ES's gains. What conceptions of unity, we ask, emerged to support this stance? Were they theory oriented even if not reductionist, or primarily grounded in experimental practices and techniques shared between laboratories and other sites of inquiry? Paradoxes emerge when we follow this topic into the present. Evolutionary biology has successfully integrated molecular techniques and gene-sequencing data. But even though molecular findings have overturned some key commitments of the early synthesis its practitioners still resist reduction and retain the stress on phenotypes. At the same time, genetic reductionism has been undermined by the very molecular findings that this aspiration stimulated, including those bearing on developmental genetics, epigenetics, and gene networks.

DS R520

15:30 – 17:00

ORGANIZED SESSION / DIVERSE FORMAT

“SURVIVING EUGENICS” (2015). DOCUMENTARY FILM SCREENING AND DISCUSSION

Organizer(s): **ROBERT A. WILSON** (University of Alberta, Canada)

In 1996, Leilani Muir won a landmark legal case against the Canadian province of Alberta for wrongful sterilization and confinement at the Provincial Training School in Red Deer, an institution for “mental defectives”. *Surviving Eugenics* is a documentary about the history and ongoing significance of eugenics in Canada. Anchored by survivor narratives from Leilani and four other eugenics survivors from Alberta, and drawing on expert testimony from those involved in the case, *Surviving Eugenics* provides a unique insiders' view of eugenic history. In doing so, the film raises broader questions about disability, human variation, and contemporary North American society.

This recently released, 44-minute documentary film is designed for classroom use in both high school and university in a wide variety of courses, and covers topics at the intersection of the history, philosophy, and social studies of biology. It was developed over the past two years as part of the *Living Archives on Eugenics in Western Canada* project (eugenicsarchive.ca). This screening will provide an opportunity to discuss both eugenics and the socially-engaged approach to the teaching the history and philosophy of biology and its contemporary significance. Discussion will be led by one of the film's co-directors and executive producer.

17:00 – 17:30

COFFEE BREAK

17:30 – 19:00

PLENARY SESSION – W. FORD DOOLITTLE | Marie-Gérin-Lajoie auditorium

19:00 – 20:30

PUB-NIGHT COCKTAIL AND MONTRÉAL BEST POSTER PRIZE | “Le Département” bar, room A-M640

THURSDAY JULY 9

DS 1520

09:00 – 10:30

INDIVIDUAL PAPERS

19TH- AND 20TH-CENTURY PERSPECTIVES ON CELL THEORY

[Darwin's reasoner: Chauncey Wright as philosopher of biology](#)

TREVOR PEARCE (University of North Carolina at Charlotte, United States)

In this paper I demonstrate that Chauncey Wright—an early pragmatist and friend of Peirce and James, whom Darwin deployed as “a sound reasoner” in his debate with St. George Jackson Mivart—was a philosopher of biology *avant la lettre*. Despite a lack of training in biology, Wright deployed his mathematical and philosophical skills to great effect in a series of articles on evolution. His debate with Mivart, in particular, foreshadowed not only the “factors of evolution” controversy of the 1890s but also the discussion—resurrected by Stephen Jay Gould in the 1970s—of internal versus external causes in evolution. Although other scholars have noted these connections, they have not pursued them in any detail, since their interest has been focused on positivism, pragmatism, or the evolution of consciousness. The paper has three parts. First, I present Wright’s positivist philosophy of science, which played a key role in his debate with Mivart. Next, I describe Wright’s conversion to Darwinism, and show that he was making mathematical and philosophical arguments about the Origin of Species within months of its appearance. Finally, I argue that although Wright, in his debate with Mivart, seems at first to be defending a strong externalist or selectionist position, he is actually making the philosophical point that proposed causes of evolution must be backed up by empirical evidence, and cannot simply be postulated in the abstract. Wright was engaged in a form of reasoning that has striking parallels with that of philosophers of biology today. He did not himself present any empirical evidence, but he did outline the form such evidence would need to take to support any purportedly new account of the evolutionary process. In this era of the so-called “extended synthesis,” Wright may still have something to teach us.

[Protoplasmic structure and the end \(?\) of cell theory in the 1890s](#)

DANIEL LIU (University of Wisconsin-Madison, United States)

This paper will argue that cytology and the concept of the cell suffered a severe crisis among many biologists in the 1890s, a crisis that would precipitate biologists’ rapid and often confusing embrace of colloid chemistry in the 1910s and ’20s. To key insiders, what had seemed like a decade of fantastic progress in the 1880s gave way to radical doubts about fundamental methods in cytology, the proliferation of terminology and neologisms

in the discipline, and even the legitimacy of the word “cell” itself. This paper will examine three biologists working in the 1890s — the botanist Alfred Fischer, the protozoologist Otto Bütschli, and the physiologist William Bate Hardy — and their critiques of the staining and fixation techniques that had been widely used the decade prior. As part of their investigation into the fundamental methods of cytology, Fischer, Bütschli, and Hardy played a pivotal role in introducing artificial preparations such as gelatine and agarose as models of protoplasmic structure, bridging an ontological and epistemological gap between cell studies and the nascent discipline of colloid chemistry. Yet, rather than solve these fundamental issues, I will suggest that the controversies they generated only prolonged the crisis in cytology, until it crisis slowly dissipated through the interwar period.

Exploratory investigation in the philosophy of C.S. Peirce

NIALL ROE (University of Calgary, Canada)

C.K. Waters (2003, 2007, 2008, manuscript) has argued for the importance of exploratory investigation in scientific practice (also Burrian 1997, Elliot 2007, O'Malley 2007, Steinle 1997). This paper determines the extent to which Waters' account of exploratory reasoning is compatible with the philosophy of C.S. Peirce. It does so in two steps. First, I describe Waters' notion of exploratory investigation, focusing on determining the necessary and sufficient conditions for calling a type of inquiry exploratory. Secondly, I look to Peirce's philosophy, determining whether exploratory investigation is endorsed on his understanding of scientific practice. I conclude that Peirce's philosophy supports the sort of exploratory investigation Waters endorses. Further, this investigation clarifies a potential role of hypothesis within exploratory reasoning. Comparing Waters and Peirce is fruitful for many reasons. First, understanding Waters in Peircean terms offers further insight into investigative reasoning. Peirce's account of inquiry is hypothesis-based. This seems to run counter to a purely exploratory investigation, which emphasizes a lack of preconceived ideas in inquiring (e.g. taking apart a watch to see how it works). As such, it is not initially clear how or whether Waters' account is able to incorporate such hypothesis-based systems. This paper uses Peirce to clarify how exploratory investigation can still flourish in a hypothesis-based system of inquiry. Secondly, Waters' epistemology is pragmatic in tenor, inviting comparisons with Peircean pragmatism. And while certain agreements between the two are evident (e.g., the importance of viewing science as a working practice), there also appear to be substantial differences (e.g. Peirce's requirement that science tends towards a “final” position). Resolving these tensions helps place Waters in a historical context and helps gauge the continued relevance of Peirce in philosophy of science.

DS 1525

09:00 – 10:30

INDIVIDUAL PAPERS

EVOLUTION AND PHILOSOPHY

Popper's puzzlement over evolutionary theory

MEHMET ELGIN (Mugla Sıtkı Kocman University, Turkey)

Popper's main thesis about evolutionary theory (ET) is that although it is the most important theory without any serious competitor in its domain, it is not a mature scientific theory in that it has not yet been fully developed and articulated. Nanay (2011) argues that Popper's assessment of ET stems from his thinking that his method of trial and error-elimination and the process of natural selection (NS) are closely related. Ruse (1977) also claims that it is possible that Popper has led to his problematic views about ET in part because of his belief that his theory of growth of knowledge and the process of natural selection are closely similar. However, Ruse's main goal is to critically analyze Popper's arguments for his assessment of ET. Stamos (1996, 2007) argues that Popper reached his conclusion about the scientific status of ET on the basis of his controversial criterion of demarcation. There are dissenters, however, Hull (1999) and Settle (1996) argue that Popper was misled by writings of some evolutionary biologists and his views on ET were misunderstood by both philosophers and scientists, noting that some of the things Popper said were not acceptable. My main thesis in this talk is that at least one aspect of Popper's views on ET still deserves a serious philosophical attention. Against Nanay, Ruse and Stamos, I argue that Popper offers philosophically interesting arguments different from the ones these authors have focused on. Against Hull and Settle, I argue that Popper's focus of attention was, as he explicitly says, on the modern synthesis theory of evolution developed especially by Fisher, Haldane and Wright and that he was not misled with respect to his claim that formulation of NS based on the statistical definition of fitness (Popper's term) is a tautology despite the fact that Popper himself also says he was misled by the writings of some evolutionary biologists. To develop this thesis systematically I will provide an answer to the following two questions: 1. Why was Popper interested in ET? 2. What are the reasons that led Popper to think that ET has not fully developed and articulated scientific theory? There are three reasons why Popper was interest in ET: 1. He thought that there is a close relationship between his method of trial and error-elimination and the process of NS as Nanay (2011) rightly emphasizes. 2. He was interested in ET because of its relation to his views on historicism. 3. He was also interested in ET because he thought that ET is the only significant theory for the solution of some important philosophical problems such as the mind-body problem and freedom in a physical universe. Although I will briefly talk about these issues, my main focus will be on the second question because it is this part of Popper's writings on ET that I believe still deserves a philosophical attention. There are two reasons why Popper thought that ET has not been a fully developed and an articulated scientific theory: 1. Although ET provides in-principle causal explanation for “apparently goal-directed” complex adaptations, it has not yet provided an actual causal explanation for any single one of them. 2. Formulation of NS based on the statistical definition of fitness (Popper's term) reduces the empirical content and explanatory power of ET. Since the first problem is a consequence of the second problem, what really dissatisfied and puzzled Popper was the

mathematical turn ET took in the hands of Fisher, Haldane and Wright. The first problem led Popper to think that ET needs improvement and the second problem led Popper to think that ET “is not a testable scientific theory but a metaphysical research program”. I will argue that Popper’s argument leading to the second claim should be taken seriously by anyone who thinks that laws or the main principles of an empirical science must be empirical. I will then argue that since ET based mathematical principles produces empirical knowledge, I will argue that any views on scientific explanation and on the relationship between theoretical part and empirical part of scientific inquiry that implies that science such as ET based on mathematical principles is not possible should be taken to be given up.

An improved relational semantics of biological modalities

MAXIMILIAN HUBER (Université de Genève, Switzerland)

Biological modalities are ubiquitous in all domains of biological research and hence seem to play an important epistemic role. For example, in ecology, the competitive exclusion principle states that for a given habitat, the stable coexistence of two species occupying the same niche is biologically impossible. However, there is no systematic theory of biological modalities. This is both surprising and problematic. It is surprising because modalities have been one of the most important topics in mathematical logic in the last decades; and it is problematic because the exact truth-conditions of claims involving biological modalities remain in the dark. The aim of this paper is to remedy this situation. In a first step, I will improve upon Dennett’s (1995) relational semantics for biological possibility. These semantics are based on the Library of Mendel which is stipulated to contain 1. every logically possible genome, and 2. for each genome, a reader-constructor capable of producing the corresponding phenotype. Then, for some genome $G1$, x is biologically possible if and only if x is an instance of a genome $G2$ or a feature of $G2$ ’s phenotypic products, and $G2$ is accessible from $G1$. There are two main challenges: First, a salient interpretation of the accessibility relation must be provided since it is left undefined by Dennett. I will argue that the notion of an edit script from bioinformatics can be put to use. Second, it must be shown how the reader-constructor can be modeled and white-boxed. Here I will propose a solution in the spirit of dynamic modal logic. In a second step, I will discuss the adequacy of my improved relational semantics with respect to a range of case studies.

Disciplinology: Or what Wikipedia thinks of philosophy and the natural science

TYLER BRUNET (Dalhousie University, Canada)

Using a computational approach, we investigated the conceptual structure of disciplines from the natural sciences and philosophy. We used Wikipedia and the Stanford Encyclopedia of Philosophy as sources of pre-defined discourses, taking them to represent the collective understanding of a large community of contributing authors. We contrasted the resulting structural patterns with prevailing conceptions of the structure of academic disciplines. The hierarchy of science (HOS) model (Fanelli and Glänzel 2013), and branching tree models

were examined in greatest detail. We argue for an unrooted reticulated tree (network)—in opposition to linear and hierarchical structures—in both natural science and philosophical discourses. We constructed networks using inter-discipline distance metrics derived from extracted keywords and whole text sources. Our methods allowed network construction even between distantly related natural science fields, and showed no immediate evidence for a strong continental-analytic divide in philosophy. We used hyperlinks to construct a graph (a connection of nodes and edges), and determine the major modular groups therein, as well as to examine the global domain architecture of the reticulated tree of disciplines. Our method allowed construction of networks based on contextual information beyond direct page hyper-linkage—such as sentence structure and common syntactical features. We see this exercise in computational “folk-disciplinology” as a useful adjunct to more traditional academic, educational, and scholarly approaches to the study of human knowledge.

DS 1540

09:00 – 10:30

INDIVIDUAL PAPERS

MODELING POPULATIONS AND GAMES

Population genetics and mechanism

LUCAS MATTHEWS (University of Utah, United States)

Philosophers of biology have made a very strong case for the role of mechanistic explanation in proximate, process-oriented sciences such as neuroscience (Craver 2007) and molecular biology (Darden 2006). Because these specialized sciences appear highly amenable to mechanistic thinking, questions arise regarding the role of mechanistic explanation in other pattern-oriented domains of investigation that make no explicit appeal to mechanisms. In this paper I investigate population-genetic, statistical approaches to natural selection, with an eye for mechanistic reasoning. I use Tabery’s (2014) conceptions of “mechanism-elucidation” and “variation partitioning” approaches to demonstrate that appeal to mechanisms plays an important role in building evidence for population-genetic, natural selection explanations.

Modeling evolutionary games in populations with demographic structure

XIANGYI LI (Max Planck Institute for Evolutionary Biology, Germany); **STEFANO GIAIMO** (Max Planck Institute for Demographic Research, Germany); **ANNETTE BAUDISCH** (Max Planck Institute for Demographic Research, Germany);

ARNE TRAUlsen (Max Planck Institute for Evolutionary Biology, Germany)

Classic life history models are often based on optimization algorithms, focusing on the adaptation of survival and reproduction to the environment, while neglecting frequency dependent interactions in the population. Evolutionary game theory, on the other hand, studies frequency dependent strategy interactions, but usually omits life history and the demographic structure of the population. Here we show how an integration of both aspects can substantially alter the underlying evolutionary dynamics. We study the replicator dynamics of strategy

interactions in life stage structured populations. Individuals have two basic strategic behaviours, interacting in pairwise games. A player may condition behaviour on the life stage of its own, or that of the opponent, or the matching of life stages between both players. A strategy is thus defined as the set of rules that determines a player's life stage dependent behaviours. We show that the diversity of life stage structures and life stage dependent strategies can promote each other, and the stable frequency of basic strategic behaviours can deviate from game equilibrium in populations with life stage structures.

The explanatory payoffs of multiple realization in cognitive neuroscience

MARIA SERBAN** (University of Pittsburgh, United States)

Given a stable higher-level theory and a theory pitched toward the lower-level of organization of a biological system, the doctrine of multiple realization claims that there are one-to-many mappings from the unified (and perhaps homogeneous) higher-level properties to the heterogeneous lower-level properties of the system. The multiple realization doctrine has been traditionally taken to license a strong thesis about the autonomy of psychology from neurobiology and to set an antireductionist agenda for philosophy of cognitive science in general (Putnam 1965; Fodor 1974). However, critics of multiple realization have contested the strong anti-reductionist consequences of the thesis. Their objections targeted both the conceptual arguments for multiple realization (Sober 1999) and the lack of empirical support for the doctrine within cognitive neuroscience (Bechtel and Mundale 1999). In response, I argue that current scientific research provides ample support for the multiple realization thesis in both biology and cognitive neuroscience. Drawing a comparison between the degeneracy thesis (Tononi, Sporns, and Edelman 1999; Edelman and Gally 2001; Price and Friston 2002; Mason 2014) and the multiple realization thesis allows us to refine some of the features and implications of adopting multiple realization as a viable research hypothesis in cognitive neuroscience. In order to illustrate the methodological and explanatory payoffs of the multiple realization thesis I rely on research on the phenomenon of recovery of language functions. This case study illustrates that the collaboration between different cognitive modeling paradigms (the lesion-deficit model, functional imaging studies of normal adult subjects and developmental models of brain function recovery) provides ample support for the multiple realization or degeneracy of higher-level cognitive functions. In this context, I show how the thesis of multiple realization promotes the development of mixed-level explanatory strategies for explaining the properties and behaviors exhibited by complex biological systems at higher (and more abstract) levels of organization.

DS 1545

09:00 - 10:30

INDIVIDUAL PAPERS

HISTORY, NATURAL HISTORY AND HUMAN NATURE

Urban anthropological fieldwork in “mixed-race” communities, Australia (1940-1965)

KATHRYN TICEHURST (University of Sydney, Australia)

Between 1940 and 1965, several anthropologists in Australia, including Marie Reay, Jeremy Beckett, Ruth Fink and Diane Barwick, worked in Aboriginal communities which they labelled “mixed-race.” Such conceptions of partial or mixed Aboriginality were not reflective of Aboriginal people's self definition. They were borrowed instead from administrative categories and they blurred the lines between race and culture. These terms referred to Aboriginal people who lived on the edges of segregated country towns and in the suburbs of Melbourne and Sydney. Fieldwork in towns and cities differed from the traditional practice of the remote Australian anthropologist. It involved attending church services, protest meetings, weekly dances and boxing matches. It posed new problems: Diane Barwick had difficulty finding her subjects amongst the broader population, whilst Ruth Fink had trouble convincing the inhabitants of Brewarrina that she wasn't a spy, or a disguised photographer for the Aborigines Welfare Board magazine. These anthropologists turned to sociology, and to theories of marginality, to describe communities which remained distinct whilst living with others. This paper will focus on the social interactions which constituted fieldwork in these studies, to examine changing anthropological practice and theory in this period. Even though these anthropologists explicitly rejected biological race as a useful concept, racial categories continued to determine who was considered an appropriate subject of study, and race continued to affect the social relations upon which such studies were based.

Kraepelin not interested in biological explanations of insanity! says Hopkins psychiatrist: Adolf Meyer's psychobiological view of dementia praecox and critique of Emil Kraepelin

SUSAN LAMB (McGill University, Canada)

The name of the German psychiatrist Emil Kraepelin became synonymous with “biological psychiatry” at the end of the twentieth century. Adolf Meyer, however (the Johns Hopkins psychiatrist whose influence on American psychiatry a century earlier equaled that of Kraepelin) publicly criticized his mentor precisely because Kraepelin refused to acknowledge the biological dimensions of dementia praecox. Historians have tended to frame developments around clinical and cultural constructions of dementia praecox in the United States in terms of disciplinary disputes over an organic/somatic versus functional/psychogenic etiology. According to traditional narratives, Kraepelin was a prominent thinker in the somatic camp, whereas, among proponents of functional theories, Meyer derived his ideas from more important theorists (e.g., Janet, Bleuler, Freud). Richard Noll recently ventured beyond this limiting dichotomy, arguing that Kraepelin's endocrinal theory of auto-intoxication to explain dementia praecox represented an alternative biological middle ground. As the fictional headline above is meant to emphasize, Meyer cried foul on this very point. He criticized Kraepelin's allusions to unverifiable biochemical processes as a “terminus technicus for our ignorance” that detracted from the painstaking work

of investigating why and how the complex biological function of mentation failed in such cases. Noll is not the first historian to characterize Meyer's own theory of "psychobiology" as hopelessly vague, and he disparages Meyer's audacity to describe his approach as "biological". Yet Meyer's ideas on dementia praecox have never been clearly restated for purposes of historical analysis, making it impossible to evaluate critically their relative significance. This paper 1) examines Adolf Meyer's conception of dementia praecox as the result of dissolution and a disorder of poorly regulated instincts and maladaptive habits, and, 2) explores the possibility that it emerged as a radical and important theory - and, the more likely progenitor of biological psychiatry in the United States today.

Why did Ernst Haeckel copy Wilhelm Giesbrecht's copepod drawings?

KATHARINA STEINER (Universität Zürich, Switzerland)

The famous drawings of the zoologist Ernst Haeckel (1834-1919), professor at the University of Jena, have been criticized for misinterpreting the appearance of organic forms to suit Haeckel's aesthetic conception of evolution. For example, the perfect symmetries and sharp points of his radiolaria depictions have been reproached as products of "Haeckelism." It is also clear, I will argue, that his plate on copepods in his *Kunstformen der Natur* (1899-1904) appropriated figures from zoologist Wilhelm Giesbrecht's *Systematik und Faunistik der pelagischen Coepoden* (1892), only reorganizing the arrangement and changing their formal-aesthetic presentation to a minimal degree. This is particularly of interest because we have here practically identical images used by researchers from different schools, distributed in two different contexts, with two different scientific aims. Giesbrecht (a student of Karl A. Möbius) wrote his study for a scientifically trained audience—methodologically it is aligned with an expedition to examine plankton carried out by Victor Hensen in 1889; it remains a key piece of basic research comprising both a systematic morphological biological description of species and a quantitative data set treating their geography and behavior. By contrast, Haeckel's *Kunstformen* was aimed at a lay audience. At the same time, however, he tied his collection of plates directly to his theoretical texts *Generelle Morphologie* (1866) and *Schöpfungsgeschichte* (1868). In doing so he sought to generate an aesthetic-morphological systematics for his natural objects, his "promorphology." In my paper, using the drawings of Giesbrecht and Haeckel I inquire into the function of epistemic images within zoological research. Haeckel's appropriation of Giesbrecht's images shows how an epistemic object can transition from an "objective", quantitative context to a "subjective", qualitative context. Giesbrecht's drawings of copepods were open to interpretation. Their use as an epistemic object by Haeckel was not contingent upon Giesbrecht's particular aims and tradition.

DS M240

09:00 - 10:30

INDIVIDUAL PAPERS

TREES AND LINEAGES: INTERDISCIPLINARY PERSPECTIVES

The priest and the tree: Augustin Augier's "botanical tree" (1801) as an image of divine Creation

NILS PETTER HELLSTRÖM (Uppsala universitet, Sweden)

The once forgotten "botanical tree" of Augustin Augier, a tree representation of the natural system, reminiscent of a natural tree and presented in analogy with a family tree, has received considerable attention since botanist Peter F. Stevens stumbled over it in the early 1980s. Originally part of Augier's taxonomy treatise, *Essai d'une nouvelle classification des végétaux* (Lyon, 1801), historians of natural history and evolutionary theory have dubbed his tree the first tree in systematics, and treated it as a precursor to Darwin's "tree of life". Whereas the "botanical tree" has been granted much attention, the identity of its author has remained completely unknown—which has complicated attempts to place it into context. Following research by myself and colleagues in France, we have been able to reconstruct the identity of Augustin Augier de Favas, a Catholic priest of the Oratorian order, who saw in the tree the beauty, order, and perfect symmetry of divine Creation. Given that the family tree, as a model for the natural system, preceded theories of evolution, I call for a re-evaluation of the place of the tree in the history of the life sciences.

A tree of trees

MARIE FISLER (Muséum national d'Histoire naturelle, France); **GUILLAUME LECOINTRE** (Muséum national d'Histoire naturelle, France); **PIERRE DARLU** (Muséum national d'Histoire naturelle, France); **CÉDRIC CRÉMIÈRE** (Muséum d'histoire naturelle du Havre, France)

In the history of science, we usually classify authors in "schools" of ideas. For example, we identify some naturalists as "Transformists", some of whom being "Darwinians" or "Lamarckians". In the twentieth century's Systematics (the science of classification), we usually distinguish "Synthetists", "Pheneticians" or "Cladists." Such categorizations are often described, but have never been formalized. In a similar way, during the history of Systematics, taxonomic groups were not formalized. This has changed in the second half of the twentieth century, with the emergence of a rigorous methodology : through coding the anatomical similarities of species into characters, by maximizing consistency among characters using a "tree", biologists could create rigorous tools (parsimonious trees) to make nested classes. With those tools, we know exactly why primates and rodents for example, belong to the mammals group, and why mammals and birds are members of the vertebrate group. We have reused these methods in order to code the similarities of ideas concerning the Tree of Life among authors. Thus, trees from 233 major works of natural history were coded. This produced a "tree of trees": a hierarchical representation of the ideas about trees shared among authors. With this tree, we formally found some already known categories, but we discovered new ones as well. We even found that some traditionally recognized groups were not homogeneous but had to be separated into two distinct "schools". Thus, the categorization tools used in Systematics may allow the study of scientific Schools of thought. This will result to a more transparent and accurate description of the history of science.

Ontological frameworks for species pluralism

JUSTIN BZOVY (University of Western Ontario, Canada)

Debates about what species are have been framed monistically. In a post-Darwinian context, philosophers and biologists have debated whether species are individuals (Ghiselin, 1974; Hull, 1976), natural kinds (Boyd, 1991), some mixture of both (Millikan, 1999; Rieppel, 2013), abstract sets (Kitcher, 1984; Valen, 1988), or processes (Rieppel, 2009; Dupre, 2012). Most have assumed that only one of these ontological accounts of species taxa will be correct. I take issue with this assumption by arguing that this ontological debate is not about what species taxa are, but about what sort of properties, be they historical or similarities, are more important for grouping species taxa. Given this simplification of the ontological debate, a resolution will require an interpretation of the role evolutionary theory plays. Those who stress the importance of evolutionary theory favour historical properties (e.g., Ereshefsky, 2001; Wilkins, 2003), and those who stress the importance of non-evolutionary factors or interests favour similarity properties (e.g., Dupré, 2001). I frame this debate in a pluralistic context. On my account, some species taxa may belong to different ontological categories. Different properties, historical or similarity, can be important in certain cases more than in others. Situating the ontological debate in this manner gives us a method for developing an ontological framework that is suitable to modern forms of realistic species pluralism. My approach is also particularly relevant to the development of the PhyloCode, a rankless or non-hierarchical approach to taxonomy that is meant to replace all existing taxonomic codes. Those hesitant to accept the PhyloCode have debated whether it stresses historical properties and treats species as individuals (e.g., Rieppel, 2006; Ereshefsky, 2007).

INDIVIDUAL PAPERS

EXPERIMENTATION AND PRACTICE IN THE FIELD, THE LAB AND THE CLINIC

Data creation and research environments: Implications for the re-use of open data

LOUISE BEZUIDENHOUT (University of Exeter, United Kingdom)

How life science data can be shared to maximize the benefits to humanity is a topic that is receiving increasing attention. In response to calls for increased openness within scientific research, the Open Data (OD) movement has been highly influential in championing unrestricted access to research data. This drive towards openness is underpinned by certain key assumptions – not only that benefits will be accrued from data re-use, but also that all online data could – can and would – be re-used. An uncritical approach regarding the feasibility and likelihood of data re-use, however, overlooks the social, historical and political issues that may influence what data are used – and what data are ignored. This talk critically engages with this assumption, asking the question: what issues about data selection (that precedes re-use) are absent from current data discussions? It becomes important to ask how scientists judge which data to re-use, and why some data are selected preferentially.

These questions stem from recent fieldwork in laboratories in low/middle-income countries (LMICs). Scientists interviewed were concerned that issues such as their use of older equipment and methodologies, the low visibility of their research institutions and the limitations associated with lack of funding would cause their data to be overlooked when placed online. These concerns influenced their engagement in data sharing initiatives, their discussions on data sharing and openness, and – ultimately – their involvement with the international scientific community. The concerns of LMIC scientists thus strike to the heart of the OD movement and force us to re-examine how far the likelihood of re-use can – and should – be assumed. Assuming both that scientists believe in data reuse and that online data are indeed reused are two topics urgently requiring further investigation.

Disseminating behavioral genetics research to the public: Evidence-based recommendations

ALEXANDRE MORIN-CHASSÉ (Columbia University, United States); **JAMES FOWLER** (University of California, San Diego, United States)

The media regularly cover scientific studies suggesting that genes are partially responsible for a particular behavior or social orientation. However, recent research shows that this practice unintendedly leads people to infer genetic causation to other traits that are not even mentioned in the news report. The purpose of the current study is to verify whether the emergence of this side-effect depends on the type of scientific evidence presented. Results from our survey experiment reveal stronger generalization effects when the news content presents high heritability estimates derived from twin studies or insights from population genetics. Based on this finding, we suggest directions of future research, and offer empirically-driven recommendations for how science journalists should – or should not – cover behavioral genetics research.

Singularization in the cancer clinic: Genomics, targeted therapies and emerging diagnostic entities and configurations

PASCALE BOURRET** (Aix-Marseille Université, France); **ALBERTO CAMBROSIO** (McGill University, Canada); **PETER KEATING** (Université du Québec à Montréal, Canada); **ETIENNE VIGNOLA-GAGNÉ** (McGill University, Canada)

Recent developments in oncology are grounded in the massive deployment of genomic technologies and of a novel category of drugs collectively known as targeted therapies, insofar as they target, at least in principle, specific pathways and molecular abnormalities of patients' tumors. Touted as the harbingers of an era of individualized, personalized, or precision medicine, these new therapeutic strategies have already become part of routine practices, and are presently the object of major clinical research initiatives both in Europe and North America. Their development is associated with a new understanding of the etiology of cancer, the attempt to replace traditional, histology-based classifications with a molecular nosology, the development of new diagnostic approaches, and the emergence of new clinical trial designs (umbrella trials, basket trials, etc.). Our paper examines these transformations by analyzing them as practices of "singularization", embedded in a regime of "intense problematization" (Callon, 2012), whereby the relevant entities – i.e., molecularly defined types of cancer, targeted drugs, targeted therapeutic regimens – are mutually (re)defined on an ongoing basis, while

DS M280

09:00 – 10:30

opening up new spaces of inter-comparability. Our approach aims at capturing the novelty of these recent developments by contrasting them with more traditional understandings of “personalization” that refer to the adaptation of existing treatments to the predefined, stable, and independent characteristics of a given patient.

DS M320

09:00 – 10:30

INDIVIDUAL PAPERS

ETHICS, RACE, AND USE-INHERITANCE

Pragmatic naturalism and the is-ought challenge

JORGE OSEGUERA GAMBA (Florida State University, United States)

In his book *The Ethical Project*, Philip Kitcher (2011) offers a naturalistic account of Ethics, which he dubs Pragmatic Naturalism. Based in evidence from primatology, archeology and anthropology, and some speculation from evolutionary biology, his account is intended to be normative and not merely descriptive, therefore it has to fulfill a challenge posed by Hume that any normative naturalistic accounts of ethics has to fulfill: how to bridge the is-ought gap, i.e. how can a prescription of an ethical practice be made from purely descriptive premises. The purpose of this essay is to explore the details of how this challenge could be met using the framework of pragmatic naturalism. My answer will be that pragmatic naturalism is able to give a logically valid argument from “is” to “ought” using descriptive claims and conceptual truths as premises. Its normative force is not delivered as an absolute authority—as some moral realists would like—but that is not a problem for pragmatic naturalism, since it does not have that aim. First, I will explain what Hume’s challenge consists in. Then I will explain the “analytical history” of our ethical practices offered by Kitcher to spell out the function of Ethics and formulate the first premise. Next, I will sketch the metaethical picture of pragmatic naturalism in order to formulate two more premises. The missing premises will be formulated as conceptual truths. As I formulate each premise I will deal with the objections that can be made. Finally, I will point out some objections—not related to the logical structure of the argument offered—that can be made, and reply to them.

Carleton Coon and the modern synthesis

DAVID DEPEW (University of Iowa, United States); **JOHN JACKSON** (University of Colorado Boulder, United States)

The physical anthropologist Carleton Coon’s *The Origin of Races* (1962) argued that five great races of man evolved from separate *H. erectus* populations before these races independently (and at different times) became *H. sapiens*. The book provoked censure from the American Anthropological Association because Coon refused to repudiate the uses to which opponents of school integration, interracial marriage, and equal voting rights were putting it. This occurred at a critical moment in the Civil Rights Movement. One of us has shown that Coon’s refusal was not just a demand for academic freedom; he was complicit with his cousin Carleton Putnam, author of a notorious book called *Reason and Race*, in leading readers to think that science supports

segregation (Jackson, 2005). The anthropologist Sherwood Washburn and the population geneticist Theodosius Dobzhansky were Coon’s most trenchant critics. In a departure from the doctrinal unity that the makers of the Evolutionary Synthesis (ES) tended to presume or require of each other, however, two other founders of the ES, Mayr and Simpson, defended Coon not just on grounds of academic freedom, but because they thought he might be right, a possibility Dobzhansky ruled out on conceptual grounds. In this paper we argue that unacknowledged differences between what Mayr and Dobzhansky meant by “population thinking,” a phrase they both had been using since 1950, may have played a role in this unexpected divergence. We make use Joeri’s Witteven’s 2013 study of “population thinking” to characterize this difference and of Mayr’s and Dobzhansky’s archived correspondence with Coon to bring it to bear on the case. We touch on the disturbing possibility that unexpected strains of disunity in the early ES may have been tied to differing views about racial equality.

Spencer, use-inheritance, and the end of liberalism

STEPHEN ENGELMANN (University of Illinois at Chicago, United States); **MATTHEW BEIFUSS** (University of Illinois at Chicago, United States)

This paper explores the political-theoretical implications of the transition from Lamarckian to neo-Darwinist evolutionary paradigms at the end of the nineteenth century, particularly in imagining a post-imperial world order. Building on the work of David Weinstein and Robert Richards, we examine shifts in the voluminous oeuvre of “our great philosopher, Herbert Spencer” (Darwin, *Descent of Man*), especially in dialogue with J.S. Mill, Darwin, and August Weismann. Spencer’s attempt to give liberal utilitarianism a naturalist basis was deeply reliant on Lamarckian use-inheritance, and the political conclusions he drew from it were anti-imperialist, but in the framework of a thoroughly imperial “civilizational” cosmopolitanism and globalism. At least in Europe, Spencer’s failure to adapt his sociology and political theory to the emerging modern synthesis doomed it to a creeping irrelevance, and ceded the scientific high ground to the racial nationalism of theorists like Rudolf Kjellen. Our point of departure is a close reading of the fascinating *Progress, Its Law and Cause* (1857), and we close with some reflections on the possible political implications of post-genomic critiques of neo-Darwinism in our neo-liberal context.

DS M340

09:00 – 10:30

INDIVIDUAL PAPERS

MODULARITY, HIERARCHIES AND VISUAL THINKING: ANALYZING APPROACHES TO BIOLOGY**The persistence of hierarchical organization in biological thought****DANIEL BROOKS**** (Westfälische Wilhelms-Universität Münster, Germany)

Despite a slew of recent (yet insightful) criticism, the concept of “levels of organization” remains a pervasive theoretical concept in the biological sciences. For one thing, the concept of levels is heavily referenced in scientific texts of all degrees of specialization, whether in general (or advanced) textbooks or original research articles. Nonetheless, the term’s admitted ambiguity poses problems. While it is doubtful that a singular conception of levels can adequately perform the many roles that are attributed to it, a plurality of more particular, mutually complementary levels concepts is possible. In other words, what the critics charge as vacuity in the concept of levels of organization, proponents may defend as a virtue of flexibility in the concept’s range of application. This presentation will offer a moderate defense of the levels concept that makes room for a more sustained constructive analysis of the importance of the concept in contemporary biological thinking. Unlike other organizing concepts in biology, such as the “tree of life,” the concept of levels of organization is more directly applied by scientists themselves to, e.g., align or contrast the contributions of their own work on a given scientific problem to other approaches in the same discipline or work in other subdisciplines of biological research. Simultaneously, scientists also use levels to orient their research towards objective features of the natural world. In more philosophical terms, the concept of levels represents an invaluable resource for understanding pluralistic explanation by helping us conceptualize relative explanatory contributions of particular disciplines to complex phenomena that are investigated by multiple disciplines that, alone, are unable to explain such phenomena.

Modularity and the limits of mechanistic explanation in biology**STAVROS IOANNIDIS** (University of Athens, Greece)

Biologists commonly describe their practice as involving the discovery of mechanisms. But is it appropriate to describe biological systems as mechanical in nature? In this paper I explore this question by focusing on the nature of mechanistic explanation. I argue that the failure of modularity in the case of biological systems shows the limitations of the application of mechanistic explanation to biology. It is a widely held view that for an explanation to be mechanistic, it has to be modular. In Woodward’s well-known interventionist account of mechanistic explanation, in particular, this means that the causal relationships within the mechanism have to be modular, i.e. it should be in principle possible to change a specific causal relationship without also changing other causal relationships in the system. In the paper, I explore the extent to which biological systems can be said to be modular in Woodward’s sense. Thereby, I investigate how modularity itself can be understood, and what is the relationship between modularity taken as a requirement for mechanistic explanation and concepts of “modularity” commonly encountered in biology. In particular, I focus on a crucial feature that biological processes have but systems commonly viewed as “mechanical” lack: in cases such as metabolic processes

and genetic networks, the causally active components of a mechanism are themselves produced during the operation of a mechanism, in contrast to cases of systems typically regarded as mechanical. If a biological system fails to be modular, it would be misleading to describe it as a mechanism, and to employ mechanistic explanations to explain its behaviour. To the extent that the failure of modularity is the norm in biological cases, the present argument shows a limitation of the mechanistic view of explanation in the biological case, and the need to develop non-mechanistic accounts of biological explanation.

Visual thinking in genetics: A case of genetic maps in Seymour Benzer**YOICHI ISHIDA** (Ohio University, United States)

In 1954, Benzer began experimental work that would produce a series of seminal contributions to molecular biology. Benzer’s research notebooks collected at the Caltech Archives show that much of his daily research activities from 1954 to the early 1960s involved genetic experiments with bacteriophage T4, construction of fine structure genetic maps of the rII region of phage T4 DNA, and exploration of physically coherent interpretations of the map. At bottom, a genetic map is a diagram that provides a visual summary of the results of genetic experiments, and Benzer used it for the purpose of organizing the experimental data. But he also used it for the purpose of sustained thinking about the structure of DNA. In this paper, I analyze the roles genetic maps played in the process of Benzer’s reasoning about DNA. Recently, multiple lines of research in information visualization, embodied cognitive science, philosophy of cognitive science, and philosophy of science strongly suggest that a descriptively adequate account of scientific reasoning must take into account the roles that perceptual processes, especially visual processes, play in scientists’ reasoning. Drawing on these lines of research as well as Benzer’s research notebooks, I will develop an account of visual thinking in genetics and show how visual properties of genetic maps can help the sort of research Benzer was doing. Moreover, the account of visual thinking in genetics that I develop will not be a simple extension of the theory developed in the lines of research mentioned above. For, as I also argue, the real-world scientific reasoning with diagrams has characteristics that are not shared by cognitive tasks commonly studied in cognitive science.

DS M460

09:00 – 10:30

INDIVIDUAL PAPERS

EXPLANATION AND METHODOLOGY IN EVOLUTION AND ECOLOGY**Evolutionary explanations****SUSANNE HIEKEL** (Universität Duisburg-Essen, Germany)

In the philosophy of biology, two opposing interpretations of Darwin’s “one long argument” are defended. The first interpretation, advocated for example by Michael Ghiselin or Michael Ruse, understands the argument in terms of a Hempelian account of historical explanation. The second interpretation, advocated by Stephen J Gould, emphasizes the historical dimension of the argument and regards it as implying a narrative historical

methodology. According to the Hempelian account, a scientific explanation is only given if the event which is to be explained can be subsumed under a law-like universal hypothesis. According to Ghiselin and Ruse, the argument of the *Origin of species* is to be reconstructed in that way. Gould, by contrast, stresses that evolutionary events are “particulars of history, rather than necessary expressions of law” (Gould, 2002). With this conflict in the background, two different, more or less tacitly presupposed methodologies of historical explanations – the Hempelian account and Arthur C. Danto’s narrative account of historical explanation – are presented in general and then transferred to an explanation of an evolutionary event: the endosymbiosis. According to the theory of endosymbiosis, recent eukaryotic cells evolved because of symbiosis events that led to the development of the organelles (mitochondria and plastids) of eukaryotic cells. More specifically, I argue that the Hempelian account – apart from the fact that it faces general difficulties such as the problems of overdetermination, of full description and of prediction – falls short of capturing a specific aspect of natural history: the particularity of evolutionary events. By contrast, a narrative account which draws on Arthur C. Danto’s explanation model avoids the problems of the covering law model and does justice to this aspect of natural history. Consequently, a historical explanation of evolutionary events is defended, which is in tune with Danto’s historical explanation.

A normative approach to resolving methodological issues in invasion biology

ERIC ROGERS (University of Cincinnati, United States)

One of invasion biology’s aims is to help control the economic and environmental costs of invasive species. Progress towards this goal is hindered by a number of methodological issues, including broad inconsistencies in the use of key terms like “invasion” and “invasive species.” This has caused problems for research integration and confounded communication between researchers and the stakeholders in invasion research. Those who have addressed this problem have largely done so on the basis of “internal” considerations, that is, in terms of the coordination and communication among researchers engaged in research activities. I argue that the nature of invasion biology’s role in the practical task of controlling invasions requires a broader perspective. Controlling invasive populations is a monumental task requiring the coordinated efforts of a diverse group of professionals, including policy makers, land managers, and governmental agencies, all of whom rely for their performance on the research communicated by invasion biologists. This means, first, that the methodological choices of invasion biologists may have downstream consequences for these other groups. If researchers cannot agree on a term, and that term is used to mean inconsistent or contradictory things, biologists cannot hope to communicate their findings effectively. This makes it difficult for those who must use this research in their decision-making, sometimes resulting in ineffective or counterproductive strategies. Second, despite the shared effort, invasion biologists have a special degree of responsibility given their control over the understanding of invasions and the available management alternatives. I argue this places a normative obligation on researchers to utilize “external” considerations – the potential consequences of their choices for those outside the field – when making methodological decisions, especially the use of terminology. I further argue that such considerations can help us resolve at least some terminological disputes, using the term “invasive species” as an example.

On the importance of answering the right question: A defence of statistical explanations in evolutionary theory

MARION DURAND (University of Toronto, Canada)

Recent work in philosophy of biology has suggested that the models of evolutionary biology appeal not to causes of evolution, but to statistical non-causal properties of populations to explain changes in trait distribution. This view has come under fire. In particular, some opponents reject the idea that statistical explanations are explanatory. Indeed, literature is replete with causal accounts of explanation. It is a widely shared intuition that an explanation should articulate the cause(s) of what it purports to explain. I argue that this is not a necessary requirement. I lay out a general account of explanation which allows for genuine non-causal explanations. Explanation is both a metaphysical concept and a practice. Explanations are formulated but also assessed and accepted or rejected. The metaphysical requirements we lay out must therefore make sense of practice. Inspired by Garfinkel (1981), I suggest that an explanation needs to answer two types of questions about its explanandum: what-if-things-had-been-otherwise but also what-needed-to-be-the-same for the explanandum to have been the same. The former has often been addressed in counterfactual accounts of explanation, particularly convincingly by Woodward (2001, 2003)’s invariance relation, but it is not enough. As Strevens (2004, 2008) highlights, one also needs a criterion for explanatory relevance. The answers to both questions are needed. Combined, they capture what I call a modal profile of the explanandum. An explanandum can have several such profiles, and part of the practice of explanation consists in matching the modal profile of one’s interlocutor. This account of explanation is compatible with but less restrictive than a number of accounts of explanation in the literature, while also making sense of practice. Statistical explanations as employed in evolutionary biology fulfill the metaphysical requirements, but capture modal profiles which do not match their opponents’.

DS R510

09:00 – 10:30

ORGANIZED SESSION / STANDARD TALKS

MECHANISMS OF EVOLUTION

Organizer(s): **ERIC SAIDEL** (George Washington University, United States)

The New Mechanistic Philosophy has provided a new and exciting way to think about explanation in biology. The new mechanists suggest that discovery and explanation in biology proceeds by searching for and finding mechanisms. In expanding the insights of the new mechanists, philosophers have wondered about the scope of mechanistic explanation. In particular, can mechanistic explanations be extended to the phenomena of evolution? This session aims to explore this question. **Lindley Darden** (an author of one of the seminal New Mechanistic texts) will discuss the role of next generation sequencing of whole genomes in the study of mechanisms responsible for reproductive isolation; her talk will put study of adaptive speciation mechanisms into the context of a multilevel view of evolutionary mechanisms. Thus, she will be applying a new method of analysis to Darwin’s principle of divergence. **Fermin Fulda** engages with an existing debate about the conceptual found-

dations of evolutionary theory: should we conceive of evolution by natural selection as a causal phenomenon or as a statistical phenomenon? Fulda will argue that a mechanistic interpretation of natural selection is in fact compatible with a statistical interpretation of evolutionary theory. More specifically, a mechanistic interpretation of selection-for explanations is compatible with a statistical interpretation of selection-of explanations. **Eric Saidel** will address the active debate about whether evolution by natural selection can be considered a mechanism. He will argue that evolution by natural selection does fit at least one conception of mechanistic explanation, but that (contrary to the claims of at least one author of this conception) successful mechanistic explanations do not require reifying the mechanisms appealed to in those explanations. **Jessica Pfeifer**, who works on philosophy of evolutionary theory, will chair.

Speciation mechanisms, genomes, and reproductive isolation

LINDLEY DARDEN (University of Maryland, College Park, United States)

Next generation sequencing of whole genomes has revolutionized the study of mechanisms related to speciation. As in many areas of biology, the generation of “big data” currently outstrips the computational approaches to analyze it. Methods are needed to relate genome differences to ecologically significant factors and identify the mechanisms for explaining the genomic patterns of species divergence. Charles Darwin would likely be delighted to see this new method for analysis of his principle of divergence and current work on ecologically driven selection in adaptive speciation. This talk will put study of adaptive speciation mechanisms into the context of a multilevel view of evolutionary mechanisms, from genetic and chromosomal mechanisms yielding variation, to natural selection as the mechanism producing adaptations, to speciation mechanisms producing biological diversity.

Natural selection, mechanistic explanation and the statistical interpretation

FERMIN FULDA (University of Toronto, Canada)

Two recent debates in the philosophy of biology concern the causal vs. statistical interpretation of evolutionary theory and whether natural selection is a mechanism. I suggest that we can gain some clarity about the conceptual and methodological foundations of evolutionary theory by asking about how these issues are related. One might think that if natural selection is a mechanism then evolutionary theory must be a causal theory. Conversely, one might think that if evolutionary theory is a statistical theory then natural selection cannot be a mechanism. The mechanistic interpretation of natural selection, it seems, is incompatible with the statistical interpretation of evolutionary theory. By using the selection-for/of distinction, I will argue that a mechanistic interpretation of natural selection is in fact compatible with a statistical interpretation of evolutionary theory. More specifically, I will argue that a mechanistic interpretation of selection-for explanations is compatible with a statistical interpretation of selection-of explanations. While the former corresponds to ecological studies of actual selective forces familiar from Darwin’s theory of evolution, the latter correspond to population-genetic studies of idealized statistical trends familiar from the Modern-Synthesis theory of evolution. Conceiving selec-

tion-for explanations mechanistically does not imply that natural selection itself is a mechanism, thus preventing unnecessary reification. It also allows us to secure the causal-mechanical basis of evolutionary theory while preserving the distinctive statistical content of population-genetic models.

Mechanistic explanation without mechanisms

ERIC SAIDEL (George Washington University, United States)

Does the New Mechanistic approach to explanation in the biological sciences extend to evolution by natural selection? According to the dominant views of mechanistic explanation, to give a mechanistic explanation of a phenomenon involves finding a mechanism that produces the phenomenon. Thus some philosophers (e.g., Skipper and Millstein (2005)) argue that even if we could make evolution by natural selection fit the required parameters demanded by the New Mechanistic philosophy, it would not be a mechanism; no single mechanism could account for the entirety of the phenomena. Others (e.g., Barros (2008)) argue that since the diverse phenomena of evolution by natural selection can be unified in an abstract mechanism schema, evolution can be thought of as a mechanism. This paper challenges the ontological shift from mechanistic explanation to mechanism. The right explanation of a phenomenon may be mechanistic even though the ontological interpretation of that explanation is not justified. There is no object that is the mechanism that produces evolution by natural selection. Nonetheless, evolution by natural selection can be fruitfully characterized as an organization of entities and activities. By so characterizing evolution by natural selection we gain explanatory purchase on the regularities that we observe in the many instances of evolution by natural selection.

DS R515

09:00 – 10:30

INDIVIDUAL PAPERS

INTERACTORS, IMMUNOLOGY AND CANCER: LEVELS OF SELECTION QUESTIONS?

Immunological individuation and units of selection

DANIEL MOLTER (University of Utah, United States)

In this essay I challenge two metaphysical consequences that Thomas Pradeu (2012) claims follow from conceiving of organisms as being physiologically individuated by their immune systems. The first consequence is that organisms achieve the highest degree of biological individuality. The second consequence is that such organisms are heterogeneous. I argue that Pradeu’s view of the organism as both heterogeneous and endowed with the highest degree of biological individuality is conceptually flawed, as both claims about organisms generate paradoxes in some biological contexts. In light of these paradoxes I argue that we should look to evolution rather than to physiology to provide a theoretical foundation for biological individuality at the level of the organism. Despite conceptual flaws in his formulation of the organism, I argue that immunity, understood in terms of Pradeu’s continuity theory, does in fact provide a physiological criterion of biological individuation,

one unique in its ability to weave heterogeneous strands of the genealogical nexus into a single discrete unit of selection. However, I argue that these heterogeneous units of selection should not usurp the name “organism”, as much of biological theory, especially population genetics, requires a homogeneous single-species concept of organism. I argue that we should retain the view that an organism is part of a single species lineage and use the term “holobiont” (Mindell 1992, cf. Booth 2014a) to refer to immunologically-integrated multi-lineage units of selection.

Pluralism and the levels of selection in cancer: Toward a genomic model

JOSEPH WU (Duke University, United States)

The recognition that cancer is an evolutionary process has yielded many insights for understanding the dynamic nature of the disease. But an evolutionary perspective bequeaths a philosophical problem that has largely been ignored by cancer researchers, namely, the levels of selection. In this paper I explain how cancer is an evolutionary process and why the levels of selection issue is central to understanding the origin and existence of cancer. I then clarify the difference between pluralist and monist interpretations of the levels of selection disputes, a philosophical distinction that many scientists are unaware of. Applying James Woodward's theory of causation, I argue for pluralism and show how a genomic model of cancer parses the causes differently to provide an equally accurate representation of carcinogenesis. I conclude by suggesting pragmatic advantages of a genomic model of cancer in biomedical research.

The return of the interactor

AUSTIN BOOTH (Dalhousie University, Canada)

The evolutionary importance of consortia of taxonomically divergent lineages has been the subject of much discussion in recent philosophy of biology. An increasingly popular unifying approach is a Hull-style perspective in which the interactor concept is revised and adapted to account for the evolutionary role of multilineage consortia. I offer an analysis of this new kind of interactor-based approach to understanding the evolution of multilineage entities. I argue that an interactor-based approach needn't be coupled with a traditional replicator concept. I then make note of some evolutionarily relevant axes along which interactors can (and do) vary in nature. At stake is whether or not multilineage interactors should be understood as units of selection, to what extent they are genuine reproducers or merely systems that recur in each generation, and what kinds of interactions between their parts bind them into genuine biological individuals.

DS R520

09:00 – 10:30

INDIVIDUAL PAPERS

MODELING EMERGENCE IN SYSTEMS BIOLOGY

Mechanistic explanation in systems biology: Cellular networks

DANA MATTHIESSEN (Georgetown University, United States)

Mechanistic philosophy draws heavily from examples in the fields of molecular biology, neuroscience, and basic cell biology. While authors acknowledge its adequacy for such fields, it is frequently contended that, as biological systems approach higher levels of behavioral and compositional complexity, the explanatory purchase of standard mechanistic concepts and strategies begins to falter. In particular, the sufficiency of mechanistic philosophy is currently being disputed for research that falls under the banner of “systems biology”. While some hold that systems biology is mechanistic, others argue that it involves a distinct, non-mechanistic form of explanation. I will evaluate these latter claims with respect to a representative program in systems biological research: the study of regulatory networks within single-celled organisms. I argue that these networks are amenable to mechanistic philosophy without need to appeal to some alternate form of explanation. My aim is not to simply redefine or expand the concept of mechanism in a way that conveniently subsumes the objects of systems biology. Rather, I intend to show how commonly accepted postulates and procedures of mechanistic philosophy apply to and are referenced within the study of cellular networks. In addressing the critics, I aim to advance a picture of mechanistic science that is in accord with the methodology of those studying cellular networks. For this I will draw on a depiction of the explanatory strategies of mechanistic science, which I owe to Craver and Darden (2013) and who cover it in greater detail. After arguing for the compatibility of systems biology with these strategies, I will consider and reject an alternative view of systems biology, which I associate with the notion of design explanation.

Canalization and developmental processes: Beyond a neopreformationist interpretation of the cryptic genetic variability

FLAVIA FABRIS (Sapienza – Università di Roma, Italy)

The concept of canalization, coined by Waddington to illustrate the complex functioning of all developmental processes, has been recently subjected to some neopreformationist interpretations centered on the role of the notion of cryptic genetic variability. Waddington attributed the evidence of the genetic assimilation of acquired characters to this concept, claiming that all organisms are complex homeorhetic systems with specific abilities to influence the evolutionary pathways through the regulation of buffering mechanisms of genetic variability. I will suggest that contemporary biotechnological approaches have misrepresented the original content of the concept of cryptic genetic variability, transforming it into a mere genetic informationism. I will argue that the heuristic value of the concept of canalization has been reduced to a static representation of an “a-contextual developmental system”, closed with respect to its environment. The idea will be evaluated analyzing the contemporary assumptions of canalization in molecular biology research with the aim to recover the original meaning of the concept as an open interaction process between the organism and its environment.

Multicellularity and the type of functional integration for organismal interaction

ARGYRIS ARNELLOS (Konrad Lorenz Institute for Evolution and Cognition Research, Austria)

Multicellularity raises conceptual challenges for understanding organismal interaction. Although multicellularity comes in different characters and in various types and forms, almost all multicellular (MC) systems (from biofilms and colonies to modular and full-fledged MC systems) exhibit some kind of functional integration that in turn allows them to deploy collectively coordinated interactions with their environments. Through such interactions MC systems are able to maintain their organization, to explore niches, and to increase the possibility of survival of their constituting units and of the systems themselves, as a whole. Notwithstanding the resulting adaptation at the global level, I argue (contrary to neo-Darwinian and adaptationist approaches) that not all MC interactions can be considered organismal. Adopting an organizational perspective, I distinguish between a constitutive level (CL – developmental and metabolic processes) and an interactive level (IL – the functional interactions that the system exerts in the environment) of a MC organization. I discuss three types of coordination of MC interaction (representing almost all cases), and I explain that their realization requires different organizational relations between the two levels. I suggest that organismal interaction requires a specialized regulatory subsystem (produced and maintained by the CL) able to modulate both the coordination of the set of structures responsible for the execution of the interactions with the environment (IL) as well as the metabolic processes that constitute and support these interactions (CL). I argue that the endogenous production and operation of such a regulatory subsystem entails a certain form of global functional integration, which in a complete contrast to the other two cases renders the related interactions genuinely attributable to the whole MC system. I discuss in detail the consequences of such type of functional integration regarding the interdependence between IL and CL, and I conclude with implications for the organismal status of several MC systems.

10:30 – 11:00

COFFEE BREAK

INDIVIDUAL PAPERS

ORGANIZATION AND COMPLEXITY: FROM PHENOTYPE TO SYSTEM

Aristotle's four causes and phenotype

ÖZLEM YILMAZ (Sabancı Üniversitesi, Turkey)

In this presentation causation in phenotype explanation is examined with its similarities to Aristotle's theory of four causes. The research of the complex pathways of interaction net between genotype, phenotype and environment needs causal investigation which involves more than a single cause. This investigation is similar to the investigation of Aristotle's material, formal and efficient causes altogether. Final cause will not be used in this consideration because with the theory of evolution, which is a fundamental principle of biology, it is

clear that there isn't any purposive happening in biological phenomena. Still the final cause gets place in many philosophical studies and keeps its importance. Here in this work the author doesn't think that there is final cause in biology, but despite this she will talk about the similarity between final and formal causes and the role of final cause within the gene-centered view. Reducing natural phenomena about living things to one cause (for example: genes) is a mistaken way in explaining phenotype which has many different probabilities and complex interactions in every parts of it. It might sometimes be easier to use parts and to reduce some phenomena into single causes while investigating but the student of nature should always keep in mind that this reducing attitude is only a practical way of understanding the features of parts themselves, and these parts are in a complex and interrelated state all together (they have different features when they are together) and they should be thought and investigated (whenever possible) in this context. As Aristotle puts it; there is no form without matter, as it will be stated in this talk: efficient cause is intrinsic to the living things too; then we can say without material, efficient and formal causes there is no proper explanation of phenotype. In other words proper explanation of phenotype is possible with the investigation of environmental, physiological, developmental, genetic and evolutionary factors in the context of their interrelated state. Maybe this research programme – explaining phenotype while evaluating all these factors – can work with asking all possible causal questions in a proper way to the subject phenomena. In this sense, thinking on Aristotle's formal, material and efficient causes altogether is similar to explaining and investigating phenotype in a most proper way. Examples from plant physiology in a changing climate will be given.

Organizing principles as tools for explaining biological complexity

CONSTANTINOS MEKIOS (Stonehill College, United States)

One of the notable features of the system-theoretic approaches to biology that emerged in the first half of the 20th century was a commitment to the articulation of a system theory of life. By the time Ludwig von Bertalanffy's *General System Theory* (1968) was published, his ideas about how such an objective could be reached – ideas which he had first introduced more than thirty years earlier – were ripe. In order to effectively address problems stemming from the complex organization of biological systems, Bertalanffy argued, the focus must turn on the identification of properties shared by systems in general, as well as on the formal expression of the principles that govern them. Among those subscribing to this point of view was Mihajlo Mesarovic, for whom the search for organizing principles was to be at the heart of the inquiry to which he first referred by the term "systems biology" in 1968. In this paper I seek to show that looking back at the conceptual foundations of these early theoretical efforts to address the problem of complexity in biology could help us think about the value of new mathematical tools for contemporary systems biology. This conclusion is not only substantiated by evidence originating from careful characterization of Bertalanffy's general system principles. It is also supported by recent work in the philosophy of biology which suggests that organizing principles have the potential to complement standard mechanistic explanations in the context of systems biology (Drack and Wolkenhauer

2011; Wolkenhauer et al. 2012; Green and Wolkenhauer 2013). The discussion culminates in the following question: would it be productive for systems biologists to invest on a search for abstract principles at a juncture when their methodology seems to be increasingly defined by pragmatism?

Entropy, the “constructal law” and the emergence of structural organization

LAURENT JODOIN (Université de Montréal, Canada)

The emergence of “order” (biological or not) based on entropy dissipation has a long story. Here, I first distinguish the substantial approach (e.g. in physiology) from the analogical approach (e.g. in population genetics) of entropic explanatory strategies. I then discuss the conditions under which a certain kind of emergence can be explained by an entropy principle. I sustain that the “constructal law” proposed by Bejan (1998, 2006, 2012), is a valid criterion to choose among various emergent relata. The upshot is that, as natural selection treats all living creatures as equals (humans no longer have a special status), this account brings closer every physical (i.e. “real”) system, the living creatures have then no longer such a special status compared to non-living things.

DS 1520

11:00–12:30

ORGANIZED SESSION / DIVERSE FORMAT

EXTENDING PHILOSOPHY OF BIOLOGY: A ROUNDTABLE ON NEW METHODOLOGIES AND DOMAINS, FROM CARTOGRAPHY TO CANCER

Organizer(s): **RASMUS GRØNFELDT WINTHER** (University of California, Santa Cruz, United States)

Participant(s):

RASMUS GRØNFELDT WINTHER (University of California, Santa Cruz, United States)

OCTAVIO VALADEZ BLANCO (Universidad Nacional Autónoma de México, Mexico)

Philosophy of Biology continues to develop, even explode. Similarly to the universe’s expansion, however, our field’s growth has hardly been uniform in all directions. Thematic clusters with highly specialised debates and agendas exist as practically separate universes. While such a divide-and-conquer strategy permits real progress by teams of researchers sharing thematics and commitments, it also encourages conservative tendencies that stultify creativity. In this roundtable, we invite philosophers of biology, as well as historians, sociologists, anthropologists, and psychologists (etc.) of biology, to reflect on new kinds of domains, methodologies, and questions that might benefit the further evolution of the field.

We invite reflection on a diversity of new socially engaged questions extending philosophy of biology. We bootstrap discussion by providing two examples of how to extend philosophy of biology. (There is recent work on each of our examples, but they are not, yet, considered a proper part of philosophy of biology.) First, in “Cancer: An Extended Philosophical Approach,” **Valadez Blanco** reflects on the domains of philosophy of bi-

ology. What would a philosophy of cancer look like? Might a philosophy of cancer move beyond epistemological and methodological matters, turning to urgent ethical, sociological, or political questions? Second, in “Maps as Vehicles of Scientific Explanation,” **Rasmus Grønfeldt Winther** examines methodologies of philosophy of biology. Consider the map analogy, most nakedly stated as “scientific theory is a map of the world.” This analogy is explored by many general philosophers of science. How might philosophy of biology benefit from this pluralistic and perspectival image of science? The two talks will then be followed by a roundtable in dialogue with each speaker and his respective themes of “New Domains” and “New Methodologies.” At the end, the time remaining will be for a general roundtable.

DS M220

11:00–12:30

INDIVIDUAL PAPERS

EVOLUTION ACCROSS BORDERS: POLITICS AND EDUCATION

The topic of evolution in textbooks of the socialist school in Mexico (1932-1941)

ERICA TORRENS (Universidad Nacional Autónoma de México, Mexico); **MA. ALICIA VILLELA** (Universidad Nacional Autónoma de México, Mexico)

Charles Darwin’s book *On the Origin of Species* introduced evolution by natural selection to the public in 1859. In Mexico, evolutionism was supported by many physicians and naturalists of the time, such as Justo Sierra, Alfredo Dugés, Jose Ramirez and Alfonso L. Herrera. However, as in other parts of the world, the acceptance and reception of Darwinism occurred in a particular and peculiar way. The Mexican scenario is interesting in this regard. In Mexico as in France, there was a delay in the introduction, diffusion and acceptance of Darwinism. According to Genovese, this happened mainly by the ongoing armed conflict of that time; according to Maldonado the most important factor was the Mexican frenchifying efforts of the Porfirian era extolling the positivist ideals. However, discussions of evolution were not absent in Mexico and were important for the development and establishment of modern biology in this country. On the subject of education: when was it that evolution found its way into classrooms and text books of basic education? We know that Dugés (1878, 1884), Ramirez and Herrera (1904) published specialized books recurring to evolutionary ideas. Regarding textbooks for basic education, which represented a topic of intense debate between the state and various other groups (positivists as Gabino Barreda and religious sectors, for example), it was up to the presidency of Abelardo Rodríguez (1932-1934) and with the socialist school of the thirties in Mexico that the issue of biological evolution began to be contemplated in the plans and curricula of primary and secondary education. This paper presents the efforts to introduce the theme of biological evolution into Mexican classrooms in the mid twentieth century and questions if the information was truly Darwinian or just evolutionist and why.

An evolutionary analysis of Strawsonian reactive attitudes

ANDREW MOFFATT (Florida State University, United States)

Peter Strawson first brought the class of emotional phenomena called the reactive attitudes (resentment, gratitude, indignation, guilt, etc.) to the forefront of scrutiny in the debate about moral responsibility; but in the past decade, research in the fields of evolutionary and moral psychology have led to a profound reimagining of what these reactive attitudes are and what place they should have in our moral landscape. Recent studies by Joshua Greene and Jonathan Haidt have suggested a new way of conceiving of our moral minds, and as such the reactive attitudes that populate them. In this paper, I apply research from moral and evolutionary psychology to critique the placement of our reactive attitudes at the center of our moral lives as Strawson suggests. I argue that the reactive attitudes are essentially evolutionarily adapted emotions, some of which permit rational justification, while others do not. Further, I contend that when rational justification does not apply to a reactive attitude, the objective attitude should be assumed instead.

Darwinism immigrates to America: A transnational social history of ideas

ADAM SHAPIRO (Birkbeck, University of London, United Kingdom)

Recent historical studies have shed new light on the differences between German and English language interpretations of Darwinism in the late nineteenth and early twentieth centuries. These differences not only shaped scientific practice, they also influenced the ways different public audiences understood and reacted to Darwinism. This raises the question of which Darwinisms hybrid and transnational communities experienced, and whether their reactions to “Darwinism” ought to be understood differently from those of groups whose experience of Darwinism were rooted in a single linguistic and cultural framework. This paper addresses the experiences of German Lutheran immigrants to the United States and their descendants from 1870 to 1920. It looks at the way that these communities formulated reactions to Darwinism and their complex relationship to American varieties of antievolutionism. Was it the case that these immigrants brought with them a Haeckelian interpretation of Darwinism and interpreted American debates over evolution’s role in education, eugenics and World War I in light of this? Or did German Lutheran seminarians and clergy encounter evolution as a part of their larger experience of adaptation and assimilation in a new national context? Though many in this community rejected or refuted Darwinism, and may have agreed with the conclusion that Darwinism was atheism, the grounds given for that conclusion were different than Fundamentalist ideas articulated in long established American denominations. This paper looks particularly at the experiences of German Lutheran immigrants and their descendants in Nebraska, a state which outlawed the German language in schools following the First World War. It explores the context of the German Lutherans who had a teacher removed from the Lutheran college in Fremont, Nebraska in 1922, which resulted in the U.S.’s first evolution trial, a slander lawsuit that took place nine months before the 1925 Scopes trial.

DS M240

11:00 – 12:30

INDIVIDUAL PAPERS

SYSTEMS BIOLOGY FROM DESCARTES AND SPALLANZANI TO DIGITAL DATABASES

Activities versus ontological parsimony in Descartes’s biological mechanisms

BARNABY HUTCHINS (Universiteit Gent, Belgium)

Illari and Williamson (2013) have recently defended the inclusion of activities in the ontology of mechanisms against the view that takes activities to be reducible to entities and their capacities. In this paper, I look at perhaps the most famously parsimonious ontology in the history of philosophy, and show that even Descartes finds activities to be ineliminable when explaining biological mechanisms. Descartes was metaphysically committed to an ontology of the material world that consists of nothing more than matter “extended in length, breadth and depth” (Principles 2/4). He consistently asserted the superiority of his approach over Aristotelian natural philosophy precisely on the grounds of its ontological parsimony. Yet his explanations of physiological mechanisms rely not only on the material anatomical structures he observed during dissections of human and animal bodies but also on the activities occurring between those structures. These activities bear more than a passing resemblance to the activities described by recent literature on mechanisms. In this paper, I analyse Descartes’s explanations of the mechanisms of nutrition, circulation, and muscle action. I show that the activities they involve are not reducible to entities, capacities, or motions, but are essential to the mechanisms being described. Thus, e.g., the pulse is an activity in the mechanism of nutrition for Descartes. But pulsation is not a capacity of the blood itself and is “as much of the heart as of the arteries” (Description of the Human Body 2): it is not localisable to any particular anatomical entity or the capacities thereof. Nevertheless, pulsation is at the core of Descartes’s account of nutrition. As such, activities remain ineliminable – even in the context of an ontology with such deep, systematic commitments to parsimony as Descartes’s.

From systems to biology: A bibliographic analysis to reveal the history of systems biology (1992-2013)

YAWEN ZOU (Arizona State University, United States)

Systems biology, an interdisciplinary field which studies complex biological systems from a holistic perspective, had mostly engineers, mathematicians and physicists as its pioneers before 1990s. However, systems biology has attracted more biologists to participate in it in the past two decades. My goal is to understand (a) the way the contributions of biologists and scientists from non-biological disciplines have changed from 1992 to 2013, and (b) the historical and philosophical implications underlying this change. In the Web of Science, I found 9805 articles in English published between 1992 and 2013 and having the term systems biology in their topics. The citation information of the 9802 articles served as the corpus of my analysis. The corpus was then analyzed through a variety of innovative computational tools and approaches, including citation analysis, text classification, and topic modeling. The results were then interpreted from both the historical and philosophical perspectives. The results are as follows: a) more biology-oriented papers, such as those focusing on biological mechanisms and medical research, were published in the field of systems biology over time, compared with

systems-oriented papers like those dealing with mathematical models; b) the institutional context for authors have stabilized since early 2000s, with authors affiliated more with biological institutions than systems-oriented institutions, however, differences were observed for most highly cited authors and general authors; c) topic modeling based on the abstracts of the 9805 articles shows that biology-oriented topics, such as medicine, vaccines and drugs, have been on the rise, further supporting the findings based on references and on institutional context. My analysis suggests that systems biology has shifted from more systems-oriented to more biology-oriented from 1992 to 2013. If the trend continues, systems biology will become more integrated with other biological disciplines, especially medical research.

Lazzaro Spallanzani studies on plant reproduction: A case study on the role of theory in interpreting observations and experiments

MARIA ELICE BRZEZINSKI PRESTES (Universidade de São Paulo, Brazil)

With the overall goal of providing empirical evidence of the unification of animals and plants in one huge family of organic beings, Lazzaro Spallanzani (1729-1799) associated his numerous studies on generation of animals to some plants species. He performed anatomical observations of floral structures and developed different controlled experiments, including procedures that were being incorporated into the experimental protocols of the time, such as parallel series. The Italian naturalist reported the existence of the “seed” inside the female flowers before fertilization, and concluded that pollen was not always needed for the development of the embryo. These conclusions were consistent with his ovist preformation ideas, as opposed to other concepts advocated by botanists of the time, both those related to the animalculist preformation and those proposing the existence of sexual reproduction in plants with the participation of two fertilizing liquids, male and female. The episode is a case study for discussion on the role of theories and their relation to observation and experiments in the construction of scientific knowledge.

INDIVIDUAL PAPERS

EMERGENCE: AGENCY, VITALISM AND HOLOBIONTS

The birth of the holobiont: Multi-species birthing through mutual scaffolding and niche construction

LYNN CHIU (University of Missouri, United States)

Holobionts are multicellular eukaryotes with multiple species of persistent symbionts. They are not individuals in the genetic sense— composed of and regulated by the same genome—but they are anatomical, physiological, developmental, immunological, and evolutionary units, evolved from a shared relationship between different species. What are the processes that constitute and maintain the multi-genomic holobiont? I argue for a new perspective: the reciprocal scaffolding of developmental processes and mutual construction of developmental, ecological, and evolutionary niches between humans and the microbiota symbionts. The case study: the

human birth process, whereby mother, fetus, and symbiotic microbial communities induce and/or constitute conditions for the development and reproduction of one another. These include the direct induction of maternal or fetus physiological changes, the restructuring of ecological relations between communities, and evolutionary selection against undesirable competitors. The mutual scaffolding and niche constructing processes start early— prior to amniotic rupture. We are evolutionarily, physiologically, and developmentally integrated holobiont systems, strung together through mutual reliance (developmental scaffolding) and mutual construction (niche construction). Bringing the processes of niche construction and developmental scaffolding together to interpret holobiont birth conceptually scaffolds two new directions for research: (1) in niche construction, the evolutionary implications of organisms actively constructing multiple overlapping niches and scaffolds, and (2) in Evolutionary Developmental Biology, evolutionary and ecological processes as developmental causes.

The discreet charm of eighteenth-century vitalism and its avatars

CHARLES WOLFE (Universiteit Gent, Belgium)

Building on some earlier work on forms of vitalism as relating to biomedical science (not metaphysics; cf. Wolfe and Normandin 2013), here, I try to investigate the still-problematic notion of vitalism, hovering in the realms of the philosophy of biology, the history of medicine, and the scientific background of the Radical Enlightenment (case in point, the influence of vitalist medicine on Diderot). This is a more “biologistic”, “embodied”, medicalized vitalism than versions of this idea found in recent “theory” discourse, e.g., on materiality. I first distinguish between what I would call “substantial” and “functional” forms of vitalism, as applied to the eighteenth century. Substantial vitalism presupposes the existence of something like a (substantive) vital force which either plays a causal role in the natural world as studied by scientific means, or remains a kind of supernatural, extra-causal entity. Functional vitalism tends to operate “post facto”, from the existence of living bodies to the desire to find explanatory models that will do justice to their uniquely “vital” properties in a way that fully mechanistic models (one thinks, e.g., of Cartesian mechanism) cannot. I discuss some representative figures of the Montpellier school as being functional rather than substantial vitalists. A second point concerns the reprisal of vitalism(s) in “late modernity”; from Hans Driesch to Georges Canguilhem (who was perhaps the first in the post-war years to provocatively call himself a vitalist, when this was still a “bad word”). I suggest that in addition to the substantial and functional varieties, we then encounter a third, more existential form of vitalism, articulated by Canguilhem, in which vitalism is a kind of attitude towards Life. I suggest that distinguishing between these three forms should lead us to revise some of our common judgments about the place of vitalism (Gilbert and Sarkar 2000) in the restructuring of biological theory. (Oyama 2010)

DS M260

11:00–12:30

Minimal agency and its discontents**ALEX DJEDOVIC** (University of Toronto, Canada)

There has been considerable interest at the boundary of philosophy, cognitive science and biology in developing an account of minimal agency, which is roughly the kind of agency that is common to living systems as such. The minimal agency project aims to clarify thinking about the continuity and embeddedness of cognitive processes in the more general class of biological processes (Di Paolo 2005, Thompson 2007, Barandiaran et al 2009, Skewes & Hooker 2009, Christensen 2012). The central claim of this project is that the defining features of minimal agents—individuality, interactional asymmetry and (minimal) normativity—are grounded in specific features of complex autonomous systems, namely their (i) organizational closure, (ii) thermodynamic openness and (iii) precariousness (Barandiaran et al 2009). The approach of locating agency in the causal architecture of complex autonomous systems is insufficient to ground minimal agency. I claim that minimal agency is not a systemic phenomenon; rather, it is an ecological phenomenon. The minimal agency project fails because it places too much emphasis on the organizational closure of complex autonomous systems, and too little emphasis on the crucial fact that agents are needfully free. For any agent, need (dependence) and freedom (organizational closure) are caught up in an ineliminable “dialectical” interplay (Jonas 1966). For instance, maintaining organizational closure relies on complex forms of openness to and dependence on the agent’s environment. This constitutes the essential predicament of all agents. An ecological account of minimal agency is better able to accommodate the conceptual nuances inherent this predicament. It also provides an account of the source of natural normativity in agency. I contend that an ecological account of minimal agency can naturalistically accommodate what is right in the minimal agency project while clarifying the difficult conceptual issues it raises.

INDIVIDUAL PAPERS

BIOMEDICAL ETHICS AND NON-HUMAN EMPATHY**A matter of national dignity? Tuberculosis, North Korean defectors, and the politics of disease management****KYURI KIM** (Korea Advanced Institute of Science and Technology, Korea); **BUHM SOON PARK** (Korea Advanced Institute of Science and Technology, Korea)

To date, historians have studied the sociocultural meanings of tuberculosis and their relationship with society, such as romanticization, stigmatization or exclusion of patients and related groups. This research argues that tuberculosis in South Korea gained meaning by being translated into politico-economic terms, and demonstrates the politicization of tuberculosis management in the late twentieth century through discourse analysis of policy papers, research publications, media reports and interviews. Tuberculosis has been largely understood

under the rubric of economic development and closely tied to the country’s identity and dignity. Until the 1990s, tuberculosis was considered an obstacle to economic development, which provided justification and motivation for rigorous policies targeting the entire population. Tuberculosis is no longer as rampant but still maintains a constant presence in South Korea, with unprecedentedly high prevalence rates despite the economic advancement. Tuberculosis has thus been described as “unfitting,” and more common among specific marginalized populations—or risk groups. In the late 1990s, the number of North Korean defectors (NKDs) entering South Korea increased exponentially, and a new socially marginalized group at high risk of tuberculosis had emerged. Extra vigilance and care in detection and treatment of tuberculosis among NKDs was institutionalized, but also resulting in the othering and blaming of North Korean public health system and the defectors for importing tuberculosis across the border. Coupled with the long-standing economic frame of understanding tuberculosis as a disease of poverty, the matter of tuberculosis prevalence among NKDs became a medium for demonstrating the capabilities and superiority of the South Korean regime over its northern counterpart. This case of tuberculosis in South Korea shows that disease lies at the intersection of both exclusion and inclusion of Others in society, and that of sociocultural and geopolitical contexts, and is mobilized for the preservation and promotion of national dignity.

A Study in nature: STS reflections on the Tuskegee syphilis study**MARGARET CURNUTTE**** (Baylor College of Medicine, United States)

The history of the Tuskegee Syphilis Study is fairly well known. In 1932 the US Public Health Service (USPHS) initiated an experiment in Macon County, Alabama, to determine the natural course of untreated syphilis in black males. The study continued for forty years, well after it was known in the early 1950s that penicillin could be used to treat syphilis. While the ethical implications of this case have been discussed in great detail, in this paper I would like to draw attention to the significance of how the study was defined. From its inception, the USPHS called the Tuskegee Study a classic “study in nature,” rather than an experiment. This paper first explores the historical origins of the terminology, “study in nature,” locating its origins with Francis Bacon’s distinction between natural experiments, which become studies in nature, and contrived experiments, which are controlled experiments in a laboratory or clinical setting. Second, this paper addresses the significance of this dichotomy, in particular for the Tuskegee Study, from a science and technology studies (STS) perspective. STS scholars, like Latour and Jasanoff, have shown that the notions of nature and politics were developed over centuries in such a way as to make any synthesis of the two terms impossible. The consequence was the separation of (scientific) facts from (social) values. Recent scholarship has shown that natural and social orders are produced at one and the same time, or co-produced. In light of these STS insights I argue that the historical terminology used to characterize the Tuskegee syphilis study reflects important historical boundary-work. The description of the case as a “study in nature” separated the collection of observed “value-neutral” scientific facts from the social and political context that allowed for such a study.

DS M280

11:00 – 12:30

In defense of bottom-up approaches to animal empathy

FÉLIX AUBÉ BEAUDOIN (Université Laval, Canada)

Frans de Waal's "Russian doll model" is a prominent example of a bottom-up approach to animal empathy. As the name of the model suggests, de Waal sees empathy as a multilayered phenomenon. He maintains that "cognitive" forms of empathy (e.g. empathic perspective-taking) are built out of simpler and phylogenetically more ancient ones (e.g. emotional contagion). Two important objections are sometimes made against such approaches. First, they overestimate the role played by lower-order mechanisms, especially in humans. Second, they offer explanations of altruistic behavior in non-human animals that are too "mentalistic". I will address both objections. Drawing on recent work on contagious yawning and autistic spectrum disorder, I will suggest that deficits in lower-order mechanisms disrupt empathetic responses all the way up to the "cognitive level", even in humans. Bottom-up approaches, therefore, are probably right to insist on the key role played by such mechanisms. The second objection draws attention to a general problem with the attribution of mental states (e.g. beliefs, metacognition, phenomenal consciousness, empathy, etc.) to non-human animals. Possible explanations of a given behavior can range from more behavioristic to more "mentalistic" ones, and it can be very hard to tell which type of explanation is preferable. In some cases, the evidence is compatible with both. I will review some of the evidence on altruistic behavior in non-human animals, both anecdotal and from controlled experiments, and argue that many examples of such behavior are best explained in "mentalistic" terms. In other words, it is quite plausible that some animals – especially non-human primates – are able to act on the basis of an understanding of a conspecific's situation, goals, etc. It is also plausible to think that such acts are sometimes motivated by a concern for the welfare of others, rather than by purely egoistic motives.

INDIVIDUAL PAPERS

FITNESS, FEMINIST VALUES AND DRIFT

Evolutionary explanations of female sexuality: Combining feminist values and new empirical perspectives

ESTHER ROSARIO (University of Alberta, Canada)

My paper explores the roles social values, particularly feminist values, and social biases play in evolutionary explanations of female sexuality, including human and non-human primates. I contend that in the case of female sexuality, bias in scientific practice leads to incomplete and empirically unfounded theories of female sexual and reproductive social behaviour. In particular, I hold that evolutionary theories such as sexual selection theory benefit from being assessed in light of feminist values. Furthermore, I argue that incorporating feminist values into theory choice helps correct social bias within evolutionary theory and yields more complete and accurate biological explanations. In so doing, I examine Elisabeth Lloyd's criticism of adaptationist accounts of female sexuality that reduce all sexual behaviours in female primates to reproduction. Lloyd argues that pre-theoretical

assumptions about gender inform and severely limit evolutionary explanations of female sexuality in human and non-human primates. However, I demonstrate how evolutionary biologist Joan Roughgarden's alternative to sexual selection, social selection theory, complements and goes beyond Lloyd's criticism. While Lloyd rightly objects to the exclusive focus on female mating behaviour in the study of female sexuality, I argue she does not do justice to the research interests of those who study how sexual behaviour enhances fitness and she does not offer an evolutionary agenda. I maintain that Roughgarden's view fills this explanatory gap by not merely elucidating flaws in theories of female sexuality that reduce sexual behaviour to mating, but by showing how a diversity of sexual and gender related behaviours comprises a social system (rather than simply a mating system) that promotes evolutionary success. Incorporating feminist values into theory choice, in my view, makes it possible for Roughgarden to identify roles among conspecifics that contribute to evolutionary fitness within a social system, which are influential social behaviours that sexual selection theory overlooks.

Selection as an explanatory shortcut and the nature of evolutionary accidents

FRIDOLIN GROSS (Humboldt-Universität zu Berlin, Germany); **PIERRE-LUC GERMAIN** (Istituto Europeo di Oncologia, Italy)

The exact meaning of "evolutionary accident" is somewhat ambiguous given that there is no intention behind evolution. This paper aims at clarifying this notion and at identifying the sense in which natural selection can be called non-accidental. Since random drift appears to be the paradigmatic example of accidental evolutionary change, we examine its causal dimension and its relationship to adaptation. We note that all accounts of drift, at least implicitly, rely on a distinction between discriminate and indiscriminate causes. We argue that this distinction requires the selective abstraction of causes from their specific context. Drawing on Gould's observations on the Burgess shale, we further argue that natural selection serves as an explanatory shortcut to evolutionary history. Evolutionary accidents, by contrast, are best understood as outcomes that cannot be explained other than by going through the actual sequence of historical events. We conclude that an explicitly epistemic view on natural selection, that focuses on its explanatory role, can promote a better understanding of evolution. This view circumvents ontological fallacies and avoids the conflation that lies at the origin of panadaptationism.

Abstraction and probabilities in evolutionary theory: Why drift is not purely (or perhaps even primarily) a function of population size

JESSICA PFEIFER (University of Maryland, Baltimore County, United States)

There are explanatory reasons to abstract from features of an organism's environment, even though these features are causally relevant to evolutionary outcomes. This has been touted as one of the main reasons biologists invoke probabilities in understanding evolutionary processes (e.g., Sober 1984, Matthen 2009). In the paper, I argue that there are different modes of abstraction, and these different modes affect how we think about the probabilities involved in quantifying fitness. This in turn helps situate the recent debate between the statisticalists and causalists about selection and makes clear why certain criticisms of the statisticalists miss

their mark. However, it also clarifies how we can and ought to think about selection causally. One interesting result of such a causal view is that random drift will not be purely (or perhaps even primarily) a function of population size. Moreover, whether population size makes a difference to the likelihood of drift occurring will be an empirical matter, not a mathematical truth. This has important implications not only for how we ought to think about and model natural selection and drift, but also how biologists might study these processes experimentally. The current paper will focus primarily on these points about drift.

DS M340

11:00 – 12:30

INDIVIDUAL PAPERS

EARLY MODERN NATURE

[Productive nature as an epistemological principle in 18th-century Naturphilosophie](#)

JOSH LALONDE (University of Ottawa, Canada)

The influence of Immanuel Kant (1724-1804) on the development of biology has been studied extensively, while that of his contemporary F.W.J Schelling (1775-1854) has not, although the latter's work was much more closely related to empirical investigations in the life sciences. In fact, a large proportion of historical research on late 18th- to early 19th-century German life sciences is devoted to demonstrating the "respectability" of figures such as Goethe and Kiehmeyer by showing them to be untainted by any association with Schelling's Naturphilosophie. I aim to counter the myth of Naturphilosophie as a flight of mystical fantasy by examining the epistemological basis of Schelling's inquiries into nature: namely the principle that explanations of natural phenomena could only be legitimate if they at the same time explained the knowability of their explanans. I will then examine Schelling's application of these principles to organic nature in his *Erster Entwurf eines Systems der Naturphilosophie* (1799) and his resultant "dynamic" conception of life as being constituted by the interaction of basic forces of matter, which he regarded as an alternative to both mechanistic and vitalist conceptions of life. Finally, I will turn to Schelling's theory of the "evolution" of organic nature as a descending series of gradations, distinguished by the diminishing degree of individuality of the products found at each stage.

[The contamination of the rhinoceros image after Dürer's woodcut](#)

ROBERTO DE ANDRADE MARTINS (Universidade de São Paulo, Brazil)

In 1515 Albrecht Dürer produced his famous woodcut of a rhinoceros, supposedly depicting an Indian specimen that had been brought to Portugal. It is well known that Dürer's woodcut was not faithful to the real animal and that it had a strong influence on zoological descriptions of the rhinoceros, until it was corrected in the 18th century. This paper will address the impact of Dürer's woodcut, describing three episodes: the wrong description of the rhinoceros by a Portuguese eye witness; the distorted description and representation of Roman coins that exhibited a rhinoceros; and the unrealistic drawings of live rhinos brought to Europe in the following centuries. Those instances show how strong can be the influence of preconceptions on observations.

[Rediscovering nature through the visual culture of the Royal Botanical Expedition to New Spain \(1787-1803\)](#)

DIANA HEREDIA (Universidad Nacional Autónoma de México, Mexico)

The illustrations made by Atanasio Echeverría and Vicente de la Cerda during the Royal Botanical Expedition to New Spain became widely known by scientists and historians alike when two thousand of them were found in a private library in Barcelona in 1980 after being lost for more than a century. Before their disappearance in 1820, the illustrations had already travelled to Madrid, Montpellier and Geneva, where they were examined by leading figures in botany at the time. However the long sought publication of these illustrations and other materials from the expedition remained unfinished until 2010. Although there is a considerable amount of scholarship on the Royal Expedition to New Spain itself, few works have analyzed the importance of the visual culture produced in this expedition under the light of new historiographical tools such as the circulation of scientific objects. This paper aims to review the work and research that has been done on each of the contexts in which the illustrations (or their absence) circulated from 1570 to 1980. This is the first and most reasonable approach in the construction of a large-scale history that uses the circulation of knowledge as a cohesive tool. Furthermore, this review shows that there is still much unwritten on the role of colonial artistic institutions in the training of draughtsmen and the establishment of scientific illustration as a practice, as well as the significance of the circulation of visual and print culture associated with the illustrations in Europe and Mexico during the nineteenth century.

DS M440

11:00 – 12:30

INDIVIDUAL PAPERS

SOCIALITY AND COMMUNICATION

[Only following orders: Are instructions the most primitive kind of semantic content?](#)

OLIVER LEAN (University of Bristol, United Kingdom)

What does semantic information look like in biological systems far simpler than human brains and language? Recent work has aimed to make sense of semantics in simple biological systems, but without assuming rich linguistic properties like subject-predicate structure or combinatorial syntax. For example, some have proposed a kind of simple semantic content that doesn't make the familiar distinction between propositions and instructions, instead carrying an undifferentiated mixture of both. This includes Millikan's notion of "Pushmi-Pullyu Representations", and William Harms's "primitive content". This content is carried by signals which simultaneously track the state of the world and govern behaviour; it's argued that it isn't until communication becomes more complex that signs begin to carry one or the other. While they shed some of the anthropomorphic baggage, these accounts of simple semantic content don't actually solve the key problems of 1) grounding content in objective facts about the systems in question, and 2) providing a clear standard of error that's necessary for semantics of any kind. Instead, under the minimal conditions given by these accounts, the only clear semantic

content is that of simple instructions. I justify this from a number of angles. In the language of Lewis-Skyrms signalling games, it's because of the conceptual priority of "receivers" over "senders": every sender is a receiver, but the reverse isn't true. In the language of teleosemantics, it's a consequence of a re-thinking of the kind of etiological functions (and their malfunctioning) that should determine this content. I'll illustrate with a number of molecular case studies, such as allosteric proteins, hormone receptors, and gene expression. However, I'll suggest that this may also be true of higher-level phenomena like simple animal signals.

"The enlightened step of rationing": Bill Hamilton, the theory of inclusive fitness, and perceptions of a post-World War II population crisis

SARAH SWENSON (University of Oxford, United Kingdom)

The limits of positive social behaviors, such as altruism and cooperation, were a pressing concern in the postwar decades. The desirability of international peace and the possibility of a global economy meant that scholars and politicians alike debated the likelihood that disparate groups could work together. Many biologists felt that their discipline was uniquely capable of understanding the nature of human conflict as well as the probability that it could be successfully eliminated, and some believed that biology should play a role in political decision making. By the late-1950s, several studies claimed that crowding exacerbated tendencies towards aggression and social deviancy. In light of these results, prominent biologists such as Julian Huxley, G.C.L. Bertram, and William Thorpe argued that the greatest danger of the time was not communism but overpopulation. As a young man in the 1960s, Bill Hamilton inherited many of these biologists' assumptions. While he developed and began to articulate the meaning of his now famous theory of social behavior, he demonstrated a deep concern for the population crisis and the threat it posed to the future of humankind. For Hamilton, the population crisis was difficult to combat because it was at its roots a biological problem: organisms had been genetically programmed to maximize the number of their genes that survived to the next generation. This paper will build upon primarily unpublished documents held in Hamilton's personal archive to illuminate the relevance of the theory of inclusive fitness to concerns surrounding population growth in the second half of the twentieth century. In doing so, we may examine the relationship between biology and policy in these years and begin to understand why, by the early 1970s, Hamilton urged that governments should make "the enlightened step of rationing" rights to bear children on scientific grounds.

The explanatory utility of "meaning" and "reference" if animal communication is indexical: A sceptical analysis

DAVID KALKMAN (Australian National University, Australia)

Should animal communication be regarded as the exchange of information between senders and receivers, or as senders merely influencing receivers? Recent work on this question has focused on the phenomenon of functional reference in order to critically analyse whether animal communication involves symbolic reference, which would set animal communication apart from mere influence if true. However, authors now mostly agree that the mechanisms underpinning the production and reception of functionally referential signals are too simple. Despite this, some still resist reverting to an influence picture of animal communication. These informational proponents have instead shifted focus towards the plasticity of signal reception in many communicative species, holding that animal communication is indexical, as opposed to symbolic. Signals carry information in the sense of raising the probability of particular world states relevant to receivers. In virtue of this, receivers may adaptively associate particular responses with signals in their own lifetimes. It is claimed that these facts warrant talking about the meaning or reference of signals as part of proximate explanations of animal communication. I argue against this. Talk of meaning or reference is not yet warranted because receivers need be responding merely to the proximal physical features of signals. I construct a three tiered hierarchy corresponding to different degrees of mechanistic sophistication that can underpin nonhuman animal communication, and locate the explanatory utility of linguistic notions like meaning and reference on the highest level only, where receivers respond "robustly" to distal features of their environment, and where for the first time the information signals carry in virtue of their relational properties can come apart from the influence such signals have in virtue of their physical properties. My main concern is that talk of meaning and reference, when not warranted by the details, attributes too much cognitive sophistication to animals.

DS M460

11:00 - 12:30

INDIVIDUAL PAPERS

GENETIC DIVERSITY, SOCIAL EMOTIONS AND SEXUAL DESIRE IN EVOLUTIONARY CONTEXT

Genetic diversity among humans: A human rights issue?

BENJAMIN GREGG (University of Texas at Austin, United States)

To manipulate a human's DNA sequence genetically is to change the genome of an individual — or an entire species. The attractions of engineering are powerful. Just consider the tremendous social consequences of an individual's skin color or sex. Many other characteristics may loom large in a person's life and may be relevant in matters of social justice. In postindustrial populations, for example, height appears to matter for both mate preference and mate choice. With identical educational levels, taller men generally enjoy better careers than short men because, for example, they tend to receive greater supervisory responsibilities. Height is also an important

factor in various sports. One might well conclude that most people would prefer to be tall than short. Within ten years research may well be able to identify the causal genes for human stature. Much more consequential, of course, is intelligence. The heredity of intelligence has been confirmed by several large-scale studies. With the completion more than ten years ago of the sequencing of the human genome, several genome-wide association studies have identified six different chromosomal regions and sixteen candidate genes associated with human intelligence as measured by IQ scores. With accelerated technical development in neuroscience, research may identify the causal genes for human intelligence within a matter of decades. Today and in the future, manipulation is motivated not only by an interest in health but also by political, economic, and cultural beliefs and goals. And, I argue, it will lead to less genetic diversity among humans — unless political community constructs a human right of “pre-personal life” (such as a fetus) not to be genetically engineered. I frame my analysis with the question: Might a human embryo be culturally understood as possessing a human right to be free of genetic manipulation, or free at least from genetic enhancement where enhancement can be distinguished from genetic therapy? And exactly what reasons speak for, and which against, political community constructing human life at the pre-personal level as human rights bearing? I answer this question in two steps: (1) I show that human nature and human culture lie on a continuum such that “human nature,” especially as it results from genetic manipulation, is nothing natural but rather a cultural choice because the legal and moral regulation of genetic enhancement finds no guidelines in nature. Genetic modification is always a political act — and the stakes of cultural and political preference and commitment only increase with biotechnological development. (2) To regard human nature as a cultural choice allows equally for opposite conclusions: either (a) pre-personal life is “human nature” or (b) it isn't. I develop a means by which a political community might determine which of these options is preferable. (a) To grant legal and other forms of recognition to an embryo or fetus would prevent their genetic manipulation — but the consequences would drastically change social and political organization. Some changes might be welcome, such as “remedial enhancement” in which political community classifies parents' genetic characteristics along some dimensions as “below normal.” Public policy might then champion embryo modification in ways that render that dimension “average” (or above) in the person who developed from that embryo. But other changes would be very unwelcome, including the criminalization of whole areas of life protected, in the United States, as matters of a right to privacy (such as abortion). (b) If pre-personal life is not a human being in the sense of a human rights-bearing life, then of course it enjoys no human right against being genetically manipulated. In that case, genetic engineering will facilitate choices by parents and others that will lead to decreased genetic diversity among humans. Consider, for example, pre-implantation genetic diagnosis (PGD), introduced only twenty years ago. It screens for genetic disease-free embryos; couples at high risk for offspring with genetically inherited disease are screened prior to implantation. Embryos without detectable genetic defects become candidates for transplantation into the mother's uterus for gestation. Although PGD is now routinely performed in doctors' offices, selection for intelligence or physical appearance has yet to be performed. But such an application one day soon could become routine wherever the relevant technology becomes available at locally plausible costs.

Emotions in social contexts in primate societies: An evolutionary approach

ALBA LETICIA PEREZ-RUIZ (Centro de Estudios Filosóficos, Políticos y Sociales Vicente Lombardo Toledano, Mexico)

The study of emotions has been addressed from different scientific disciplines. These areas of research have given as result the development of several theories of emotions. This work focuses particularly on scientific studies of emotions in nonhuman primates from an evolutive approach. It is known that emotions, commonly described as human subjective experiences, were considered inaccessible for animal research. Nowadays this position has changed. From an evolutionary perspective, emotions can not be assumed as a human exclusive trait because most of brain structures related with emotions are similar in all primates. Darwin in *The Expression of Emotions in Man and Animals* wrote that humans and animals, at least mammals, express their emotions in similar ways. Moreover, the expression of emotions has been related with survival and individual fitness. Scientific research on emotions related with social relationships in nonhuman primates is complex, mainly, among other variables, because of subjectivity. Nonetheless, important systematic studies have been developed. The approach to the study of emotions is from two levels ontogenetic and phylogenetic. Emotions are modulated by the synergic effect of different factors that can be internal and external. According to this, emotions are multi-determined and are product of internal states and external context, as well as physiological and behavioral changes. In a primate group, individuals behave differently according with the circumstances of social context and they interact in a different way with the distinct members of the group. In well established groups of primates, aggressive episodes between individuals disturb their social relationships. This change in the social relationship is related to changes in emotional responses. Aggressive interactions that damage social bonds and affiliative interactions that restore social relationships are examples of emotional variation in nonhuman primates.

Science and sexual desire

SHARYN CLOUGH (Oregon State University, United States)

Philosophers of science have not had much to say about the sciences of sexual desire. And what little relevant philosophy of science research there is, remains focused on methodological missteps in psychiatry, evolutionary psychology, behavioral genetics, endocrinology, and neurophysiology—typically as applied to human behavior more generally—with concerns about the science of sexuality used only as examples. Of these examples, most focus on problems with the scientific investigations of male homosexuality. While we are interested in methodological problems with the science of sexual desire—including the pathologizing, heterosexist focus on male homosexuality—we are mostly interested in what would count as methodologically sound, compelling, and insightful scientific investigations of the broad spectrum of sexual desire. Answering this question requires examining some common themes of resistance to the very idea of a science of sexual desire: Why do scientific approaches to sexual desire, even at their methodologically most sound, seem unable adequately to capture the variation of interest, to (many of) us, as desirers? Why do some of us (all of us?) feel threatened when we discover that some of the variation of interest can be explained by scientific approaches? We propose that the

answers to these questions are related to our collective and common failures to understand both what it means for human sexual desire to be an appropriate object of scientific investigation, and how scientific investigation is a practice of humans with (sexual) desires. Stated positively, we have a collective need to remind and be reminded that the moral/intentional realm of sexual desire is fact-laden, i.e. there are patterns to examine, predict, and explain. And on the flip side, the factual domain of the sciences of sex is laden with the moral/intentional all the way down.

DS R510

11:00 – 12:30

ORGANIZED SESSION / STANDARD TALKS

DE-EXTINCTION

Organizer(s): **MARKKU OKSANEN** (University of Eastern Finland, Finland)

Bringing extinct species back to life may be possible in the near future. If researchers are successful, this challenges the basic assumption of conservation: extinction need no longer be forever. Terms “recreation”, “resurrection”, “reviving”, “resuscitation” and “extinction reversal” have been used to denote this action but it seems that the new term “de-extinction” has now become prevalent. **Oksanen** and **Siipi** have edited a volume *The Ethics of Animal Re-creation and Modification* (Palgrave, 2014) that includes their and **Turner**'s contributions. This session will further elaborate the theme by focusing on three interrelated ideas: the concept of irreversibility, de-extinction as a form of selection, and the commodification of de-extinct animals.

De-extinct species as property objects and as wildlife

MARKKU OKSANEN (University of Eastern Finland, Finland)

The paper will examine the clash between commodification and rewilding of de-extinct animals. On the one hand, the re-creation of such animals is likely to be driven by financial incentives: it is easy to picture to oneself how live creatures could be used commercially (in the spirit of *Jurassic Park*) or some aspects of the re-creation processes could be protected by means of intellectual property rights. On the other hand, as far as de-extinction is used as an instrument for biodiversity conservation, the animals it produces should be classified as wildlife because the original species was never domesticated. Because of the dominance of financial interests, however, the rewilding of de-extinct animals in the proper sense is a highly improbable scenario. The reason for this is that rewilding would mean that one should renounce one's property rights to those animals.

De-extinction and the finality of extinction

HELENA SIIPI (University of Turku, Finland)

The fast developments in cross-species cloning have inspired numerous writers to state that soon extinction no longer needs to be forever (see e.g. Rosen 2012; Redford et al. 2013; Sherkow and Greely 2013; Kumar 2012; Phillips 2013). These statements rest on the presupposition that finality of extinction is not necessary but something can be changed by technological development. Yet, differing views have been presented: “Extinct also says something about the future of the class – that once it becomes a null class, it can never come to have members again. It may be claimed that this is what extinct means” (Gunn 1991). In this paper, I examine the possibility of fitting the current technological developments in resurrection science together with the idea of finality of extinction. The following three alternatives are discussed: (1) Animals born from de-extinction procedures fail to be members of the original species. Rather, these animals belong to a new human-created species (Garvey 2007) that is a copy of the original species. (2) Animals born from the de-extinction procedures are members of the species that once died out, but despite their existence, the species remains extinct. There are two types of extinct species: ones that have not been re-created and the ones that have been re-created. (3) Animals born from de-extinction procedures are members of the original species but extinction did not take place before they came into being. Extinction means loss of information necessary for producing an individual with characteristics of the species (see Delord 2014), and in the case of animal re-creation, the original species never went extinct.

De-extinction, biodiversity loss, and artificial species selection

DEREK TURNER (Connecticut College, United States)

Species selection is an idea that emerged from the work of paleobiologists in the 1970s and 1980s, with prominent advocates including Steven Stanley, Stephen Jay Gould, Elizabeth Vrba, and David Jablonski. Much of the discussion of species selection has focused on (and at times gotten bogged down in) conceptual issues. Although there are a few important studies that put the idea to work, it's not clear that species selection theory has generated much fruitful empirical research. Nevertheless, the concept of artificial species selection could turn out to be useful in conservation biology. One way to think about the biodiversity crisis is to focus on extinction rates, and to project recent trends forward with the aim of assessing the probability of a mass extinction event over the next few centuries. But this focus on the rates and amount of biodiversity loss overlooks the fact that the biodiversity crisis also involves a species-level sorting process. Lately there has also been a great deal of hype about de-extinction, or the possible future use of biotechnology to reverse recent extinctions. That, too, would be a straightforward case of artificial species selection. Species selection theory can help us to think through the ramifications of de-extinction.

DS R515

11:00–12:30

ORGANIZED SESSION / STANDARD TALKS

BEYOND “INFORMATIONISM” AND MACHINE MODELS: RADICALLY RETHINKING THE PHYSICAL BASIS OF LIVING SYSTEMSOrganizer(s): **LENNY MOSS**** (University of Exeter, United Kingdom)

Could molecular biology have been a mistake? Are the avatars of “The New Mechanism” barking up a dead tree? Drawing upon aspects of biophysics, biochemistry and theoretical biology, this session will critically assess the shortcomings of “informationist” and “mechanical” models in meeting current challenges in the life sciences and suggest some radical alternatives. The meaning and place of “reductionist” methods will also be addressed in this context as will the idea of “top-down” causation. **Newman**’s paper will make a case for the role of “generic” physical processes in morphogenesis, and the inapplicability of cybernetic approaches to biology. **Moss**’s paper will focus more specifically on the ubiquitous roles of aqueous chemistry including hydrogen bonding, the transfer of hydrogen atoms as well as protons, and the role of “hydrophobic hydration” in constituting the organisational and functional conditions of any living system.

A renewed physicalism for organismic biology?Organizer(s): **SAHOTRA SARKAR** (University of Texas at Austin, United States)

In recent decades philosophical work in biology has veered between two extreme agendas. The first is one that presumes concepts and techniques borrowed from the philosophy of mind are of relevance to biological research. (An example is the use of arguably dubious teleosemantic analyses in attempts to explicate a concept of biological information.) The second, which is embraced by this paper, presumes that biological systems must be understood in continuity with physical systems, that is, apparently unique biological features are expressions of physical constituents and interactions that do not distinguish between animate and inanimate matter and have no irreducible intrinsic teleology between them. This “new physicalism” has typically been expounded as some form of reductionism. After motivating the physicalist agenda for biology, this paper turns to the varieties of reductionism and develops one in which a carefully explicated mereology becomes central to epistemological projects. The paper then turns to the recent excitement about the new mechanism. It points out that what is valuable in it has long been embraced by this form of reductionism and was central to debates between mechanists and emergentism in the 1920s and 1930s. More controversially, it argues that the rest of the new mechanism embraces a metaphysically naive realism about the status of mechanisms which are not only typically left ill-defined but also misses the crucial insight (due to the logical empiricists) that the same system can be multiply (and inconsistently) decomposed into groups of mechanisms for different explanatory projects. Finally the paper ends by noting the complex conceptual relations between the new physicalism and various forms of emergentism.

Evolution of development was empedoclean, not cyberneticOrganizer(s): **STUART NEWMAN** (New York Medical College, United States)

Present-day animal embryos derive from ancient cell clusters that exhibited forms and patterns based on their material properties. For example, the clusters assumed multilayered, hollow, segmented, elongated and appendage-bearing configurations depending on conditional physical effects mobilized by the resident genes and the resulting interactions among the cells, and between the cells and the external environment. Over time, the loosely organized morphological motifs of phenotypically plastic pre-metazoans were compounded into integrated, reliably generated wholes by entry into “satisficing” (as per Herbert Simon) ecological niches and relationships. This view, which is similar to that advanced by Empedocles of Agrigentum 2500 years ago, is more consistent with experimental and paleontological evidence than that of standard evolutionary theory, in which machine-like, gene-controlled developmental programs were built up in a gradual fashion by stringent adaptive regimes, with morphological complexity only achieved after numerous selection cycles. These points will be illustrated by examples of discontinuous change and discordances between genes and form in animal development and evolution.

DS R520

11:00–12:30

ORGANIZED SESSION / STANDARD TALKS

WORLDS APART? ARISTOTELIAN AND CONTEMPORARY BIOLOGICAL EXPLANATION AND THE PRIMACY OF THE ORGANISMOrganizer(s): **ANNE PETERSON** (University of Utah, United States)

Aristotelian biology is often described as “essentialist” in a way that over-emphasizes the role of the species form and under-emphasizes the role of the individual organism in biological explanation. This focus on form at the expense of the organism leads to a devaluation of the emphasis Aristotle placed on the organism, both with respect to the developmental process and with respect to the reproductive process. Restoring the organism to its rightful place in biological explanation for Aristotle leads to promising points of connection with contemporary evolutionary developmental biology and evolutionary theory more generally. It also supports a view of Aristotelian form that underscores form’s dependence upon the way of life of a certain group of organisms, along with form’s teleological connection to matter. In general, the priority Aristotle accorded to the role of individual organisms in answering biological questions about generation, development, and being is a clear point of contact with contemporary biology. Where do the points of conflict between contemporary and Aristotelian biological explanation lie, and can Aristotelian models, including concepts such as matter and form, potentiality and actuality, still be helpful for answering questions that arise on the contemporary scene?

Aristotle on bodies, souls and ways of life

JAMES LENNOX (University of Pittsburgh, United States)

There seems to be a rather fundamental tension in Aristotle's *De anima*. It begins by arguing that organisms' organic body is their matter and their soul is their form—form understood as the perfected capacity of an organic body. But it also argues that there are many distinct soul capacities, and different organisms may have organ systems capable of expressing one or more of these capacities. How then are we to understand the unity of an organism—is an organism simply the sum total of its organs and organic capacities, or is there an account of why different organisms have the particular set of structures and capacities they do? In this paper I argue that an overlooked concept that is central to his biological enterprise, the concept of βίος (way of life) is the key to answering this question. This concept plays a central role both in Aristotle's systematics and in his explanatory theory, in accounting for why different kinds of animals have the distinctive structures and capacities they do; but it also explains the coordinated nature of an organism's parts and behaviors—what Cuvier, an attentive reader of Aristotle, referred to as the “correlation of parts”. In order to drive this point home I look carefully at the closing paragraphs of his philosophical introduction to zoology, *Parts of Animals* I.5, and then examine his account of the different adaptations of birds to their different ways of life, especially in *PA IV.12*. Implicit in his theory and practice is the view that the unified organism, adapted to a particular way of life, explains the particular organization of organ systems and living activities that different kinds of organisms have, rather than the other way around.

Mechanism or hylomorphism? A plea for organisms

DENIS WALSH (University of Toronto, Canada)

One of the impediments to a thoroughgoing organicism is methodological. The properties of organisms that influence evolution—their plasticity, their self-synthesising, self-regulating, goal-directedness—are emergent properties. But the very idea of emergence is thought to have been rendered incoherent by reductive mechanism. Everything that wholes can explain can be explained by parts. Contemporary “anti-emergence” is predicated on two implicit metaphysical assumptions about causal powers: intrinsicity and foundationalism. Together they entail that the causal properties of a complex entity are fixed exclusively by the causal properties of the parts. There has been recent interest in exploring an updated version of Aristotelian essentialism for evolutionary biology. The leading idea, deriving from recent work by Lennox, is that an organism's βίος—“way of life”—is an explanatorily basic teleological property, a “nature”. An organism's nature in turn, according to Aristotle, is the consequence of the reciprocal constraints of its form and matter. Form consists in an organism's purposive capacity to organise matter in ways conducive to its pursuit of its way of life; matter consists in the range of possibilities for an organism's pursuit of a way of life. One unappreciated virtue of biological neo-Aristotelianism is that it offers an argument against anti-emergentism (and a fortiori for organicism). There is a reciprocity between the capacities of organisms and their parts that reflects the reciprocity between Aristotelian form and

matter. The explanatorily salient properties of organisms—as manifested in their goal-directedness—are fixed by the causal properties of their parts. Yet, reciprocally, the salient properties of organisms' parts are fixed by organismal goal-directedness. Where causal (material) properties are allowed to be relational and contextual (rather than intrinsic and foundational) the kind of part/whole reciprocity that is characteristic of emergence is entirely coherent. Neo-Aristotelianism about organisms is a form of emergence.

Reproduction, form, and organism in Aristotle's metaphysics and biology

ANNE PETERSON (University of Utah, United States)

Passages from Aristotle's metaphysical and biological writings alike suggest that an organism's father, rather than its species form, is (if all goes well) the primary or fundamental cause of that organism's generation and of its characteristic features. Understanding a father's role in reproduction primarily in terms of a vehicle for transmitting the species form is therefore misleading because it glosses over the Aristotelian priority of organism over form. Generalizing from “father” to “parents,” it is better to say that Aristotelian biology agrees with contemporary evolutionary theory in maintaining that an organism's parents are the fundamental locus of explanation for the generation of that organism with its characteristic features. How, then, should we understand the role of form in reproduction? The explanatory priority of organism over form suggests that for Aristotle, a species form corresponds to generalized capacities that are dependent upon fully determinate capacities within individual organisms of that species. It is these fully determinate features and processes that are, per se, transmitted from generation to generation, with this transmission being caused by the parents; the species form is carried along for the ride. However, Aristotle's view that the explanatory role of form in reproduction is posterior to that of the organism does not divest form of its metaphysical status as a genuine component of organisms. Moreover, the way in which Aristotle privileges the explanatory role of the organism over that of form in the reproductive process means that on his view there is no metaphysical barrier (though there may be other sorts of barriers) to the generation of new forms and hence of new species. I will end by suggesting some consequences of this Aristotelian priority of organism over form for the relevance of Aristotelian metaphysical concepts within contemporary biology.

12:30 - 15:30

LUNCH BREAK

13:00 - 15:00

COUNCIL MEETING | Room DS-1955

DS 1520

15:30–17:00

ORGANIZED SESSION / STANDARD TALKS

ONTOLOGY AND EPISTEMOLOGY OF IDENTIFYING CHARACTERS AND GENESOrganizer(s): **SHUNKICHI MATSUMOTO** (Tokai University, Japan); **ALAN LOVE** (University of Minnesota, United States)

Identifying characters in organisms is a starting point of almost all biological explorations. Researches in systematics, evolutionary theory, genetics, physiology, pathology, etc. depend on the precise description of characters. However, biologists have always been puzzled about characters, not only because the discernibility of characters among closely related organisms is not always warranted but also because the factors that are responsible for bringing about those characters are intertwined. These puzzles raise many related questions: To what extent and by what approaches can we individuate characters and their variations? Are the individuated characters character types or individual characters? To what extent and by what approaches can we identify causal factors (typically, genes) that are responsible for characters? Are the identified genes gene types or individual genes? To date, biologists have been able to individuate characters and genes via different approaches. Evolutionary theory, developmental biology, classical genetics, molecular biology, and other biological sciences offer different approaches that may be separated or related. Our session aims to explore the problems of how separated or related those approaches are. **Suzuki** and **Tanaka** address the issue about how to understand homologous characters. In order to overcome the problems in each of the currently prevalent two theories about homology — the individuality theory versus the homeostatic property cluster (HPC) kind theory — they propose their own reproducible-persistent-module (RPM) theory. **Matsumoto** discusses the case of the discovery of the cystic fibrosis gene to examine what methodology was employed in the identification process. He especially notes the relevance of evolutionary gene concept in the modern molecular biology. **Chen** explores the individuation of genes from the experimental perspective. He argues that the theory of classical genetics and its attendant experiments actually individuated only some types of gene, while experiments from the biotechnology of transgenes could individuate a particular gene.

Beyond the dichotomy of individual and kind: The reproducible-persistent-module (RPM) theory of homology

DAICHI SUZUKI (University of Tsukuba, Japan); SENJI TANAKA (Keio University, Japan)

Homology is one of the central concepts in biology, but its ontological status is still controversial. We consider it by comparing two theories: the individuality theory and the homeostatic property cluster (HPC) kind theory. According to the individuality theory, homology is a relation of correspondence between parts of individuals (Ghiselin 1990, 2005). According to the HPC kind theory, a homologous character (or a homologue) is a natural kind defined by a homeostatic property cluster (Assis & Brigandt 2009, Brigandt 2009). Both theories have not only their own advantages, but also problems. For example, it is difficult for the individuality theory to accommodate the fact that homologous characters are often genetically discontinuous, and the fact that they are often abstracted to some kind-like “types” or “body plans” even by the contemporary biologists. On the

other hand, properties and underlying mechanisms of homologous characters (e.g., molecular components of vertebrate lenses, regeneration/developmental mechanisms of newt lens) are often too variable for the HPC kind theory to explain. Moreover, the HPC kind theory is likely to blur the boundary between homology and analogy (Brigandt 2009), which is important and useful for biologists. So here we propose a new conception of homology: the reproducible-persistent-module (RPM) theory. According to the theory, homologous characters are modular structures that are reproducible and persistent in evolutionary/biological (life history) processes. Homologous characters as modules are not only spatiotemporally restricted (because they are actual modular structures realized in some specific processes), but also have properties that are homeostatic to some degree (because they are persistently reproducible). Thus the RPM theory accommodates both individual-like and kind-like characteristics of homologous characters.

Cystic fibrosis as a case study for the identification of the gene

SHUNKICHI MATSUMOTO (Tokai University, Japan)

I will take up Collins, Riordan, Tsui, and colleagues' historical feat of identifying the cystic fibrosis transmembrane conductance regulator (CFTR) gene in 1989 as a case for studying the issue concerning the identification of the gene. What is noteworthy about their work is that it employed the approach of “reverse genetics,” for they had to set out for the endeavor while knowing little about the protein synthesized from it. On the other hand, discovering the mutations that give rise to pathological symptoms involved the approach of “forward genetics,” for it started with the CF phenotypes of patients and then went downward to track down the underlying genotypes (mutations). As for the causal pathways concerning how these mutations actually cause CF symptoms, the explanations available today still remain more or less sketchy although the genotype-phenotype relationships in the modern molecular biology have been described far more in detail, as compared to those counterparts in the old classical genetics. From the analysis of this case, the following points can be obtained. First, we can point out a kind of conceptual isomorphism between “the gene for X” talk emblematic of evolutionary biology and “the gene for CF” one which is one of the exemplars of molecular biology. Second, more important, in some context it is a prerequisite for an arbitrary DNA sequence to be identified as a gene (coding region) that it is an evolutionarily conserved sequence. For, the researchers eventually managed to track down the gene for CF by comparing the DNA sequences they had just decoded with DNAs from other organisms, based on the idea that evolutionarily conserved sequences across species are highly likely to encode some functional polypeptides. Thus, I will argue for the relevance of the evolutionary point of view in the modern molecular biology.

The experimental individuation of genes

RUEY-LIN CHEN (National Chung Cheng University, Taiwan)

Recently, biological individuality has become a central issue in the philosophical discussion of biology. Philosophers focus on the question of what counts as biological individuals and usually approach this question via theories – evolutionary, physiological, or immunological (Godfrey-Smith 2013; Clarke 2013, Pradeu 2010, 2013). They view different biological theories as providing different principles of individuation for defining biological individuality. However, theories are not the only access to the definition of individuality; experimentation may offer an alternative approach. Even experimentation can individuate a particular object while theories can only individuate a kind or a type. In the case of the gene, for example, Gregor Mendel assumed that hereditary factors of features are unitary and corpuscular things – scientists called them genes later. The classical geneticists built up a theory of genes and performed experiments to identify some individual genes. In this sense, one might well say that the classical geneticists experimentally individuate genes. However, I will argue the genes that the classical geneticists had individuated were no more than the gene kinds or types. Genes as particular objects had not been individuated till biotechnology of transgenes was invented. Here I presuppose a distinction between the individuation of kinds and the individuation of particular objects. I will also explore the relationship between the two kinds of individuation.

ORGANIZED SESSION / STANDARD TALKS

FAILURE IN SCIENCE

Organizer(s): **ANN-SOPHIE BARWICH** (Center for Science and Society, Columbia University, United States)

Science fails. And it fails on a daily basis. Experiments go wrong, measurements do not deliver anticipated results, probes are contaminated, models are considered too simplistic and not representative, and some inappropriately applied techniques lead to false positives. When philosophical debate has dealt with scientific failures, it predominantly focussed on justifying the success of the scientific enterprise in terms of its capacity to represent reality. An often-overlooked characteristic of science—not at least in the quest for more grants and media suited success stories—is that it inevitably must fail to do the job it sets out to do. For scientific research to exceed our initial modelling assumptions and to continuously trump our ever-adjusting experimental limits, things have to go wrong. We want to investigate different aspects of failure as integral to science. Our interest in failure refers to more than the obscure “element of surprise” or an incentive to do better next time. We think that failures in science are beneficial in their own right. Not only because failures might lead to accidental findings, or because they correct prior assumptions in an experimental set-up. Rather, we think failures guide scientific enquiry on a par with success stories. Failure complements success more than in some proverbial sense: While a success enforces a current research strategy, failure opens up many different alternatives routes

broadening our inquiry. By asking why something appears to present a failure, different possibilities are conceived. Each of these possibilities can be investigated by designing constraints under which different features and behaviours of research materials are modelled and simulated. Failure requires creative and flexible reasoning that exceeds a given modelling outset. The importance of failure in science lies in its demand to rethink the constraints that underlie our models and, moreover, our current successes.

Explicit failure

STUART FIRESTEIN (Columbia University, United States)

Public support (i.e., money) for science is critical, but we find a public ever more excluded from the scientific process, left with second hand newspaper accounts of a stream of discoveries. This is further distorted by an educational program that presents science as an impenetrable mountain of facts often presented in an equally impenetrable language. The problem is not significantly remedied by presenting the public with outreach programs of “science for dummies” lectures by leading scientists. Although these lectures, when done well, are often entertaining and provide the public with a slightly friendlier view of science, the problem in the end is not one of information but of attitude. Scientists know implicitly that it is questions that count more than facts and that failure is an integral part of the scientific process. Certainty is rare and because of its common association with authority is usually suspect. Thus science is most creative because it traffics in ignorance, failure, doubt and uncertainty. Remarkably these add up to a 400 year record of success and progress unparalleled in human history. Why is it so difficult to make this implicit scientific method of failure and ignorance, the real scientific method, explicit to the non-professional scientist? Are failure and ignorance the possession of an elite corps of PhD scientists? Indeed are they even the possession of many working scientists? Do pressures of funding and promotion steer most scientists away from risky questions that have a high potential for failure, pushing them instead to adopt safe if less interesting research programs. With a low tolerance for failure and uncertainty we promote a science that lacks courage and patience and sacrifices creativity for the mundane. Can this be rectified? Galileo changed the attitude of both church and public towards science with a single book.

Intrinsic hidden constraints in data-intensive biology

ISABELLA SARTO-JACKSON (Konrad Lorenz Institute for Evolution and Cognition Research, Austria)

Biology is progressively changing into a data intensive science. Advocates of big data are thrilled about the prospects that the limitations that previously forced researchers into hypothesis-driven research can now be overcome by using data-driven approaches. Concomitantly, these experts urge that science has to get past its historically rooted obsession with causal explanations in favor of revealing relationships of data by correlation methods. They claim that knowing what, not how, is good enough for answering scientific questions. And in fact, data intensive success stories have opened new empirical avenues in biology, such as designing diagnostic tools and developing high-throughput technologies. These advances have proven particularly valuable in

DS 1540

15:30–17:00

applied sciences. However, the unwaning enthusiasm for a successful strategy often comes at the expense of overlooking hidden constraints. Scientific observation is perspectival, the nature of instruments, the methods, and the data measured reflect only a selected aspect of reality through which researchers interact with the world. The vast scale notwithstanding, scientists still apply well-established, standard scientific methods to get from the actual data to models. Thus the practice remains internal to the scientific perspective. This is irrespective of the underlying data volume and analyzing methods. To make matters worse, the more successful (in terms of richness of answers) a strategy seems, the more negligible it seems to go beyond its borders. But this is where intrinsic constraints are concealed. In line with Firestein, I believe that basic science begins where data run out and new questions must be created. To draw (causal) conclusions going beyond the current scientific perspective, researchers have to move to a broader theoretical perspective by temporarily neglecting facts and correlations in a controlled manner. I will support my claim using recent examples from big data approaches of molecular and structural biology that are used for “rational drug design”.

“Simply” failure or delayed success? Mapping smells in the brain

ANN-SOPHIE BARWICH (Center for Science and Society, Columbia University, United States)

What is considered a failure or a failing research strategy in scientific practice? It is often not obvious whether a lack of success is based on the characteristics of the target-system, the choice of theoretical concepts or current instrumental boundaries. I want to understand what forms of failure render the need for alternative research strategies visible by analysing when modelling limits become interpreted as failures (rather than delayed successes) of standard approaches. I address this question by looking at contemporary research mapping smells in the brain. It was long thought that the olfactory pathway works similarly to the visual system, forming topographic activation patterns in the cortex. Previous studies had successfully established a clear activation pattern in the olfactory bulb (a multilayered neural structure situated in the frontal lobe of the brain). But the apparent lack of a clear spatial organisation of activation patterns in the olfactory cortex presents one of the major research puzzles today. A recent study (Chen et al. 2014) now indicates that olfactory processing in the piriform cortex (PC) exhibits a different organisational principle. In this study, the experimental method was old but the conceptual modelling strategy was new. Drawing on this study, I examine when research strategies—such as modelling possible cortex activations based on bulb patterns—require re-examination. What is considered a modelling constraint and what a failure? And how are previous experimental failures influencing the conceptual development of alternative questions?

DS 1545

15:30 – 17:00

ORGANIZED SESSION / STANDARD TALKS

EVOLUTIONARY NEUROLOGY, HEREDITARIANISM, AND THE FORMATION OF MEDICAL GENETICS

Organizer(s): **STEPHEN CASPER** (Clarkson University, United States)

The papers in this panel trace a narrative from evolutionary neurology through to the formation of modern biomedicine. As these papers showcase, questions of evolutionary descent and future shaped geneticist science and medicine in modernity and after. Many Victorian scientists and clinicians claimed that the study of the evolution of the nervous system in animals and human beings, nervous diseases, and the hereditary circumstances of both the organ and its pathologies, was central in the political debates of the day. Victorian evolutionary neurology, grounded in comparative anthropology, physiology, and zoology, provided an essential theoretical conception of the structure and function of the nervous system that subsequently framed explanations of, and treatments for, nervous diseases. Nervous diseases, so many argued in the hereditary discourses of the day, made the natural history of human beings manifest. Thus in this way the discovery of new and supposed neurological conditions shed light on the descent of human beings and permitted speculation about their future. Down’s syndrome, in particular, showcased human development, and, by corollary, when no hereditary component was immediately evident, as in cases of epidemic encephalitis, specialists in nervous diseases still sought refuge in the evolutionary morphology of the nervous system to conceptualize symptoms and to re-imagine autonomy. Much was at stake in this discourse, not least the naturalistic foundations of the human and life sciences and the application of those foundations in policy prescriptions and medical practices. Indeed, the subsequent emergence of medical genetics would be highly dependent upon those lines of reasoning even as the science of human genetics would significantly problematize their scientific and ideological assumptions.

Time, deep history, and the evolutionary neurology of nervous disease

STEPHEN CASPER (Clarkson University, United States)

Victorian clinicians, scientists, anthropologists and naturalists were fascinated by the question of how the passage of time left traces of a deeper history in the nervous system of animals and human beings. Following this logic, human nervous diseases could be used to situate human beings in evolutionary time, as those disease states seemed to disinhibit primitive centers that had served long-passed evolutionary descendants. In this way, nervous diseases transcended mere pathology: the excitation and release of primitive functions in unhealthy human beings appeared as evidence of past modes of the species’ existence. The language of nervous disease that ultimately sprang from these theoretical conceptions animated the natural history of degenerative, vegetative, and senescent states. Similarly, the comparative zoology of the nervous system situated the organ system in time as well; embryological and comparative morphological studies traced the evolution of the nervous system from lower to complex forms, while physiological experimentation augmented these studies by theorizing the accumulation of inhibitory processes that had advanced the organism’s complexity. In this way nervous diseases functioned as natural experiment and metaphor. Evolutionary neurology ultimately provided a powerful

methodological, deterministic, and sometimes fatalistic narrative about time and the nervous system, one that came to underpin many of the premises and assumptions of geneticist, eugenic, evolutionary, physiological, and psychological discoveries of the twentieth century.

Epidemic encephalitis and the invention of the sub-cortical subject in interwar Britain

KENTON KROKER (York University, Canada)

Sociopolitical power and brain science were intertwined long before our current neuroscientific regime. The outbreaks of epidemic encephalitis during the 1920s attest to a complex relationship between neurology, eugenics, and the reconstruction of British public health. Where other neurological conditions offered a high degree of professional and symbolic capital linked to inheritance (neuresthenia, idiocy, chorea), epidemic encephalitis resisted such interpretations. It did not “run in families,” and Britain’s system of epidemic surveillance (the most sophisticated in the world) failed to localize its outbreaks in any meaningful way. Yet the chronic after-effects of the disease, known as “post-encephalitis,” generated many of the same sociopolitical anxieties posed by its dysgenic counterparts; namely, the immanent threat represented by a growing population of failed human beings requiring provision. By the early 1930s, neurologists and the British state alike had adapted to the novel and mysterious biological threat posed by epidemic encephalitis. They had jointly (but imperfectly) transposed earlier hereditarian discourse with a language better suited to the new public health’s concern with risk and individual autonomy. Like the genetic material responsible for inherited degeneration, the viral cause of encephalitis was material, sub-microscopic, but poorly defined and unidentified. But “healthy carriers” spreading “aborted forms” of the disease put all Britons at risk. And the deficiencies of post-encephalitis were less focussed on the intelligence of the cortex than they were on the sub-cortical systems thought to regulate morality, emotions, and movement. These differences translated into a dramatic change of fortunes for those unable to exercise their autonomy in an expanding bureaucratic state. Legislative changes to the 1913 Mental Deficiency Act, coupled with new diagnostic approaches that classified patients according to their capacity for self-care, enabled those marked by post-encephalitis to retain much of what their dysgenic predecessors had lacked: political and moral subjectivity.

From evolutionary neurology to genetics: Tracing the deep history of Down’s syndrome

ANDREW HOGAN (Creighton University, United States)

In 1866 British physician John Langdon Down adopted the term Mongolian Idiocy to describe a form of feeble-mindedness that he had identified in a number of patients at the Earlswood Asylum. As head of this institution, Down oversaw the clinical evaluation of hundreds of patients. The regular collection of anthropometric data from each got Down thinking about links between physical and mental abnormalities, facilitating his delineation of this disorder characterized by mental deficiency and distinctive facial features. Down felt that the condition gave affected Caucasian children a Mongolian appearance. From this, he inferred that this neurological

disorder in some way returned a child of Caucasian ancestry to an evolutionarily more primitive Mongolian state. His interpretation was grounded in a liberal understanding of race for its time, one assuming that all human races were evolutionarily unified, and that the biological boundaries between them could occasionally break down. While the biological basis of Down’s theory was largely discredited by other physicians over the coming decades, the viewpoint that this form of feeble-mindedness involved some sort of racial reversion influenced eugenic ideas about mental defect throughout the early-20th century. As genetics came to shape understandings of disease, it was proposed that Mongolian Idiocy represented the uncovering of a primitive trait that had largely disappeared from expression, but still existed in the deep history of human genetics. A more clear cut genetic explanation of Mongolian Idiocy was proposed in 1959 by Jerome Lejeune, who identified an extra copy of chromosome 21 in affected patients. While mid-20th century physicians largely moved away from earlier racial understandings of Mongolian Idiocy, I argue that this new genetic etiology continued to reflect conceptions of neurological disease as having a basis in the uncovering of traits that still lurked somewhere in the deep history of the human genome.

DS M240

15:30 – 17:00

INDIVIDUAL PAPERS

EXPLORING ECOLOGICAL THEORY

History Earth: How the geo-physical globe put together our planet

SIMON WHITEHOUSE** (Florida State University, United States)

The photographic image of Earth has become a common mental representation of the Age of Ecology since the advancement of Cold War satellite technology. Little scholarship, however, has examined how the planet increased in its visual accuracy during the post-war era and how artists and scientists came together to present the Earth to the general public. In many major North American scientific institutions where the evolution and physical make-up of Earth is studied, the Rand McNally Geo-Physical Earth globe has been the main artifact that helped the public visually conceive the planet. Although the globe has been commonly appreciated for its aesthetic appeal in natural history museums, planetariums, university departments, and public libraries, little recognition has been given to how the holistic image of Earth was incrementally put together. This study rests on a broad foundation of primary source research. Through photographic representation in major American magazine publications, archival research from the Rand McNally and Company records in Chicago, oral history interviews with globe manufacturers, geographers, museum professionals, and cartographers, the proposed paper hopes to show how some of the top post-war visual artists and scientists painstakingly put the Earth together in globe form. This presentation aims to ask the following questions: How does an artifact like the six-foot Earth globe represent the development of inter-disciplinary fields of post-war biology, astronomy, oceanography, geography, geology, and cartography? How can the globe continue to be used as an object to communicate global environmental problems of the present day?

Telling the origins of the neutral theory of ecology

WILLIAM BAUSMAN (University of Minnesota, United States)

The unified neutral theory of biodiversity and biogeography has proved to be both very controversial and a last- ing presence in community ecology. One persistent epistemological question asks how the neutral theory can be useful given its “obviously false” assumption that all individuals in a community are functionally equivalent. I believe asking this question is prompted by a particular narrative about the origin and development of the neutral theory - the origin story Stephen Hubbell, its chief innovator, tells. In this way, the philosophy of the neutral theory has been founded upon its history. But that history is not the only one available. Different epistemological questions and different answers to these questions can be prompted by different narratives of the origin and development of the theory. In this paper I take Hubbell’s origin story as the jumping off point for telling the origins of the neutral theory. I critique his origin story considered as a historical claim by outlining three different but interrelated narratives of how the neutral theory of ecology grows out of the history of community ecology after 1950. The first narrative foregrounds the construction of formal models of biodiversity patterns. The second narrative foregrounds empirical and theoretical work on whether tropical communities are in taxonomic equilibrium. And the third narrative foregrounds the existence of Kimura’s neutral theory, the MBL model in paleobiology, and the debates over the proper role of “null hypotheses” in biology. A very different historical picture of the origins of the theory emerges from these narratives than from the origin story. And a different epistemic picture of the usefulness of the neutral theory follows from these different origins. For example, empirical work on tropical forests has evidenced that tropical trees are functionally equivalent and so this assumption is not obviously false in general.

From Pierre-Joseph Van Beneden (1809-1894) to microbiome: History of commensalism

BRICE POREAU (Laboratoire Sciences, Société, Historicit ,  ducation et Pratiques, France)

Commensalism is a biological association in which one partner (the commensal) benefits while neither harming nor benefitting the host. Parasitism and mutualism were well defined during the nineteenth century and commensalism was theorized during the second part of that century. Pierre-Joseph Van Beneden (1809-1894), a Belgian professor at the University of Louvain, developed this concept of commensalism. In his 1875 publication *Animal Parasites and Messmates*, Van Beneden presented 264 examples of commensalism. His conception was widely accepted by his contemporaries and commensalism has continued to be used as a concept right up to the present day. In our presentation, we examine the development of commensalism during the nineteenth century and the use of the concept in contemporary science. We have used hitherto unpublished archival material for Pierre-Joseph Van Beneden to explore the pertinence of his concept. From an epistemological point of view, commensalism can be seen as a marker of the new domains in the life sciences such as microbiology and genetics. Through their use of different models of the concept, these two sciences gave a new sense to commensalism with the new concept of microbiome. We propose to establish the historical and epistemological links between the past concept of commensalism and the microbiome.

DS M260

15:30 - 17:00

INDIVIDUAL PAPERS

HUMAN NATURE, MORAL NORMS AND SOCIOBIOLOGY

Looking for moral norms in all the wrong places? On the nature and significance of nonhuman animal “entangled normativity”

ANDREW FENTON (California State University, Fresno, United States)

There are at least three distinct approaches to critically discussing nonhuman animal morality among those sympathetic to its existence. The first examines selective pressures on capacities that are implicated in what is recognizably moral (e.g., Cartwright 2010). A second approach typically highlights various pro-social capacities exhibited by various nonhuman animals as well as what may also be virtuous (or vicious) behavior (e.g., Bekoff and Pierce 2009). The third approach provides analyses of what is taken to be constitutive of human moral agency and shows where these elements are present among nonhuman animals (e.g., Flack and de Waal 2000). Among the challenges facing those participating in this discussion is the development of an empirically tractable program that does not confuse the relevant behavior with something else (e.g., something more political or better described as “social etiquette”). I suggest that morality as we currently understand it should only be sought among domesticated or habituated nonhuman animals. This is largely because of two factors (i) the significance of principled action historically emphasized in human morality and (ii) the likelihood, even within the relatively recent past of *Homo sapiens*, that morality as we currently understand it was too entangled with what we would now regard as law, politics and social etiquette to permit strict separation. (i) allows room for an emergent morality in, say, *Homo-Pan*, *Homo-Canis*, or *Homo-Tursiops* cultures but not in free living communities of the relevant nonhuman genera. (ii) not only permits a non-anachronistic gaze at the normative structures and practices of ancient or early classical human cultures, it permits re-seeing what has already been labeled as, say, politics (see, e.g., de Waal 1998), as something so entangled with moral elements or what we might regard as social etiquette to undermine attempts to separate them. This possibility opens up a new, and perhaps more empirically tractable, project of studying nonhuman animal “entangled normativity.”

Sociobiology and the staying power of inflammatory rhetoric: How scientific objections became a “delayed scientific critique”

SAMUEL KETCHAM (Indiana University, United States)

In 1975, Edward Wilson provoked an ongoing controversy over adaptationism and the study of human beings in an evolutionary context with his book, *Sociobiology: The New Synthesis*. The initial response to the book by critics in the Sociobiology Study Group, which included Richard Lewontin and Stephen Jay Gould, listed methodological problems that Sociobiology had in common with eugenics and racially motivated IQ tests. While they did not call E.O. Wilson a Nazi, they expressed deep concern that a failure to maintain high standards of scientific evidence made Sociobiology vulnerable to the same sort of biases that suborned scientific integrity during WWII. This criticism initiated an extreme polarization of the debate, and made it difficult to

discuss evolutionary claims about human beings without also discussing their political or moral motivations and ramifications. In an interview with the sociologist Ullica Segestråle in 1981, Ernst Mayr complained that the initial political criticism made it falsely appear as though there were no real scientific grounds for objection. In her canonical account, *Defenders of the Truth: The Battle for Science in the Sociobiology Debate and Beyond* (2000), Segestråle presents Lewontin's 1979 paper, "Sociobiology as an Adaptationist Program", as a delayed scientific critique, validated by both Mayr and E.O. Wilson's concession that, unlike the initial political response, this paper amounted to good scientific criticism. Yet a comparison of these documents shows that they contain very similar scientific arguments! The only senses in which scientific criticism was "delayed" was that it was presented in this later paper in expanded detail and without discussion of the social threat posed by poor standards of evidence. Segestråle's appeal to Mayr as an arbitrating scientific authority is therefore misleading, and fosters a sense that the initial objections to Sociobiology were not only political, but that they were merely political. In the paper that follows I re-examine this historical episode and show how methodological and political concerns are not so easily disentangled, and how provocative rhetoric from all sides has complicated both the episode and its subsequent analysis.

Evolution, human nature, and the location problem

JOSHUA FILLER (Ripon College, United States)

Recent literature on the possibility and desirability of identifying a biologically founded "human nature" have largely agreed that this "nature" will have been (1) formed by evolutionary processes and almost certainly will be (2) normatively uninteresting. More specifically, this recent literature (or so I will argue) has settled upon the position that whatever traits constitute human nature, these traits will be dispositional in character and should not be identified with a fixed expression of a phenotype as such expressions are not expressions of a human nature due to the influence of environmental factors during development. In this paper (and following Louise Antony's work on the political implications of a biologically founded human nature), I argue that a dispositional account of a biological human nature is the most plausible account of the traits that make up that nature. Yet a lingering problem remains: where, precisely, are we to "locate" human nature within a dispositional account of the traits that make up that nature? On a standard account of dispositions, the relevant options are the categorical base of the disposition, the disposition itself, and the relevant outcome of that disposition being triggered. In the literature on human nature, these correspond (roughly) to the genotype, a norm of expression, and the resultant phenotype. In this paper, I will explore the biological and metaphysical issues with locating human nature at any one of these locations. In particular, I will argue that the proper "location" for the dispositions constitutive of human nature is a matter of convention - where one will (and should) locate human nature will depend crucially on one's interest. That is, what constitutes human nature will depend, for example, on whether we approach the question from genetics or human behavioral ecology. As such, there is no one "fixed" human nature in biology.

DS M280

15:30 - 17:00

INDIVIDUAL PAPERS

MODELS, THEORIES AND COMPUTATION

The strategies for morphology formation model building of ammonites

RYOTA MORIMOTO (Health Sciences University of Hokkaido, Japan)

When some different models in the same phenomena exist, how should we evaluate them? If there is only one type of criterion, e.g. describing reality, we wouldn't be bothered by choosing the best model. However, building models includes some other goals, such as explanations, predictions, and goodness-of-fit. The aim of this paper is to examine morphology formation models of ammonites as examples. David Raup builds, for instance, a well-known model which explains shell forms of ammonites. However, his model can't reveal morphology formations of heteromorphs ammonites, e.g. Nipponites and Polyptychoceras. In contrast, Takashi Okamoto provides a less famous but more general model that can explain formation patterns for every ammonite including heteromorphs, which the Raup's model fails to do. Furthermore, Okamoto's model is more refined, and his model reveals the morphology formation process of ammonites. Thus, based on the comparison between Raup's and Okamoto's models, I provide my analysis of the criteria for good models and the philosophies behind the model building strategies.

The limits of equilibrium concepts in evolutionary game theory

AYDIN MOHSENI (Carnegie Mellon University, United States)

Within the modeling framework of evolutionary game theory, equilibrium concepts adapted from rational choice game theory are employed to identify the probable outcomes of evolutionary processes. Over the last several decades, results have emerged in the literature demonstrating limitations of each of the proposed equilibrium concepts. We present a comprehensive story circumscribing the shortcomings of the primary candidate equilibrium concepts. We argue that these results rely on an implicit notion of evolutionary significance, and propose a novel account of evolutionary significance. We show how this formulation brings clarity to assessments of the success and failure of equilibrium concepts and demonstrate that, even under quite favorable assumptions, each equilibrium concept is simultaneously too weak and too strong.

Reconsidering the game of life: Weak emergence and interventionism

CORY LEWIS (University of Toronto, Canada)

The relationship between interventionism and emergence has recently come into question. Some say that interventionism, Woodward's (2003, 2010) proposal for how to understand causal explanation, gives us reason to accept emergent properties (Sober and Shapiro 2007). Others argue the opposite, that interventionism makes emergence impossible (Baumgartner 2010). I try to navigate a path through these arguments, using Bedau's (1997) notion of weak emergence. This shows a way through the tangle, while also casting new light on weak emergence itself. Sober and Shapiro (2007) argue that interventionism provides us reasons to reject

Kim's (1997) causal exclusion argument. But Baumgartner (2010) argues that interventionism makes downward-causation, the usual causal interpretation of emergence, impossible in principle. It seems that interventionism tells both for and against emergence. But Bedau's position is specifically addressed to emergence without downward causation, so it provides a way to see the merit in both positions. And interventionism can also offer something to downward causation – specifically, the notion of stability. Bedau caches out the contingency of micro-level processes in emergent phenomena in terms of the requirement that they can “only be simulated”, or that they are explainable only complexly. Woodward's (2010) distinction between stable and unstable causal relations offers a way to cash out the notion of contingency in ontological terms. This causes us to have to reconsider one of Bedau's canonical examples, Conway's Game of Life. Seen in terms of causal stability, we find that it does not have especially emergent dynamics. The micro-dynamics that produce gliders, to take Bedau's example, are extremely widespread across the game's space of possibilities, and are therefore “stable”. So applying interventionism to weak emergence not only clarifies the debate between Sober, Shapiro, and Baumgartner, it also gives us a new perspective on weak emergence itself.

DS M320

15:30 – 17:00

INDIVIDUAL PAPERS

INDIVIDUALS, SPECIES AND HIERARCHIES

Grounding individuals in hierarchical processes

JAMES DIFRISCO (Katholieke Universiteit Leuven, Belgium)

Dupré (2012) argues that apparently substantial biological entities (genes, organisms, populations, etc.) are best conceived as abstractions from biological processes, and that processes should be the fundamental units of an ontology of the life sciences. Assuming this is biologically well-motivated, I explore some of the philosophical consequences for conceptions of individuals and hierarchy. Instead of rejecting biological continuant-individuals altogether, I attempt to show how the appearance of stable continuants and the apparent truth of substance-talk can be generated out of a process-based perspective. Following Simons (2000), continuants are construed as abstractions based on equivalence classes which pick-out invariant properties among the successive states of the relevant biological processes. The relation between a continuant and its corresponding processes is accounted for as a type of grounding relation. Accordingly, I argue, the truth of propositions referring to continuants can be grounded in truth-makers which are just processes. One revisionary consequence follows, however. If biological continuants (genes, organisms, populations, etc.) are abstract entities then they lack causal efficacy. Arguably, scientific realism about biology requires that biological entities have causal efficacy, and therefore, that we be realist only about the hierarchy of biological processes. I conclude by examining the important ways in which this hierarchy of processes differs from the traditional levels of organization hierarchy of continuants.

After interaction: Why interdependence is difficult to think about, and why to do it anyways

KRITI SHARMA (University of North Carolina at Chapel Hill, United States)

In the early 21st century – a time when the terms “networks”, “connections”, and “complexity” are in high circulation – the theme of interdependence is in the air. Nowhere, perhaps, is interdependence evoked as vividly and often as in the biological sciences. Yet the ascendant view of interdependence at play in biology (as in popular culture) is not, I argue, a view of interdependence at all. It remains a view of independence. By and large, we think that interdependence just means “independent objects interacting.” We say that things interact strongly, weakly, reciprocally, sequentially, and so on, but their ultimate independence from one another remains intact. As long as the ascendant view of interdependence continues to collapse implicitly to a view of independence, I believe that we continue to miss important implications of our own biological findings. I demonstrate how a coherent theory of interdependence – that is, a theory of causation that takes seriously the claim that things themselves do not exist except in dependence on other things – can help us make sense of disparate biological phenomena, from signal transduction, to symbiosis, to the nature-nurture complex.

Why do scientific laws tend to ignore species?

SINAN SENCAN (University of Calgary, Canada)

Whether there are natural kinds and scientific laws in biology is controversial. In particular, some philosophers of biology argue that biological species are not natural kinds, rather they are individuals (e.g. Hull, 1978; Ghiselin, 1989). Their reasoning assumes that scientific laws should be generalizations about classes of individuals and not about individuals. Yet, some others argue that there can be scientific laws concerning particular species (e.g. Lange, 1995). Lange thinks that statements of the form “The S is a T” (S is a species and T is a biological property) can be dubbed as scientific laws because these statements can perform the function of scientific laws in scientific practice. This paper critically evaluates the relationship between the concept of scientific laws and the concept of biological species. I agree with Lange that scientific practice must have priority to evaluate the status of scientific statements. Yet, I do not agree with Lange that biological practice offers a plausible reason to defend the idea that there are biological laws concerning biological species. This paper's thesis is that if there are statements which express scientific laws in biology, these statements will not refer to species because of two reasons. The first reason is that statements concerning species are usually merely descriptive or informative, i.e. they are not explanatory. The second reason is that causal biological statements in biology usually refer to properties of species but not to species directly. From these reasons, I argue that there are no strong reasons to think that there are scientific laws concerning particular species.

DS R510

15:30–17:00

ORGANIZED SESSION / STANDARD TALKS

EXPERIMENTS IN GENETICS EDUCATION: REPORTS FROM ACROSS THE DISCIPLINESOrganizer(s): **GREGORY RADICK** (University of Leeds, United Kingdom)

What should the teaching of genetics look like in the 21st century? What principles ought to guide efforts at reform of conventional teaching? Each of the papers in this session will report on innovative classroom experiments aiming, in various ways and from different disciplinary perspectives, to throw light on these questions. Biologist **Rosie Redfield** will describe the motivations behind her Useful Genetics MOOC. Science-education researcher **Brian Donovan** will discuss his latest studies into the cognitive effects on children who learn about genetic disease as linked with race. And historian of science **Greg Radick** will draw some lessons from a recent project to devise and teach a basic genetics course organized not around Mendel's pea-hybrid experiments but around the insights of the most penetrating critic of early Mendelism, the Oxford biologist W. F. R. Weldon (1860-1906).

The Useful Genetics project: Let's stop wasting our students**ROSIE REDFIELD** (University of British Columbia, Canada)

Genetics is everywhere in our lives now, but the standard introductory genetics course is a waste of our students' brains and efforts. We ask them to memorize the genetics of Mendel and Morgan, of fruit flies and mice, when they need to understand personal genomics and DNA fingerprinting, GMOs and cancer genes. We teach them to run gels and analyze crosses when they need to evaluate services such as 23andMe, Ancestry.com, and the Who's Your Daddy mobile DNA-testing truck. Useful Genetics is the first modern genetics course designed to serve the students' needs rather than the instructor's preconceptions. It's taught both as a Massive Open Online Course (MOOC) on the Coursera platform and as a for-credit replacement for a conventional university genetics course. In this talk I'll discuss both the motivations behind these changes and the challenges and rewards of delivering them to both global and university audiences.

The educational debt of school biology? Evidence that students' intentions to fix the racial achievement gap are affected by subtle racial framings of monogenic diseases**BRIAN DONOVAN** (Stanford University, United States)

Recent experimental research by Donovan (2014) suggests that indirect references to race in the biology textbook curriculum can influence how some adolescents conceptualize race in the United States (US). In the present study, the findings of Donovan (2014) are replicated and extended through a randomized double-blind field experiment that investigates the impact of subtle racial framings of human genetic diseases on ninth graders' intentions to redress the racial achievement gap. The mixed-method study was carried out in a public high school in the California Bay Area. Students recruited for the study (N = 86) read either a racially framed or a non-racially framed textbook passage on human genetic diseases. After a short distracting task they

completed two different racial essentialism scales. Then they read a New York Times article describing a test score gap between races in New York City. Following this reading students responded to an instrument that assessed their explanations for the racial achievement gap and their intention to volunteer their free time to fix it. The quantitative results demonstrated that students in the racially framed condition exhibited greater agreement with the genetic basis of racial difference than students in the non-racially framed condition after reading. Furthermore, students in the racially framed condition were more unwilling to volunteer their time to fix the racial achievement gap than students in the non-racially framed condition if they believed races were biological kinds. The qualitative results demonstrated that more students in the racially framed condition gave genetically deterministic explanations of the achievement gap than students in the non-racially framed condition. These findings open up new interdisciplinary research questions for science education and science communication in light of the fact that US science journalists tend to use racial frames to explain medical genetics research.

The Weldonian alternative: Steps towards a de-Mendelized, developmentalist curriculum in genetics (and towards students less prone to genetic determinism)**GREGORY RADICK** (University of Leeds, United Kingdom)

Between 2012 and 2014, the Genetics Pedagogies Project at the University of Leeds set out to develop, deliver and assess an experimental, "de-Mendelized" curriculum in genetics, taking inspiration from the work of the Oxford biologist W.F.R. Weldon (1860-1906). Weldon is well remembered as a critic of early Mendelism. What is less well remembered is that behind his objections lay a vivid sense of the environmental conditioning of hereditary effects, and of the variability and complexity that come from such interactions. As biology after the "century of the gene" has come increasingly to recognize interactions of this kind as primary, the case for retaining the traditional Mendelian starting point in genetics teaching has grown ever less persuasive. In this talk I'll report on the attempt at Leeds to devise an alternative that, in taking Weldon's perspective seriously, aimed at producing students not just better informed about twenty-first biology but, in keeping with that biology, less prone to genetic determinism than they were when they started.

DS R515

15:30–17:00

ORGANIZED SESSION / STANDARD TALKS

HEALTH, DISEASE, AND WELL-BEINGOrganizer(s): **SALLY WASMUTH** (Indiana University–Purdue University Indianapolis, United States)

A model of health that takes into account both the biological functioning of an organism and psychosocial experiences of wellness matters to medicine. Thus a goal of this session is to detail a "theory" of health, sensitive both to human experience and biological function; a theory rooted in biological detail that doesn't simplistically focus on absence of local dysfunctions. In this session, **James Krueger** will call into question Lennart Nordenfelt's claim that an understanding of health must proceed from one of two dominant perspectives: the disease

model, which locates pathology in biological and chemical abnormalities, and a holistic approach that draws on concepts from psychology, sociology, and anthropology to understand problems in human health/wellness. **Phillip Honenberger** will review the naturalist-normativist debate in the interpretation of health and disease concepts, arguing for a view that recognizes both the reality of norm-like structures in biological systems, and the plasticity of such structures, as well as the open-endedness of normative questions in general, within human lives and societies, thereby connecting issues of medical normativity to philosophical anthropology and biopolitics. **Sally Wasmuth** will discuss clinical findings from a study of 7 socially displaced individuals as they move from the disease of addiction toward efforts at striking a something like this “psycho-social balance”. Data illustrate how different kinds of detachment- compensatory participation show up as more or less contributory to experiences of wellbeing as defined by these individuals’ experiences.

Between illness and disease: Towards a more holistic holism?

JAMES KRUEGER (University of Redlands, United States)

In *On the Nature of Health*, Lennart Nordenfelt suggests that there are two basic perspectives from which one can approach the understanding of health and disease. The analytic approach focuses on the parts of the organism and draws upon biological, chemical and statistical concepts in formulating an account. The holistic approach, by contrast, begins with the (human) organism as a whole, and draws upon concepts from such disciplines as sociology, psychology, and anthropology to construct an account. Nordenfelt goes on to argue that any account of health and disease is going to have to take one of these approaches, that there cannot be an adequate account that utilizes both perspectives simultaneously. One must be regarded as the more basic. It isn't hard to understand why he claims this. It would seem that we either have to regard every underlying deviation as pathological (regardless of the effect that it might have on the whole organism) or we have to take holistic considerations as conceptually basic, constraining how we should regard underlying structural and functional features of the organism. At the same time, however, it seems odd to suggest that these are irreconcilable differences in perspective. Any adequate anthropology is going to have to take account of human beings as biological beings. The possible ways that human beings can live together (can live together healthily) is in no small part affected by how we function biologically. This suggests that concepts drawn from sociology, psychology and anthropology are not going to be wholly independent of biological concepts. This paper aims to evaluate Nordenfelt's contention that an understanding of health must proceed from one of these two perspectives in part by asking if a biologically sensitive philosophical anthropology could ground an approach to health that integrates concepts drawn from each perspective.

Medical normativity between anthropology and politics

PHILLIP HONENBERGER (Consortium for History of Science, Technology, and Medicine, United States)

A longstanding debate in the philosophy of medicine concerns the question of how to understand the apparent normativity of medical concepts like health and disease. In particular, the question has been: Are health and disease natural kind concepts? Or are they rather social constructions that reflect culturally relative norms? Or, finally, are they some combination of the two? Through discussion of prior work by Marc Ereshefsky, Marjorie Grene, Hans-Georg Gadamer, Georges Canguilhem, and others, I argue for realism about certain norm-like structures, including in biological contexts, while expressing skepticism that such structures could foreclose debates about the content of normative medical concepts like health and disease, primarily because of the extraordinarily plastic operation of normativity in human social systems. From this perspective, medical normativity must either become self-limited and partial, or open to the higher-order normative question, “What should we (either as individuals or as societies) favor or do?” This approach to medical normativity opens philosophy of medicine and medical ethics to evaluation from two previously underappreciated quarters: those lately taking shape under the headings of “philosophical anthropology” and “biopolitics.”

A normative scale of compensatory action

SALLY WASMUTH (Indiana University – Purdue University Indianapolis, United States)

Impoverished understandings of health and disease limit the goals and development of much-needed innovative treatments for addiction. For example, the predominant biomedical model locates the causes of craving, compulsive drug use, and diminished satisfaction with other typically rewarding engagements in dopaminergic reward center circuitry changes of the midbrain. These neurological changes, however, are not sufficient to produce the behavioral profile of addiction. Nor do treatments targeting these problems improve the lives of people trying to recover. Moving beyond biological targets, interventions targeting discrete psychosocial aspects of addictive behaviors also fail to result in lasting or noteworthy changes to overall function and experience of the human organism. In short, problem elimination whether at the level of biological disease or psycho-behavioral phenomena does not in itself yield health. A different approach is made possible by viewing addiction through the lens of a philosophical anthropological understanding of human action. From this perspective, the human organism shapes its life-world through engagement in social institutions (Gehlen). The way in which humans engage in institutions has the power to shape and reshape both how they experience their worlds and, as more recent research indicates, their biological structures (e.g. the restructuring of neural networks). However, the health value and/or potential harms inherent in different ways of engaging in the world are not straightforward or well understood. In previous work a normative model of human compensatory action that balances compensatory structure and focus (Gehlen's relief) with residual flexibility and autonomy was delineated, on which we could theoretically locate the gains and harms of addiction. In order to further detail how health and disease appear in this context, the current paper reports findings reflecting how individuals compensatory action changes as they move from the disease of addiction (and its self-reported harms) to self-reported experiences of wellness in recovery.

DS R520

15:30–17:00

ORGANIZED SESSION / STANDARD TALKS

COOPERATION, SIGNALS, AND MORAL NORMSOrganizer(s): **BEN FRASER** (Australian National University, Australia)

Human social life has changed significantly over time. This session investigates the role norms play in human social life, from three different yet interlocking perspectives. **Justin Bruner** discusses the stability of egalitarian hunter-gather social norms, drawing on game theoretic models. **Kim Sterelny** discusses the role of norms in the economic and social transition from hunter-gather to agrarian life, with an eye to the “Big Gods” account of social complexity. And, **Ben Fraser** discusses the current role of moral norms, suggesting there is significant mismatch between evolved human moral psychology and modern social contexts.

The stability of the egalitarian social contract: Bully control and social cohesion in early man**JUSTIN BRUNER** (Australian National University, Australia)

Explaining the transition from small roaming egalitarian bands to large sedentary farming communities has generated considerable interest in recent years. Yet any account of this transition must first importantly explain how the original hunter-gatherer social contract was stabilized. Predatory bullies, among a variety of other things, are a constant threat to the tranquility of the community and can often only be successfully dealt with through the coordinated action of a number of individuals. We consider two game-theoretic models which capture this strategic situation and outline under what conditions the egalitarian social contract can be upheld.

Norms, gods, and social complexity**KIM STERELNY** (Australian National University, Australia)

In previous work, I have argued that normative thinking emerged (or perhaps became much more important) in response to economic and social transition in human forager life in the later Pleistocene. On this model of the evolution of normative thought, the emphasis was on the reduction of transaction costs and in the solution of coordination problems, as forager lives became more complex at and over time, rather than on the control of cheating, and on amplifying prosocial motivation (the main factors emphasised in other views of the evolution of normative thought). The aim of this paper is to test these ideas through consideration of a somewhat later social transformation, the transition to complex sedentary societies in the Neolithic revolution, and to compare and contrast this approach to the Neolithic with the currently salient “Big Gods” account of the cognitive and motivational foundations of social complexity.

Mismatch and moral conflict**BEN FRASER** (Australian National University, Australia)

Evolutionary mismatch occurs when a trait that evolved in one environment proves deleterious in a new environment. Some elements of our evolved moral psychology may be cases of current moral mismatch. Our tendency toward in-group bias, our taste for retributivist punishment, and our inclination to objectify moral norms: all have a plausible adaptive explanation, yet each presents problems in our modern context. This moral mismatch hypothesis has interesting implications for debates about moral abolitionism, the view that we are better off without morality.

17:00–17:30

COFFEE BREAK

17:30–19:00

AWARDS CEREMONY AND ISHPSB GENERAL MEETING | Marie-Gérin-Lajoie auditorium

19:30–22:00

BUFFET DINNER (“COCKTAIL DÎNATOIRE”) | Salon Urbain, Place des arts

FRIDAY JULY 10

DS 1520

09:00 – 10:30

INDIVIDUAL PAPERS

EMPIRICAL ETHICS AND NATURAL NORMATIVITY?

[Evolutionary debunking in ethics: The empirical turn](#)

JEROEN HOPSTER (Universiteit Utrecht, Netherlands)

Sharon Street's *Darwinian Dilemma for Realist Theories of Values* (2006) has sparked ongoing (meta-)ethical debate. According to Street, our evaluative attitudes have been saturated with evolutionary influence. As a result, these attitudes are unlikely to track mind-independent moral truth. This is the essence of Street's Evolutionary Debunking Argument (EDA) against moral realism: if our moral evaluations have a contingent evolutionary genealogy, then moral facts cannot be "real" in any robust sense. Appearances notwithstanding, Street's EDA barely relies on empirical input: the "evolutionary influence" she alludes to is extremely generic. In this presentation I elucidate what Street means by evolutionary influence, and analyze her treatment of empirical evidence. I argue that Street's argument is successful in weeding outgrowths of (meta-)ethical discourse, which are oblivious to basic evolutionary facts. Although this may be considered a modest success, EDAs can have greater significance – and more intricate application – once they are informed by actual details of evolutionary biology. Street has given debunkers a hammer; the real challenge is to turn it into a chisel.

[Evolutionary debunking of fairness norms](#)

ELIZABETH O'NEILL (University of Pittsburgh, United States)

Sharon Street and Richard Joyce have advanced "global" evolutionary debunking arguments that appeal to the evolutionary origins of moral faculties to cast doubt on all moral or normative beliefs. By contrast, Daniel Kelly has argued that because different types of moral beliefs may have different evolutionary histories, there is value in "selective" evolutionary debunking arguments that target only subsets of moral beliefs, such as moral beliefs about purity. In this paper, I advance a selective evolutionary debunking argument targeting beliefs about the fair distribution of resources. In particular cases in which resources must be distributed, people frequently have conflicting intuitions about which distribution scheme is fair—for instance, resources might be distributed equally among individuals involved, distributed according to the contribution each individual made, or distributed according to each individual's level of need. I argue that evidence from developmental psychology, comparative economics, and primatology suggests an evolutionary history for resource distribution norms that gives

us reason to decrease confidence in intuitions about whether competing schemes for distributing resources in particular cases are fair. This case of the evolution of fairness norms shows, contra an argument from Edouard Machery and Ron Mallon, that we have empirical information about the evolutionary origins of at least some moral beliefs that leads to significant ethical conclusions. This project also engages with the question of in what sense it is useful to say that morality evolved.

Natural normativity: A defense of neo-Aristotelianism in ethics

ERIK ANDERSON (Furman University, United States)

An influential group of neo-Aristotelians in ethics including Phillipa Foot, Rosalind Hursthouse, and Michael Thompson have recently argued that appeals to natural teleology are essential to theories of human virtue and flourishing. For example, Foot argues that just as we say that a particular oak tree is “a good oak” by appealing to its success at performing the functions that constitute the “life form” of an oak, we say that a particular human being is “a good person” by (at least implicitly) appealing to her success at performing the functions that constitute the human life form. This is not to say that there are not important differences between human beings and other species. “Good human functioning” involves engaging well in the activity of practical reason, which makes the human case significantly different from the case of other animals. But it remains true that the assessment of human beings as good or bad, flourishing or not flourishing, and the identification of certain character traits as virtues or vices relies on an implicit teleological background—a conception of characteristically human functions that it is natural for human beings to perform. This appeal to natural teleology in ethics has come in for heavy criticism by philosophers of biology, many of whom follow William FitzPatrick in thinking that a proper understanding of evolutionary theory undermines appeals to natural teleology in ethics. FitzPatrick claims that once we recognize natural selection as concerned with “the inter-generational replication of certain germ line copies of genes of the types represented in the organism’s co-adapted genome” rather than with the flourishing or welfare of organisms, we will see the idea that humans or other organisms are “naturally designed” to flourish is based on a misunderstanding of evolution. In this paper I will defend the neo-Aristotelian approach. I will do so in part by explicating what I take to be the most plausible neo-Aristotelian account of ethics, the “capabilities approach” developed by Martha Nussbaum. After showing how Nussbaum’s theory exemplifies Foot’s idea that there are natural human functions and that a good life consists, in part, in performing those functions well, I will argue that there is a sense of “human nature” and “human function” that is biologically respectable, immune to FitzPatrick’s criticisms, and can undergird the appeal to natural teleology in neo-Aristotelian ethical theories.

DS 1525

09:00 – 10:30

INDIVIDUAL PAPERS

NEUROSCIENCE: EXPERIMENTATION, PSYCHOLOGY AND PHILOSOPHY

Convergent perspectivism

NINA ATANASOVA (University of Toledo, United States)

I advance convergent perspectivism as an account of experimental neurobiology that makes sense of the multiplicity of experimental protocols for the study of identical phenomena employed in the field. The thesis is that such multiplicity is necessary under considerations for the validity of animal models which are the main experimental tool in the field. Animal models in neurobiology are used as representational models in which the experimental animals serve as proxies for humans. Their representational validity is established through a calibration strategy which requires the results of multiple experiments aiming at explaining identical phenomena to converge. The strategy is similar to the perspectival pluralism advanced by Giere (2006) as a principle for maximizing instrument-mediated observational knowledge. It also unifies accounts of the experimental practices of neuroscience that have traditionally challenged each other. For example, Sullivan (2009) argues that neither of the competitors for an account of the unity of neuroscience proposed by Bickle (2006) and Craver (2007) adequately explains the multiplicity of experimental protocols in neurobiology. She concludes that a unified account of neuroscience is not likely to be successful. On the contrary, I show that the multiplicity of experimental protocols is beneficial for establishing the validity of knowledge claims in neurobiology. This is so because different experimental protocols provide different perspectives to the study of complex phenomena which would hardly be captured by the limited representational powers of the models available in experimental neurobiology. Thus, the experimenters in this field are confined to studying these phenomena from limited partial perspectives. This leads to the inconclusiveness of the experimental results produced on the basis of the partial experimental perspectives provided by the limited representational capacities of the models. This obstacle can be overcome when multiple experiments employing different experimental protocols, and thus different perspectives, converge in the results they produce.

Autism, sociality, and human nature

GREGORY HOLLIN (University of Nottingham, United Kingdom)

The 1990s saw the birth of “the social brain” and the claim that social processes, such as empathy, are central to both the brain’s functioning and its evolution. A full understanding of the social brain is believed to require analyses of both “normal” individuals and those with particular “social abnormalities”. Autism, as a disorder of social functioning, thus holds an important position within contemporary neuroscience and analysing its various constructions becomes an important task when searching for insight into contemporary understandings of human nature. Here I will seek to interrogate these three constructions – “autism”, “the social”, and “human nature” – and the inter-relations between them. I will argue that the relationships are far from stable and that, at the present moment, autism occupies two distinct positions, each with relevance to constructions of sociality and

human nature. First, autism signifies an absence; a qualitatively distinct state characterised by empathetic and social dysfunction. Within this narrative, autism offers a pure case of human-minus-social wherein an investigation of the social hole in autism offers a glimpse at human nature. I will argue that this construction of autism as absence emerged as a result of particular descriptions of the social and human nature which developed within the biological and human sciences in the latter half of the twentieth century. Second, autism marks a presence; a normally distributed and quantifiable trait applicable to all individuals within the general population. Within this body of thought, intimately linked with molecular genetics, the relationship between autism and human nature is quite different. Autism no longer reveals something about human nature through contradistinction to normalcy; autism is normalcy and feeds back into constructions of the social and human nature. I will conclude with some remarks on the importance of these dual narratives of autism for understandings of the human.

Minimal and narrative aspects of the self

VICTOR ROMERO SANCHEZ (Universidad Juárez del Estado de Durango, Mexico)

The self is considered one of the hallmarks of our species given its association with reason and language, also has been considered the source of our personal identity and it seems that our conscious decisions come, in certain sense, from it; we frequently affirm, for example, “I have decided to do this or that”. Recently, some scientists and philosophers have considered the human self as some kind of cognitive illusion that enables us to explain the behavior and mental states of others and even of ourselves. We will see particularly Michael Gazzaniga’s and Thomas Metzinger position and briefly address some of the theoretical assumptions of their claims. The self is, very often, regarded as the source of our personal identity, we attribute all events that befall us to a single subject, and it seems that our conscious decisions and psychological traits depend on that self. Although this is a classic theme in psychology and philosophy, currently, both philosophers and neuroscientists have made attempts to explain the self supported by some empirical sciences, as well as searching in the neuronal, biological and physiological processes that lead to the eventual formation of a self. It seems that humans have a worldview according to which our personal egos run all the time our actions. Our-selves would be the “headquarters”, the focal point of any conscious act: for Gazzaniga (1998, 2011), certain research in neurophysiology, particularly the one that he has done for more than four decades, show that such a thing is merely an illusion (a concept, image or sensory element deceiving us about the characteristics of its existence). According to this author, automatic brain devices, shaped by millions of years of evolution, run all the time our actions so the self is illusory (is not in charge of the actions). This is due to a particular “device” that Gazzaniga calls “the interpreter”. This “brain artifact” or “device” produces the illusion that is in charge of our actions but it is just interpreting verbally and reflexively the past, that is, the previous brain and nervous actions, which would be, from this perspective, automatic; they “govern” the body, while the emergence of the self and the conscious mind comes later, once the automatic brain has done the job. We will try to show, in contrast, that identifying the self only with its linguistic and conscious aspects is misleading: the self is not exhausted by those aspects

(as Gazzaniga seems to believe) as seen when we consider, for example, the phenomenon called blindsight: some patients with a lesion in the occipital cortex, where the visual information is processed, cannot consciously see, though his eyes work perfectly. However, the visual information can be processed at least partially: if these patients are asked to guess what objects are in front of his eyes (sometimes geometric figures projected in the wall by light) they guess right in many cases, more than would be expected by chance alone. A person with blindsight claims she sees nothing, but when forced to decide which figure is in front of his eyes, performs the task properly, she sees unconsciously. Analyzing the anatomy of the visual pathways, it has been found that connections coming from the eye go to other places in the brain, in addition to the visual cortex, so this information can influence behavior even if it is not registered consciously (a task supposedly performed by means of the narrative, linguistic and reflective self, of course). Now, in this case, would you say that the self did not perform the guessing activity, just because the subject was not fully conscious of his guessing? So what if the perception moves between conscious and unconscious levels of processing? So there seems to be more in the self than the narrative, linguistic and reflective aspects. Besides, we will see that, while explaining and considering what Thomas Metzinger (2009, 2011), Antonio Damasio (1994, 2010) and others call “the minimal self” or the “core self” (that is, all those traits that function below the level of conscious awareness that influence and affect what many consider thoughtful and reflective), we can have a notion of the self that is more comprehensive, robust and has more explanatory power than the position that assumes that the self is just some kind of narrative illusion.

DS M220

09:00 – 10:30

INDIVIDUAL PAPERS

FITNESS, MODELING, AND MEDICINE

Stochastic gene expression and fitness

THOMAS HEAMS (AgroParisTech, INRA, France)

Stochastic gene expression (SGE) is not only a background noise, but a constitutive parameter of all living beings. It challenges the view of adaptative evolution at the molecular level as a fine-tuned process of precise regulations in multicellular organisms. It has been described as a source of flexibility, of intercellular synchronization, and a potential driver of gene evolution. Additionally, experimental evidences can lead to encompass transcriptional stochasticity as a component of darwinian-like chance/selection processes in clonal cell populations. This has several consequences relative to evolutionary studies. First, intercellular relations might be described in terms of short-term adaptations relying on variable and/or unpredictable cellular behaviors in homogeneous environments. Here, macroscopic (tissue, organ) reproducibility would result from variations/selection of elementary (cellular, intracellular) events, ranging from simple statistical reproducibility to internal constraints that would dynamically stabilize individual cells in an adapted state. This would expand darwinian

dynamics within organism. Consequently, this would be an additional level of selection. In the context of recent debates about group selection, such endodarwian dynamics could challenge the fact that in the multi-level theory, evolutionary transitions from one level to another rely on the loss of competitive interactions at the lower level. Thus, how SGE would unify (and therefore strengthen) the theory in life sciences or generate interferences between levels (and possibly weaken it) needs investigation in the context of an extended evolutionary synthesis. An orthogonal issue is how SGE relates with classical deterministic pathways. Models are needed to describe how selective pressures can take advantage of either flexibility or reliability of cellular events. Finally, SGE occurs alongside other sources of somatic variations leading to cellular heterogeneity whether they are due to genetic, epigenetic, and expression factors. The actual relation between these mechanisms and SGE, from synergy to competition, is a promising field for evolutionary studies.

Looping effects in the case of medical empathy

RIANA BETZLER (University of Cambridge, United Kingdom)

Empathy has become a subject of much public interest lately and is viewed as a highly valuable capacity across various domains of culture and society. In this paper, I discuss how the valuation of empathy (1) interacts with conceptual confusion surrounding what empathy is and (2) may facilitate changes in behaviour — such that we see “looping effects,” in Ian Hacking’s (1995) sense of the term. It affects our understanding of what empathy is as well as how it operates. I illustrate how these looping effects occur by looking at the case of medical empathy in particular. Contemporary literature on clinical practice carries the assumption that empathy amongst clinicians is a good thing, that it facilitates the clinician-patient interaction, and that it promotes healing (Pedersen, 2009). However, this was not always the case; from the 1950s-80s, it was thought that an attitude of “detached concern” was needed in a clinical context (Halpern, 2001). These changing values have stimulated reflection on what it means to be empathic in particular contexts, raising questions about whether definitions of empathy coming from empirical psychology are useful in clinical practice. They have also influenced the way that medical education proceeds; medical students today are taught to cultivate empathy—a very particular form of empathy—and this changes the way that they behave in their interaction with patients.

Consider the mosquito

DYLAN GAULT (Laurentian University, Canada)

One of the counterintuitive aspects of the fight against malaria is that, to successfully rid humans of this disease, we may have to consider, and even promote, the health of mosquitoes. This is of interest as it conflicts with what we assume is the common value judgment regarding the mosquito: most people view mosquitoes as a nuisance and devoid of value. Even the literature on malaria uses the language of mosquitoes as a “vector”, and as a more-or-less passive element of the environment. This risks missing the important active biology and ecology of mosquitoes. The most obvious example of this is the failure of DDT to rid the world, other than North

America, of those mosquitoes that transmit malaria: the evolutionarily adaptive biology of the mosquito was able to produce populations resistant to the pesticide. A subtler example of this bias may manifest in the failure of some malaria researchers to account for, and possibly take advantage of, the fact that there exist mosquitoes that are themselves naturally resistant to malaria, even though this resistance was a significant problem for researchers seeking to breed mosquitoes to study malaria in laboratories. Even work on the genetic modification of mosquitoes seems to see biological agency as resting in the hands of humans, not mosquitoes. However, some research on the possibility of making genetic modifications to mosquitoes shows that successful modifications must not only fight malaria, but must also increase the fitness of certain mosquito populations. Thus, the future of fighting malaria may lie in considering the health of mosquitoes and in promoting that health. This presentation argues that we should take the history of malaria and mosquitoes as a warning of the possibility that our value judgments about the biology we study may be an impediment to our own practical progress.

DS M240

09:00 – 10:30

INDIVIDUAL PAPERS

UNDERSTANDING EVOLUTION: PEDAGOGY AND POPULARIZATION

Visual representation of evolution in sixth grade free and nation-wide Mexican textbooks

DAVID AKLE (Universidad Nacional Autónoma de México, Mexico); **ERICA TORRENS** (Universidad Nacional Autónoma de México, Mexico)

Interest in the role and influence of evolutionary ideas outside scientific circles has pushed the frontiers of social studies of science into the pedagogical ambit. In the field of Scientific Imaging and Visualisation, a growing interest in the role and nature of images in the teaching process and concept understanding has brought to attention the social dimension and implications of scientific images and visual knowledge in the classroom. However, studies of the introduction of evolutionary theory in the classroom in Mexico and the role of images in knowledge production are scant. The aim of this paper is to highlight aspects related to the social dimension of some of the scientific images used in the evolution chapter in the free, nation-wide textbook for sixth grade. Mexican sixth grade students who are enrolled in primary schools get a free textbook which is sometimes the only pedagogical material they use. Basic schooling is based on these textbooks and therefore may be qualified as the repository of teaching material available to students (and some teachers) across the nation. The creation and distribution of the textbooks is relegated by the Public Education Secretariat (SEP) to the National Free Textbook Commission (CONALITEG) and should be subject to scrutiny since it is material to be used for long periods of time. Merging the interest of the social dimension and implications of scientific imagery and the pedagogical connotation of using nation-wide free textbooks is the motivation of this study. Biology has been taught around evolutionary theories and cannot be understood without them. The production and delivery of these pedagogical materials as well as the imagery used to represent evolution in the textbooks used by sixth grade Mexican students should be analysed in the context of social studies of science.

Public understanding of biotechnology in the age of evo-devo**RAMSEY AFFIFI** (University of Toronto, Canada)

Since the commercialization of transgenic organisms in food production in the late 1990s, the debate surrounding the potential health and environmental impacts of GMOs has featured prominently in the media. However, the issue has become very polarized with both sides presenting partial and distorted conceptions of the behaviour of genes in organisms. Anti-GMO activists highlight the interconnectedness of the genome, emphasized through gene networks as well as phenomena such as pleiotropy and epistasis. From this perspective, the genome appears to be an integrated and well-orchestrated ecosystem of untold complexity and adaptedness and any intervention likely deleterious for reasons we are not expected to necessarily anticipate or immediately detect. On the other hand, biotech's most vocal proponents often fail to discuss genomic integration entirely, presenting the genetic code as though it were, by and large, composed of completely segregable Mendelian factors, programmed to produce predictable and reliable phenotypic outcomes. The understanding of the relationship between modularity and evolvability currently emerging in Evo-Devo (Gerhart and Kirschner, 1997; West-Eberhart, 2003; etc.) is revealing a more complex and nuanced picture of the relationship between the genotype and the phenotype that sees modularity and integration as complementary aspects of biological systems. In this paper, I will highlight the implications of this emerging understanding for our assessment of the potential safety, risks, and prospects of transgenic technologies. When scientific fields such as genetics become increasingly specialized, communicating a comprehensible description of current understanding to the public requires simplification. In practice, this means foregrounding certain details while deemphasizing others, taking on gruesome caricatures on either side of the GMO-debate. This raises difficult questions on the political, ethical and pedagogical factors involved with public education.

Characterizations of modularity: An evo-devo approach to transitions of individuality**MARIA REBOLLEDA GOMEZ**** (University of Minnesota, United States)

Modularity is an abstract concept referring to a unit of interacting components characterized by a relative high number of internal interactions and a relative low number of interactions with other similar units. I will argue that—as an abstract concept—modularity allows us to understand general patterns and translate between disciplines. But that we also want to understand and describe the biological world at multiple spatial and temporal scales; that we care about particularities of these systems because they are the result of different evolutionary histories and ecological needs. Thus, if we also want to be able to describe this heterogeneity, we will require multiple particular descriptions of modules characterized by the type and strength of their interactions. In this paper, I argue for the productive value of the coexistence between an abstract definition of modularity and a multiplicity of particular characterizations defined by the questions, the biological phenomena of interest and scientific practices involved. I argue that this pluralism provides insight into transitions in individuality and provides a way to translate between two different research programs: one interested mainly in the description of particular transitions of individuality and their developmental machinery (e.g. the evolution of metazoans) and a second one interested in a more general model of the evolution of individuality.

DS M260

09:00 – 10:30

INDIVIDUAL PAPERS

HUMAN NATURE: LANGUAGE, MUSIC, TECHNOLOGY, AND WITTGENSTEIN**Life and language through the lens of Wittgenstein****JUAN GUEVARA-ARISTIZABAL** (Universidad Nacional Autónoma de México, Mexico)

Within the life sciences language has been studied by using two main approaches: the genetic-molecular and the psycho-social. The first one acquired a significant place after the discovery of gene FOXP2 and the myriad of studies that have shown its relation to human language development and other sort of behaviors in non-human animals that appear to be linked to conditions that would favor the rise of language. The second one, although with a longer history, has gained a prominent place in biology after the advent of the social understanding of life: the importance of sociality for the development of a great deal of animal species. Although the two seem to have different aims and methods, they both share a common presupposition: evolution, regardless of the specific evolutionary mechanism. This means that they both deal with a question concerning the origins of language. However, this question is biased by another presupposition: that language is a unique feature of humankind. My main objective is to look at the problem from a different perspective, using the late Wittgenstein's thoughts on language and open the question on the possibility of language beyond the human (even beyond the animal). There are two concepts that I would particularly like to stress: language-games and forms of life. How these terms are intertwined in Wittgenstein's philosophy and how we understand the game wherein language and life appear could lead us to open them up and face a different way of regarding language, even in an evolutionary context, that is not founded on the idea that the evolution of language has to necessarily culminate (or find its best exemplary) in us humans.

“Technologies of life”: Darwin, biology, and the demographic transition**GIULIANO PANCALDI** (Università di Bologna, Italy)

This will be an exercise in the history of the life sciences in a long-term perspective. It will combine the history of science and technology with data from human population dynamics. I will examine briefly three episodes referring to the period from 1859 to the 1970s. The episodes, it will be claimed, suggest some little-explored connections among otherwise well-known trends in the history of the life sciences and the history of human populations. The first episode will focus on Charles Darwin, his views on the “technology of life”, and his attitudes towards birth control. The second, some fifty years later, will consider J. B. S. Haldane and his pamphlet “Daedalus”, which advocated the biologists' control over human reproduction in an age marked by ambitious plans for political reform. Another half century later, the third episode will consider the social background of some of the biologists who were at the origin of recombinant DNA technologies. I will use the episodes to suggest that historians should try to address together a few issues that so far have been treated separately: the spread of a “technology of life” approach in biology, secularization, fertility decline, and the expansion of the middle classes.

Music and human evolution: Philosophical aspects**ANTON KILLIN** (Victoria University of Wellington, New Zealand)

Music is a truly ancient aspect of human social life. The archaeological record boasts sophisticated Upper Palaeolithic musical technologies that betray even more ancient musical practices. Considering music's role in the context of human evolution raises a number of questions. Why did our ancestors spend time, energy and resources on music? Are music's origins intertwined with the evolution of language, or mother-infant communication, or group socio-psychological grooming, or sexual selection? Are there musical universals? Is music an adaptation? This paper will review philosophical implications of the (interdisciplinary) research on music, cognition, and human evolution. I will discuss methodological issues for the building of evolutionary models of music, critique the ever-increasing dispute over music's status as an adaptation or otherwise, and begin to integrate some recent scientific and theoretic work.

INDIVIDUAL PAPERS

MORAL NICHEs AND NATIVES: GENE/CULTURE EVOLUTION**Patterns and processes in gene-culture evolution****MICHAEL BRADIE** (Bowling Green State University, United States)

One of the motivations behind the move to "Darwinize" culture is that it will provide a unification of the human sciences in much the sense that Darwin's theory provided a basis for unifying the biological sciences (Dobzhansky, Mesoudi, Blute et al.). Peter Godfrey-Smith has recently argued that no such unification is forthcoming given the fact that much cultural change at what he calls the "meso" and "micro" levels proceeds by significantly non-Darwinian processes. Here I review some of the relevant stances on process and patterns in cultural evolution and suggest an alternative additional reason for being skeptical about the ability of a Darwinian approach to produce a unification of the human sciences.

Some controversies around moral nativism**ROGER REX** (Universidade de Brasília, Brazil); **PAULO ABRANTES** (Universidade de Brasília, Brazil)

The theory of evolution sparked a series of questions about the origins of moral judgments and the underpinning principles. In particular, it reinforced the debate about moral nativism. In this paper we scrutinize two research programs that advocate respectively the existence of an innate ability to judge morally and a predisposition to moralize behaviors with certain contents. The best-known version of moral nativism argues for the existence of a moral grammar, by analogy with the Chomskyan model of principles and parameters in linguistics (Universal Moral Grammar). The second program argues for the existence of a moral domain, i.e., of a small set of moral intuitions found in all societies (Moral Domain Theory). We critically evaluate the arguments commonly used to ground both theories: ease of learning even in face of poverty of stimulus; the pre-established order of

moral development in individuals; universality and antiquity of the moral phenomenon; distinction between moral norms and conventional norms; the principle of double effect. We are concerned with how they fare at relevant contemporary research in Cognitive Science and meet constructivist arguments proposed by Jesse Prinz and Kim Sterelny, among others. We found out that there is little evidence that our moral judgments follow the model of principles and parameters, although it can be useful as a heuristic device for guiding future research. At the same time, ease of learning suggests that the human brain is somehow prepared to learn moral rules and that the types of rule we adopt are constrained by our biology. Furthermore, the fact that the capacity to make moral judgments develops according to a similar schedule in different cultures indicates that it is an endogenous one. Although it depends, for sure, on the existence of culture, it is not reducible to cultural phenomena.

Constructing the moral niche**JOERI WITTEVEEN** (Universiteit Utrecht, Netherlands)

In a series of recent publications, Nicolas Baumard and colleagues have argued that humans possess an innate "moral sense"—a domain-specific cognitive system for making moral judgments. They contend that this cognitive system evolved through natural selection in "biological markets" that were present in late Pleistocene hominid environments (André & Baumard, 2011; Baumard et al., 2013; Sperber & Baumard, 2012; Baumard, forthcoming). Baumard et al.'s account is pitted against influential cultural group-selectionist explanations for the evolution of morality, which typically deny that humans evolved a specialized cognitive moral subsystem (Boyd et al., 2003; Chudek et al., 2010; Gintis et al., 2003). I will argue that although Baumard et al. are right to be skeptical about group-selectionist models of the evolution of morality, their market-based (individual-selectionist) alternative is itself problematic, for a variety of reasons. Most importantly, I will argue that for the specified biological market configuration to have come about, a transition from ancestral primate social configurations was needed which relies on a capacity for (proto-)morality having evolved already. In consequence, Baumard et al.'s market-based account for the evolution of morality becomes superfluous (and is therefore likely false). In the second part of my talk, I will take cues from recent synthetic accounts of human evolution (e.g. Boehm, 2012; Dubreuil, 2010; Sterelny 2012, 2014) to sketch an alternative account of the evolution of the capacity for morality. I will argue that the evolution of morality began with humans niche constructing each others' ecological, reproductive and informational environments in the early Pleistocene. The evolution of mutualism could only get started when trust—itself rooted in an evolved capacity for positive affect and collective intentionality—allowed humans to cooperate in situations with immediate, automatic payoffs. Only after evolving a basic capacity to trust one another in these simple cooperative ventures, could late Pleistocene hominids establish and support the inverse dominance hierarchies that would then form the bedrock for the elaboration of the human capacity for morality. The full evolutionary account that I will present casts doubt on the hypothesis that human capacity for morality (in the context of mutualistic interactions) forms a psychological natural kind. Instead, it suggests that the human capacity for moral judgment relies on a multitude of capacities with different, partially overlapping functions, and with different evolutionary trajectories.

DS M280

09:00 – 10:30

DS M320

09:00 – 10:30

INDIVIDUAL PAPERS

IDEAS OF HEREDITY AND ANCESTRY IN DISCIPLINE FORMATION**Against the grain: An investigative model for the ancestral health movement****RICK MORRIS** (University of California, Davis, United States)

The ancestral health movement (AHM) is an attempt to integrate concepts from evolutionary biology into the human and health sciences, in e.g. evolutionary medicine or the “Paleo diet”. The AHM looks to evolutionary biology not only to develop hypotheses about the causes of human health outcomes, but also to develop recommendations for health interventions. Needless to say, the AHM has been extremely controversial. Critics have characterized the AHM as making vague and inaccurate claims about human behavior and health outcomes. I discuss six questions which the AHM must answer to achieve its explanatory and interventionist goals in relation to one of its central claims: many negative human health outcomes are the consequence of a “mismatch” (Gluckman 2009, Nesse 2012) between contemporary human environments and “the” evolved physiology of the human organism. I call the first question the mapping question: the AHM advocate, in suggesting that human populations are better-suited to some environments than others, must identify on principled grounds which populations she will examine. Second, the epidemiological question, which requires the advocate to delineate the differing health outcomes between populations. Third, the evolutionary question, which requires the advocate to show the relevant genetic similarities between the populations. Fourth, the causal question, which requires the advocate to provide causal mechanisms for the outcomes seen. Fifth, the intervention question, wherein the advocates propose their interventions. Finally, the evidential question, which requires that the advocate demonstrate empirical support for her claims. My intent here is not to make a positive claim about how well (or poorly) different branches of the AHM make their case. Instead, I propose a model for investigating their claims which will simplify the discussion for the advocate and the skeptic alike by clarifying the disputed claims and providing a rubric by which each can evaluate the AHM.

Social heredity: The germ-plasm theory and the development of the American social sciences**EMILIE RAYMER** (Johns Hopkins University, United States)

Prior to August Weismann’s 1889 germ-plasm theory, which denied that the inheritance of acquired characters played a role in evolution, social reformers believed that humans could inherit the effects of a salubrious environment and, by passing environmentally-induced modifications to their offspring, achieve continuous progress. But Weismann’s theory disrupted this logic, and caused many to fear that they had little control over human development. As numerous historians have observed, this contributed to the birth of the eugenics movement. However, I argue that Weismann’s theory also led to the creation of a theory of human evolution in which the social environment had a central role and biological heredity had a diminished one. The origins of this theory are found in the work of nineteenth-century social scientists Lester F. Ward, Richard T. Ely, and Amos Warner. It was further developed by biologist Herbert Conn and sociologists Walter Smith and L.L. Bernard in the 1910s

and early 1920s. These thinkers used Weismann’s theory to differentiate between organic and social evolution, and argued that although Lamarckian inheritance did not occur in biological evolution it was at work in social evolution, through a process called “social heredity,” which entailed the external transmission of civilization’s accumulated traits. Relatedly, they asserted that because organic and social evolution were governed by different laws, the social environment played a crucial role in advancing humanity despite Weismann’s contention that the environment played a limited role in organic evolution. Furthermore, these thinkers used Weismann’s theory to demonstrate the limitations of biological evolution. They asserted that when compared to the social environment, organic heredity played a small role in human development. They also rejected biological theories of progress, and contended that humans were responsible for their own advancement, which was achieved by strengthening the social environment.

History of biology as a curricular component in teacher education in Brazil**TATIANA TAVARES DA SILVA** (Universidade de São Paulo, Brazil); **MARIA ELICE BRZEZINSKI PRESTES** (Universidade de São Paulo, Brazil); **NELIO BIZZO** (Universidade de São Paulo, Brazil)

This presentation will discuss a research promoted in Brazil about the History of Biology as a curricular component in teacher education. In curriculum official documents for Biology’s under graduation, in Brazil, is expected philosophical and social fundamentals and basic knowledge of History of science. To investigate how is the interpretation of this document and the implementation of History of Biology in teacher education will be research in site of the MEC (Ministry of Education) of Biology’s under graduation (teacher education) and research of the curriculum subject of History of Biology, Philosophy of Biology or similar words. It is expected that data can contribute to the development of strategies for teacher education and for “add-on approach” of History of Biology in Science education.

DS R510

09:00 – 10:30

ORGANIZED SESSION / DIVERSE FORMAT

SITUATING ORGANISMS: PERSPECTIVES ON 20TH CENTURY BIOLOGYOrganizer(s): **SABINA LEONELLI** (University of Exeter, United Kingdom); **RACHEL ANKENY** (University of Adelaide, Australia)

Participant(s):

RASMUS GRØNFELDT WINTHER (University of California, Santa Cruz, United States)**EDMUND RAMSDEN** (Queen Mary University of London, United Kingdom)**ROBERT KIRK** (University of Manchester, United Kingdom)**NATHAN CROWE** (University of North Carolina at Wilmington, United States)**SABINA LEONELLI** (University of Exeter, United Kingdom)**RACHEL ANKENY** (University of Adelaide, Australia)

The organisms that biologists study can be situated in at least three distinct ways: (1) concretely, either as living beings that need to survive and develop in laboratory environments or as unpredictable objects of study that need to be tracked in the field as they interact and change; (2) conceptually, as complex entities that need to be modeled and idealized in order to investigate specific questions; and (3) institutionally within the complex infrastructures (whether in the lab or in the field) in which they are used, which include material resources, labor and support which in turn shape the direction and outcomes of the research. This session brings together four papers that analyze these situated aspects of organismal research from philosophical, historical and sociological perspectives, both in terms of specific case studies and in terms of macroscopic trends in 20th century research.

Life on a behavior farm: Howard S. Liddell and the study of experimental neurosis

EDMUND RAMSDEN and **ROB KIRK**

Inspired by the work of Ivan Pavlov, and seeking a scientific approach to human psychopathology, from the 1920s, American psychiatrists, physiologists and psychologists turned to the animal laboratory. The field of "experimental neurosis" united a diverse array of actors, methods and ideas. This paper will focus on one of the most important and successful of its interdisciplinary research centers, the Cornell Behavior Farm Laboratory, directed by the psychobiologist Howard Liddell from 1923 to 1962. By focusing on the development of the farm through time, we shall examine how a research community evolved and continuously redefined itself, combining an array of psychoanalytic, Pavlovian and ethological theories and methods. Critical was the role of the animal, the farm employing pigs, goats, sheep and dogs. Not only did the choice of animal reflect specific research purposes, but their idiosyncrasies as individuals, their relationship to specific physical environments, and even their personal and emotional relations with each other and those who worked with them, became the subject of analysis. Through this intense focus on the life histories of the animals and the environments in which they lived, the Behavior Farm was able to procure relevance to clinical methods of diagnosis and treatment while producing more generalizable psychophysiological knowledge.

The pragmatic cartography of population biologists: Army ants, flour beetles, and the lab-field border

RASMUS G. WINTHER

Maps and cartographic reasoning play important roles in biological practice (e.g., Hall 1992; Gannett and Griesemer 2004; Turnbull 1993, 2004; Winther under contract). While significant attention has been paid to mapping in population genetics and genomics (e.g., Haraway 1997; Gaudillière and Rheinberger 2004, 2011), the importance of mapping to population biology in general has been underappreciated. I track mapping practices—actual and analogical—in two influential moments of ecology and animal behavior. (1) T.C. Schneirla's laboratory (American Museum of Natural History, NYC) and field work (Barro Colorado Island, Panama) on army ants (genus *Eciton*) from the 1930s to the 1960s. Maps played a critical role in Schneirla's theorizing, laboratory, and field practices. In his published work, they were often combined with other visual and pictorial representations/performances to produce integrated knowledge (e.g., Figure 1 from Schneirla 1957 *Theoretical Consideration of*

Cyclic Processes in Doryline Ants). (2) Thomas Park's contemporaneous work at the University of Chicago on the "population physiology" of flour beetles (genus *Tribolium*). Park used maps to a lesser extent. Yet, representing and analyzing the structured spatialization of his laboratory populations involved implicit mapping practices. Map tracking is useful in that "maps can provide valuable markers of changing theoretical interests, goals, commitments, and values" (Gannett and Griesemer 2004, 84); maps are also a central metaphor for the pragmatic production of scientific knowledge (e.g., Peter Galison; Ronald Giere; Thomas Gieryn; Thomas Kuhn; Bruno Latour; Helen Longino; Stephen Toulmin). I nestle my concrete map tracking analysis in the broader philosophical contexts of (i) the activities and nature of the lab-field border (Kohler 2002), (ii) the trichotomy of theoretical, laboratory, and natural populations (Winther, Giordano, Edge, and Nielsen forthcoming), and (iii) the sustained impact of pragmatic map analogy discourse across the sciences and humanities (Winther under contract).

Patterns of development: Trends in model organism use by embryologists (1949-1963)

NATHAN CROWE

Over the past 30 years, historians, philosophers, and sociologists of biology have articulated how particular laboratories, problems, and communities have been important to the creation and adoption of prominent experimental organisms. Using case studies, scholars have been particularly good at identifying how relationships between advisors, students, and visiting researchers can create lasting traditions of experimental organism use. This paper describes a project which focuses on analyzing a large and international data set (containing several thousand data points) of developmental biologists in the 1950s and 1960s using the General Embryological Information Service, a periodical that tracked biologists, their fields of research, and the organisms they used, for several decades. Using this data set, the paper explores whether there were larger trends of organism use that can be seen beyond the intellectual genealogies that are often used to track experimental organisms adoption. These trends may include larger patterns beyond the scale of laboratories to include institutions, regions, or nations as well as how closely organism use is related to research areas such as descriptive, comparative, and experimental embryology.

How simple organisms grew into model organism communities: The role of repertoires

RACHEL A. ANKENY and **SABINA LEONELLI**

How effectively communities of scientists come together and co-operate is crucial both to the quality of research outputs and to the extent to which such outputs integrate insights, data and methods from a variety of fields, laboratories and locations around the globe. This paper focuses on the ensemble of material and social conditions within which organismal research is situated that makes it possible for a short-term collaboration, set up to accomplish a specific task, to give rise to relatively stable communities of researchers. We refer to these distinctive features as repertoires, and investigate their development and implementation in a key case study in contemporary biological sciences, namely how research on individual organisms evolved into model organism communities. We conclude that whether a particular project ends up fostering the emergence of a resilient research community is partly determined by the degree of attention and care devoted by researchers to material and social elements beyond the specific research questions under consideration.

DS R515

09:00 – 10:30

INDIVIDUAL PAPERS

MODELING ECOLOGY AND EVOLUTIONARY BIOLOGY**Scientific methods in ecology and evolution and their epistemic values****STEPHANIE MEIRMANS** (Universiteit Leiden, Netherlands)

How do scientists in ecology and evolution arrive at knowledge claims? I have used published debates on the values of different methods in the field itself to approach this question. From these debates, it is clear that practitioners have a good intuitive understanding of the value of different methods. I have then made these insights more rigorous and explicit by subjecting them to a more systematic investigation. I found that there are three different basic methods used. First, there is the study of theoretical causal relationships, which is often expressed in mathematical language, but also comprises e.g. thought experiments. Second, one can perform experiments; typically manipulations done in a simplified and controlled environment that can point to the existence of simple causal relationships between natural entities. Third, one can observe nature, typically in a structured and systematic manner, such as the search for natural patterns. These methods can be done with different types of tools and at different levels of organization and timescales. The three methods are often, but not always, exemplified in the scientific cultures of theoreticians, experimenters, and naturalists. The methods can also be combined in various ways, leading to some of the apparent complexity of scientific research methods. Furthermore, I argue that each basic method has its own specific inherent advantages and limitations. Often, the methods are used in combination with each other because they can cover each other's weaknesses. One very important way to establish robust evidence therefore comes from using several lines of evidence that are derived from different basic methods. Notably, this account of robustness distinguishes itself from other accounts of robustness in that it explicitly addresses the different epistemic values of the three basic methods.

Reconciling community ecology with evidence of animal cultures and social learning: Socially-adapted, localized community dynamics?**CHANTELLE MARLOR** (University of the Fraser Valley, Canada)

A growing body of empirical research suggests many animal species are capable of social learning. Social learning has implications for community ecology; changes in behavior can lead to changes in inter- and intra-specific (between and within species) interactions. This paper explores possible implications of social learning for ecological community dynamics. Specifically, it examines the trophic cascade model, using the classic sea otter—sea urchin—kelp cascade as an example. Incorporating social learning and animal culture into models such as this suggests that ecological community dynamics have the potential of being highly localized. Other possible implications of social learning, namely interspecific cultures, species invasion, and socially-created microevolutionary selection pressures are also explored.

Implicit idealizations in biological modeling**ALEX VON STEIN** (University of Arizona, United States)

Models of biological systems employ idealizations to make the models simpler, more tractable, and to isolate core features of the phenomena under study. Most attention to the idealizations of models have focused on idealizations that are explicit in the presentation of the model—e.g. the use of continuous functions to represent population size or parameters held constant even though the observed values are known to vary. While attention to explicit idealizations is important, biological models often also rely on implicit assumptions—assumptions necessary for the model to work, but which are not explicit in the presentation of the model, e.g. assumptions which do not appear in the equations themselves. I discuss the presentation of models in a way that emphasizes the culpability of modelers to make explicit the relevant assumptions of their models and from this discussion I draw criticisms of modeling practice—in particular, I criticize debates in ecological theory about niches and neutral theory for arising from and persisting due to inadequate presentations of assumptions by modelers and theoreticians.

DS R520

09:00 – 10:30

INDIVIDUAL PAPERS

EXPLANATION, EXPERIMENT, AND MECHANISM**Is Brownian motion a mechanism?****ARCHIE FIELDS** (Indiana University, Bloomington, United States)

The mechanistic account of explanation has received a great deal of attention over the past decade, especially in the domain of biology. By many accounts, mechanistic explanation is the dominant mode of explanation in the biological sciences. I argue that there are a large number of biological phenomena that cannot be explained fully in terms of mechanisms. I begin by briefly describing a general mechanistic account of explanation and highlighting some of the required features of mechanisms discussed in the literature, particularly regularity of operation and having fine-tuned organization. I then show that the motion of motor proteins, which are enzymes that metabolize molecular energy sources like ATP to do mechanical work, cannot be completely explained mechanistically. These proteins often rely upon Brownian motion to move them down microtubule tracks within cells in a way that fails to adhere fully to both the regularity and fine-tuned organization that is required for mechanistic explanation. Generalizing from the motor protein case, I argue that Brownian motion cannot be explained mechanistically and that because Brownian motion is causally efficacious in many biological phenomena, those phenomena also cannot be fully explained mechanistically. This demonstrates that Craver's principal normative requirement of mechanistic explanations, which is that the mechanistic explanation must account fully for the explanandum phenomenon, cannot be fulfilled for explanations of many biological phenomena. Thus, the scope and explanatory power of the mechanistic strategy is drastically reduced since many biological phenomena involving Brownian motion cannot be given complete mechanistic explanations.

“How possibly” explanation in biology: Lessons from Wilhelm His’ “simple experiments” models

CHRISTOPHER PEARSON (Southern Illinois University Edwardsville, United States)

One common characterization of how possibly explanation in biology is that they are incomplete, non-autonomous explanations. For some, this lack of completeness and autonomy does not, however, undermine fully the value of how possibly explanation to the biological sciences. Despite their presenting as incomplete and non-autonomous, how possibly explanations occupy an important heuristic role in biology by, for example, setting out novel research programs. The case favoring an important role for how possibly explanation in biology I think is exceptionally strong however, limiting that role to heuristic, I believe misdiagnoses to some degree the ways in which how possibly explanation functions within biology. Indeed, characterizing the role of how possibly explanation as one of mere heuristic is crucially contingent on the view that how possibly explanations are incomplete and non-autonomous. I maintain, to contrary, that there are how-possibly explanations in biology that are, in a substantive way, both complete and autonomous. My defense of this claim stems from an analysis of Wilhelm His simple experiments, in which His attempted to construct manipulable physical models of mechanical explanation of development. These 2 interpretations depend on adopting one or the other of 2 contrastive explanatory contexts. The first of these how possibly can mechanical principles explain an embryo’s transition from one stage to the next is set against the context of non-mechanical factors being required to explain animal development. The second how possibly can mechanical principles explain an embryo’s transition from one state to the next set against the context of seeking an inventory of factors sufficient to account for actual embryological development. The latter of these contrastive explanatory contexts fully supports the view that how possibly explanations are incomplete and non-autonomous, though eminently useful as heuristic. Alternatively, the former contrastive explanatory context demonstrates His’s model derived explanations as both complete and autonomous.

Omics experimental strategy (OES) as a scientific epistemology for system-driven research

EVE ROBERTS (Dalhousie University, Canada)

Omics disciplines (genomics, proteomics, metabolomics, exomics, and the like) challenge the standard view that all biological/biomedical research must be hypothesis-driven. Previously I have argued that omics research is “system-driven research”, in which the complexity of a biological system is addressed directly. Furthermore, although system-driven biological/biomedical research operates within a hierarchy of hypotheses, what actually shapes system-driven experimental design is the system itself, not a proximate hypothesis. Evidently omics methodologies produce new scientific knowledge: the question is how?—given that such research is not hypothesis-driven. Taking proteomics as exemplar, I identify the strength of system-driven research as its ability to generate detailed, inclusive accounts of natural biological systems. I call its scientific epistemology the Omics Experimental Strategy. OES involves a well-designed experiment, specifically with a detailed descrip-

tion of the system under investigation, empirical data produced competently by reliable technology according to peer-generated standards of best practice, and finally contextualization of data within the system. For system-driven research, validation takes place within the system, which is driving the experiment. (Importantly, a similar validating relationship holds for hypothesis-driven research, where validation takes place in relation to the proximate hypothesis driving the experiment.) These contextualized findings provide new insight into how that system functions. Indeed some of these findings may prove to be entirely novel and unexpected. Arguably, for the OES, novelty serves as an epistemic virtue. Supported by a scientific epistemology, system-driven research carried out according to the OES constitutes scientific research, not a run-up to “real” science.

10:30–11:00

COFFEE BREAK

DS 1520

11:00–12:30

INDIVIDUAL PAPERS

MAKING BIOLOGICAL CATEGORIES: SPECIES AND OTHER KINDS

Race: The very idea of a biological basis

CHRISTOPHER CLARKE** (University of Cambridge, United Kingdom)

Geneticists know that the connection between genetics and race is a relatively loose one. There is no gene for example that is possessed by (almost) all people racialized as Asian, but that is possessed by (almost) no people racialized as Native American. Philosophers such as Appiah, Glasgow, Mills, Root, Sundstrom and Zack take facts like this one to prove that race is not a “real biological kind”. It lacks a “principled biological basis”. But Andreasen, Sesardic, and Spencer argue that these anti-realists about race are too restrictive in their standards for what counts as biologically real. I provide a novel argument for Kitcher’s deflationary stance towards this debate: for any project one can distinguish between those categories/classifications that will be helpful and those that will be unhelpful in pursuing the aims of that project. But there is no aim-independent distinction, I argue, between those categories/classifications that have a biological basis and those that do not. So both sides are mistaken. Racialized categories don’t deserve to be called biologically real, but this is because nothing deserves this empty honorific. I distinguish this deflationary stance from the much more moderate stance taken by Spencer and by Kaplan and Winther.

Lineages and identity in systematics: A critique of de Queiroz

CELSO ANTONIO ALVES NETO (Leibniz Universität Hannover, Germany)

Species are traditionally seen as evolving lineages (Hull, 1978). They are taken to be population-level lines of descent which speciate, change and go extinct across evolutionary time. For instance, de Queiroz (1997, 1999) claims that all species concept in the literature tacitly agree on the ontology of species, assuming that

species are biological lineages. Insofar the conflict concerning how to delimit such lineages is unsolvable, there is no more no solution to the species problem other than say that species are lineages. In this paper I criticize de Queiroz's solution to the species problem as a mean to reflect on lineages identity. My criticism assumes that the species problem is essentially about identity. First, I claim, the author promotes an ontological division of labor: species are committed to one and the same ontological status, but they are individually committed to different identity criteria. De Queiroz detaches ontological status from identity. But that is not a good way to solve the species problem in systematics, as I defend. Species problem concerns how to count species and not simply how to characterize their ontological status. My hypothesis is that de Queiroz does not take the difference between the uses of "lineage" in systematics and evolutionary biology seriously enough. As an evolutionary concept, "lineage" can be applied loosely without presupposing a unique and precise identity criterion. But if "lineage" is to be applied in systematics as a classificatory concept, this is not an option. There must be a single clear identity criteria associated to it. Such a difference can be made clear by contrasting selection-based and phylogenetic explanations, as well as appealing to the role of pattern and processes in evolution and systematics. After exploring such concepts, it will be clear that de Queiroz ontological division of labor is the wrong way to explain away the species problem.

Homologizing and other kinding practices

CATHERINE KENDIG (Missouri Western State University, United States)

Homology is a notoriously elusive concept to pin down (Hall 1992, 2003, 2012; Love 2007; Brigandt 2007; Ereshefsky 2012; Minelli 1996, 2003). There has been sustained debate over the nature of its correspondence and the units of comparison. I address some of these debates by analysing the nature of the comparative approach through the epistemological practice of homologizing. Consideration of practice provides not only potential for further understanding of the process of homologizing but also of kinding in general, insofar as homology is a kind of kinding. I suggest that the processes of homologizing are constitutive of natural kinding activities. As such, it is the activity that precipitates what has been called "homology thinking" (Ereshefsky 2012). Although infrequently discussed in the philosophical literature, the emphasis on comparative practice is not new. A record of comparative anatomy and the identification of sameness of form in different animals has been observed and documented since Andreas Vesalius (1543) and Nehemiah Grew (1681). The extensive anatomical collections of John Hunter (1835) and Richard Owen (1843) exemplified the making, displaying, and tracking the sameness of form in different organisms. These curated collections, their identification of type specimens, and the meticulous descriptions of these served as the epistemic estate required for adjudicating whether a particular organism belonged to, or lay outside of, a particular kind. Homologizing can be understood as a set of kinding activities that continue to shape the meaning and use of homology. Investigation into historical as well as current comparative practices reveals the diversity of these kind-generating practices, the nature of correspondence, and the units of comparison.

DS 1540

11:00–12:30

INDIVIDUAL PAPERS

MODERNITY, BIOTECHNOLOGY AND ENGINEERING NOVEL PROTEINS

"Theoretically elegant, but technically demanding": Somatic hybridization and biotechnology (1960-1995)

MATTHEW HOLMES (University of Leeds, United Kingdom)

A key barrier to the development of new forms of biotechnology – the cell wall – was removed by plant scientist Edward C. Cocking in 1960, creating what is termed a protoplast. Protoplasts appeared to possess great potential in the breeding of new plant varieties, through the fusing of entire cells of completely different species, complete with their genomes. This technique, termed "somatic hybridization," was the particle collider of the biological world, fused protoplasts resulting from crosses containing a vast range of genetic data. Fused cells were used to create a tobacco plant in 1972, somatic hybridization demonstrating its commercial viability. This paper will examine the development of somatic hybridisation from 1960-1995, disease-resistant tobacco formed by the process being commercially grown in Ontario by the latter date. Despite some successes, somatic hybridization ultimately proved a low-key biotechnology, lacking the status and international uptake of recombinant DNA techniques. Using this comparison, this paper considers the limiting factors which restricted somatic hybridisation as a commercial technology, from ongoing technical difficulties to isolation from the biotech industry. Another context is relevant to this discussion, as recombinant DNA would go on to be an environmentally controversial technology in the 1980s, an outcome avoided by somatic hybridization, despite higher risks of transmitting negative traits and genetic instability. The question will therefore be asked of why the same challenges were not faced by advocates of somatic hybridization.

Victorian science: The milieu in which it was born, the modernity into which it evolved

GEORGIA RAE RAINER (Florida State University, United States)

The British Association for the Advancement of Science (BAAS) was founded in 1831 by several prominent scholars of the day including Cambridge thinkers William Whewell, Charles Babbage, and indirectly, John Herschel. This Association changed the practice of science and established the professional discipline that we know today. One way in which the BAAS made a significant impact to the scientific community was by encouraging women to attend the research presentations, which not only increased the role society played in promoting these annual meetings, but more importantly, it opened the door for women to actively participate in the scientific community. Also, the BAAS restored the practice of a question and answer period following each presentation (having been previously discontinued by the Royal Society). This promoted diversity in the BAAS where the benefit of this practice increases the probability of objective science given the different perspectives that critically examine the work. The various commentators have the advantage of potentially different background assumptions that can affect the observations and foreseeable flaws noticed by the particular observer. This is crucial to modern scientific practice and is demonstrated in the values ascribed to peer reviewing and repeatability of experiments. While these changes may seem mild to the modern reader, they set a trend in the practice of science that has become ingrained. The modern scientific community widely uses the presentation format established by the British Association, and in large part, is better for it.

Engineering novel proteins with orthogonal tRNA: Unusual causes that make a difference

JANELLA BAXTER (University of Illinois at Chicago, United States)

Recent defenses of causal specificity in biology have attempted to justify their views by appealing to the explanatory values of biologists. Kenneth Waters defends his account of actual difference makers on the basis that biologists are primarily interested in causes that actually obtain. (Waters 2007) Similarly, Marcel Weber argues that genes are the most specific potential difference-making cause in biology on the basis that biologists are primarily concerned with biologically normal interventions. (Weber forthcoming) Both views express a widely received attitude about the interests and goals of biologists as being primarily concerned with the contingent facts of our world. While I agree with this general attitude about the contingent nature of biology, I argue that neither view fully accounts for the diversity that distinguishes the discipline. By emphasizing the actual or the biologically normal, Waters and Weber rule out unusual causes as biologically interesting. The use of orthogonal tRNA/aminoacyl-tRNA synthetases to engineer novel proteins is one case of unusual causes in biology; causes that are neither actual in Waters' sense nor biologically normal in Weber's. Unusual causes can be of significant research interest to biologists for the purposes of developing biotechnology as well as for observing the causal mechanisms of development. (Axup et al. 20012; Ivanova et al. 2014) I maintain that unusual causes in biology provide some pragmatic reasons for why describing the interests of biologists in terms of a single set of values may not be appropriate.

INDIVIDUAL PAPERS

BRAINS, RACE AND GENES: IMPLEMENTING BIOLOGICAL CONCEPTS

The biological reality of race does not underwrite the social reality of race: A response to Spencer

KAMURAN OSMANOGLU (University of Kansas, United States)

In this paper, we criticize Quayshawn Spencer's (2014) "radical" solution to the race problem in his *A Radical Solution to the Race Problem*. Spencer defends the biological reality of "race". He argues that "race", as used in the current US racial discourse, picks out a biologically real entity. He lays out his argument in two steps: first, he argues that race, in the US racial discourse, is a proper name for a set of human population groups, second, by relying on recent data from human population genetics, he contends that the set of human population groups matches the Blumenbachian partition, i.e. the US meaning of "race" is the set of populations at the $K = 5$ level of human population structure. Therefore, Spencer argues that "race", in its US meaning, picks out a biologically real entity. We raise two criticisms against Spencer's account. First, we argue that limiting the racial discourse to the current US Census is not the right way to talk about "race". We find limiting the racial discourse to the US Census problematic. Why do we need to care only about what the US racial discourse tells us about human population groups? We think that Spencer, by limiting the racial discourse to the US race, does not do justice to the culturally diverse social reality of racial discourse. We argue that "race" is a fluid

concept and it takes different shapes in different cultural and historical contexts. Second, we argue that there are other biologically interesting ways to classify human populations into different groups (such as classifying human populations according to their hemoglobin production, lactose resistance, or classifying human beings into different groups by examining if they have Denisovan gene or not etc.) as opposed to $K=5$ clustering that Spencer defends. Therefore, Spencer needs to answer the following two questions if he wants to argue for the biological reality of race in the US racial discourse: First, how is it even possible to biologically support an inherently social category like "race"? Second, what makes the Blumenbachian partition better than hemoglobin production (or any other biologically interesting classification) for social clustering of human populations? Unless this is done, his account cannot be considered successful.

The brain-as-instrument: A new approach to probability in biological systems

CHRISTINA STISO (Indiana University, United States)

Graves, Horan, and Rosenberg (1999) proposed that the processes of evolutionary biology can only be understood as deterministic and epistemic, i.e., that the chance seen in fitness and natural selection is a result of our own uncertainty rather than real indeterminism in the world. But, this subjective notion of probability in a deterministic universe raises deep philosophical concerns. If probability is epistemic, a property of the observer, then it seems illicit to use it in models of objects in the world. I would like to propose a new way of thinking about epistemic probability that alleviates these worries. This involves looking at the brain not as an outside observer looking out at the world, but as an instrument within a system of instruments. In doing so, this new interpretation shows that Rosenberg et al.'s conclusion, that epistemic probability necessitates an instrumentalist view of evolutionary theory is misguided.

The evolutionary gene and the "extended evolutionary synthesis"

QIAOYING LU (Sun Yat-sen University, China); PIERRICK BOURRAT (University of Sydney, Australia)

The increasing profile of epigenetic inheritance raises the question of whether it has major implications for evolutionary theory. In this paper, we argue that the many disagreements on this matter are partly caused by the fact that people from different sub-fields have different notions of the gene, the phenotype and the environment. Based on Haig's conception of the strategic gene, we define a notion of evolutionary gene stripped-down that includes only what is needed for genes to play their role in formal evolutionary models. This concept of the evolutionary gene incorporates not only nucleic acids but also other heritable materials such as epialleles. Once coherent notions of gene, environment and phenotype are distinguished and it is recognized that they are not equivalent to what molecular biologists usually understand, we show that the main contentious claims originating from epigenetic studies disappear, and that current evolutionary theory can easily accommodate them.

DS M220

11:00 - 12:30

DS M240

11:00–12:30

INDIVIDUAL PAPERS

DEVELOPING EVOLUTIONARY UNDERSTANDING

The space between explanation and understanding**JAKE WRIGHT** (University of Minnesota Rochester, United States)

One of the most pressing questions in recent discussion of the relationship between explanation and understanding is whether understanding, properly understood, is a species of explanation. In other words, if one understands a phenomenon in the right sort of way, does it follow that this understanding is the result of the ability to explain said phenomenon? Recently, Khalifa has argued for an Explanatory Knowledge Model of Understanding (EKMU). EKMU posits that “wherever there is understanding without explanation, there is always a knowable explanation of the same phenomenon that would provide greater understanding than its non-explanatory counterpart.” I argue against EKMU via a discussion of Rohwer and Rice’s hypothetical pattern idealizations (HPI). Specifically, I argue that HPI models provide understanding of phenomena while either (a) precluding explanation or (b) forcing one to accept the view that understanding and explanation are indistinguishable, rendering the question moot. HPI models, like the Hawk-Dove game, present impossible scenarios that lend justification to “how possibly” claims. For example, Hawk-Dove is frequently used to justify accounts of the evolution of altruism or restraint in combat by providing understanding of how these traits could have evolved. The scenario presented in Hawk-Dove games is impossible. Thus, if one accepts that explanations must be true in some important sense, is either forced to conclude that a corresponding explanation is impossible, while if one admits false explanations, the line between explanation and understanding disappears.

Evolutionary first laws: A philosophical history**DEVIN GOUVEA** (University of Chicago, United States)

Amidst continued calls for its demise, the analogy between Newtonian mechanics and evolutionary biology has recently splintered around two rival interpretations of Newton’s first law—the traditional version, based on the Hardy-Weinberg principle of population genetics, and a newer rival, the Zero-Force Evolutionary Law (ZFEL). I have argued elsewhere (forthcoming in *Philosophy of Science*) that neither analogy can lay exclusive claim to first-law status; instead it is best to understand them as complementary epistemic tools with unique strengths and weaknesses. In this talk, I will use the long history of first-law analogies to clarify how their particular epistemic roles arise within a larger matrix of explanatory agendas in evolutionary biology. Analogies between physical forces and evolutionary processes date back at least to Darwin’s notebook musings of 1838, but distinctly Newtonian statements first emerge in the formative years of population genetics. I will trace their usage from Dobzhansky’s foundational text, *Genetics and the Origin of Species* (1937), through a hodgepodge of biological and philosophical works in the 1960s and 1970s on to the textbook population genetic formulations that first appeared in the 1980s and are still commonplace today. This history reveals that the analogy has been called upon to perform a surprisingly diverse array of conceptual tasks. Depending on what questions have

been asked of it, for example, the Hardy-Weinberg principle has been understood both as a fundamental empirical law and as a trivial mathematical theorem. Recent philosophical attacks on the principle indicate renewed interest in the relationship between natural selection and random drift. The checkered past and troubled present of the first-law analogy suggest that its epistemic functions are ultimately quite sensitive to the particular biological problems in whose service it is deployed.

Putting the “co” in community: codevelopment, coevolution, and cognitive constitution**EHUD LAMM**** (Tel Aviv University, Israel)

Evolutionary history can be inferred either from historical (diachronic) evidence, that can at least be chronologically ordered if not precisely dated, such as fossils and artifacts, or from properties from a single point in time. Examples of the latter are the current properties of extant organisms such as anatomical similarities between species, developmental similarities and genomic comparisons. The distinction is not always clear-cut, however generally speaking it is clear that relying on non-historical data that is more complete and amenable to experimental manipulation has epistemic and practical advantages. On the other hand, such evidence does not directly provide information about historical development. Hence one inferential challenge facing evolutionary biology is to identify and assess patterns of inductive inference that go from non-historical evidence to evolutionary conclusions. A particularly interesting case involves the use of developmental interactions between cognitive characters to deduce conclusions about their evolutionary past. Developmental evidence is uniquely applicable for studying to cognitive-cultural coevolution and evo-devo inspired approaches to the coevolution of culture and cognition more generally. Coevolutionary hypotheses of this nature have received a lot of attention, including in the philosophy of biology community (e.g., Tomasello 1999 Donald 2000 Sterelny 2010 Stotz 2010). In this paper, we discuss two inference patterns for inferring the coevolution of two characters based on their properties at a single point in time and elaborate on the applicability of the arguments for several kinds of cases and on the strength of their conclusions. We conclude that co-developmental interactions are good evidence for coevolution and that coevolution of the relevant kinds of developmental systems likely leads to co-development. Furthermore, co-developmental interactions help deduce evolutionary order. This coevolution is typically mediated through cultural institutions. Using agent based modeling I will explore culturally-mediated coevolutionary dynamics between cognitive characters, specifically the evolutionary and developmental functions of norms.

DS M280

11:00–12:30

INDIVIDUAL PAPERS

SYSTEMATICS AND CLASSIFICATION

Diachronicity and the contingency of species membership**ALEX LEVINE** (University of South Florida, United States)

This paper turns to the consequences of time-irreversibility for one aspect of the familiar debate on the ontology of species. The causal theory of reference (Kripke 1974, Putnam 1975) offered much promise in resolving philosophical puzzles solved by the theory and practice of taxonomy. Species names could be treated as rigid designators (Hull 1982, Stanford and Kitcher 2000). But this promise comes at a cost (Levine 2001), prompting a reexamination of the semantics of taxon names, the practices whereby the scientific community accepts and changes those names, and the modal significance of both (LaPorte 2003, Haber 2012, Witteveen 2014). I argue that the ensuing debate can best be moved forward by attention to the dynamics of speciation, a process driven partially by the phenotype-blind sampling of individuals from a parent population (as in founder effect speciation). When speciation events are in principle datable, the membership of a given organism in its species must be a contingent, historical fact. At risk of violence to the evolutionary foundations of contemporary systematic biology, it must never be taken as a conceptual, or even a causal necessity. I conclude by returning to the method of types in taxonomy, a frequent target of recent philosophical scrutiny. The lesson to be drawn by the success of this method in avoiding taxonomic confusion is that being made into a type specimen situates an organism within a web of scientific conventions, allowing the name attached to it to serve as a quasi-rigid designator for those observing these conventions. But such quasi-rigidity is itself contingent on a given, historically situated scientific practice. As such, it is nothing like the rigidity attributed to proper names or natural kind terms by Kripke or Putnam.

Roxie Laybourne and the development of forensic ornithology**GABRIELLE GRAHAM** (Florida State University, United States)

In the 1960s, working from the Division of Birds in the Smithsonian Museum of Natural History, Roxie Laybourne pioneered the field of forensic ornithology. In October of 1960, the Federal Aviation Administration (FAA) turned to the Smithsonian to identify the birds which struck down Eastern Air Lines Flight 375. The work was passed to Laybourne, whose visual acuity and determination not only resolved the cause of Flight 375, but set forth the methods and markers for microscopic identification of feathers by species. Originally working with slides using light microscopy, Laybourne single-handedly developed a comprehensive library of slides to be used in what she referred to as “feather work.” Laybourne provided research and investigation services for the FAA, the U.S. Fish and Wildlife Service, the U.S. Federal Bureau of Investigation, Pratt and Whitney, Rolls Royce Limited, and the U.S. Air Force. The feather identification work conducted by Laybourne over the next forty years of her life touched areas of technology and society ranging from aeronautics safety and design, to endangered species poaching and trafficking, to criminal justice. Although Roxie Laybourne’s work has

contributed to increased aircraft safety worldwide, few know the origin story of the field of forensic ornithology and the woman responsible for its founding. This paper seeks to highlight the extraordinary work conducted by Laybourne during a time when women were only just beginning to gain acceptance in scientific fields.

Species concepts and the promiscuous grape**GEORGE GALE** (Concordia University, Canada)

H. A. Prichard argued that we all know, intuitively, what is right or wrong, and that it is only when we begin to philosophically examine the processes of our moral judgments that we lose our way. Thus, he argued, moral analysis rested upon a mistake. I think philosophical analysis of species rests upon a similar mistake. In what follows, I focus upon our attempts to systematize grapes *Vitis* genus, subgenus *vitis* as ample demonstration of this mistake. I begin with the point that up until now species concepts analysis has focussed mainly upon animal species. These attempts have so far failed to reach any settled conclusion. Unfortunately, it gets worse when botanical species are considered. One example should make this clear. Grape taxonomists ampelographers agree that there are somewhere between eighteen and thirty-two good species of *Vitis vitis* in North America. In the field, grape species are nearly as recognizable as the bird species in your backyard feeder. (Or as clear as they were to Mayr’s New Guinea hunters.) Yet, when close morphological and DNA methods are invoked, grape species seem to disappear. Indeed, DNA differences intraspecies are typically greater than differences interspecies. And one grape fact that tells crucially against most received species concepts, especially against the Biological Species Concept, is that all *Vitis vitis* species worldwide can successfully mate. Obviously, species concepts crafted for fauna simply cannot deal with such promiscuity. After a thorough review of grape systematics, and its attendant conceptual issues, I examine some of the rare approaches to botanical issues in the species concept problem, specifically those provided by Holsinger and Mischler. My conclusion is that, once botany is factored into the species concept question, the only possible options are an extreme pluralism or a Prichardian fallback into intuitionism. Given the success of field identification, I prefer the latter.

DS M320

11:00 – 12:30

INDIVIDUAL PAPERS

ECOLOGICAL THEORY AND PRACTICE: PHILOSOPHICAL PERSPECTIVES

Ecological theory and the niche**JAMES JUSTUS** (Florida State University, United States)

At least until Hubbell's neutral theory emerged, no concept was thought more important to theorizing in ecology than the niche. Without it—and its highly abstract definition by Hutchinson in particular—technically sophisticated and well-regarded theories of character displacement, limiting similarity, and many others would seemingly never have been developed. The niche concept is also the centerpiece of perhaps the best candidate for a distinctively ecological law, the competitive exclusion principle. But the incongruous array of proposed definitions of the concept squares poorly with its apparent centrality. I argue this definitional diversity reflects a problematic conceptual imprecision that challenges its putative indispensability in ecological theory. Recent attempts to integrate these disparate definitions into a unified characterization fail to resolve the imprecision.

Might organic feed the world? On the use of probabilities in modeling practice**DANIEL HICKS** (University of Western Ontario, Canada)

Philosophy of probability is generally divided into two camps, with two corresponding statistical methodologies. On the one hand are frequentists, who interpret probabilities as long-run distributions of measurement outcomes and who advocate the family of statistical methods grouped together under the name “null hypothesis testing.” On the other hand are Bayesians, who interpret probabilities as subjective doxastic probabilities (credence levels or degrees of belief) and who advocate statistical methods based on the use of Bayes' theorem. This paper argues that the use of probabilities in hierarchical Bayesian modeling does not fit into either the frequentist or Bayesian camp. This technique is illustrated with a recent paper on the “yield gap” between organic and conventional agriculture (Ponsio et al. 2015). Ponsio et al. find that multi-cropping and crop rotations “substantially reduce the yield gap” between organic and conventional agriculture, which suggests that organic agriculture could “feed the world.” This finding is based on the construction of a hierarchical Bayesian model. Because hierarchical Bayesian models do not use null hypothesis testing, they do not fit into the frequentist camp. On the other hand, the probabilities in these models are often distributions of observed or simulated frequencies, not subjective doxastic probabilities thus they do not fit into the Bayesian camp either. Finally, because these models involve idealizations and simplifying assumptions, there is reason to think that they should not be evaluated in terms of truth or credibility, but rather in terms of context-specific practical usefulness (Wimsatt 2007, Parker 2010). I discuss some implications of these philosophical observations for the interpretation of Ponsio et al.'s findings.

Resilience: Meaning, model and metaphor**LEILA CRUZ** (Universidade Federal da Bahia, Brazil); **CANDELARIA ESTAVILLO** (Universidade Federal da Bahia, Brazil); **CLARISSA MACHADO LEITE** (Universidade Federal da Bahia, Brazil); **CHARBEL EL-HANI** (Universidade Federal da Bahia, Brazil)

The idea of resilience is at center stage in current sustainability debates. Like many scientific concepts, early technical and academic usages alluded to its popular sense, subsequently continuously modified in different features as every concept has a multifaceted character. These modifications either foster or hinder concept's practical application and integration into theory. Resilience concept was originally a capacity of entities for quick recovery after disturbances, or an object's physical property of returning to its original shape after deformation. In recent ecological and conservation literature this meaning has been refined and enriched substantially, acquiring particular properties according to different discourses. In this work we analyze the resilience concept in ecology and conservation biology along three dimensions, following Pickett and Cadenasso (2002) and Pickett, Kolasa and Jones (2007): meaning, model and metaphor. “Meaning” refers to a general proposition stating concept's fundamental elements and their relations, in a scale-independent manner, aiming at broad application. “Model” specifies the classes of phenomena represented by the concept, for practical descriptive or experimental purposes. “Metaphor” refers to ideas explored in non-technical discourses, attached to it by actual instances and idiosyncrasies, as in communicating with general audiences. We present results of an exploratory research on these dimensions of the resilience concept as used in ecological and social-ecological academic literatures, specialized and non-specialized digital media, after analysis of most cited articles in 10-year intervals of articles published in these fields since 1980. Preliminary results indicate expansion of meaning dimension: system's characterization shifts from emphasizing stability to emphasizing constant variation plus adaptive capabilities. In model dimension, results indicate development of applications mainly concerned with system stability but lack of implementation strategies considering the expanded notion and for metaphor dimension, usages in specialized media followed academic discourses while in general media usages were largely unrelated to environmental themes.

DS R510

11:00–12:30

INDIVIDUAL PAPERS

EVOLUTIONARY LAWS? RANDOMNESS, CAUSALITY

[Evolution as involving laws and inconceivable without them](#)**RICHARD CREATH** (Arizona State University, United States)

There are those who say that there are no laws in biology and especially none in evolution. We are told that biology and evolution are “historical” fields, and such laws as may be appealed to must come from chemistry and physics or at least outside biology. While there is a great deal to be said for such claims, they are strictly speaking incorrect. This paper will show that for broadly Darwinian evolution by natural selection to provide an account of the origin of (current) species it must appeal to laws. And these laws are, at this level, fully biological. Whether such laws can or cannot be reduced to non-biological laws is irrelevant. The paper then goes on to argue that this conclusion is, to an important degree, compatible with the central point being made by those who say that there are no laws in biology.

[The world is more random than we realize: Proteins as a complex system](#)**LEONORE FLEMING**** (Utica College, United States)

Within the last ten years there has been a shift in how we understand proteins. The “sequence-structure-function” paradigm, which is based on the notion that a specific string of amino acids codes for one uniquely folded protein, is slowly being replaced with the understanding that intrinsically disordered proteins (IDPs) play an important role in molecular biology. It is now clear that a complete folded structure is not necessary for a protein to function. In fact, the dynamic nature of an IDP—the ability to shift between unfolded, partially folded, and fully folded forms—confers upon it the ability to fill a variety of different roles. Thus, understanding protein function requires insight beyond the mere sequence of amino acids; it requires knowledge of environmental contingency and variation. A reductive exploration of proteins as pre-programmed entities provides only a snapshot of current structure and function, whereas an account of proteins as part of a complex system explains their structure and function as largely a result of networks of interactions. One consequence of this approach is that evolutionary questions about adaptation must be addressed at the higher level, investigating system dynamics like plasticity and evolvability.

[Population-level and organism-level causal processes in natural selection](#)**STEVE ESSER** (University of Pennsylvania, United States)

Roberta Millstein has argued that natural selection should be understood as a population-level causal process. In a recent article, she sought to support this thesis by applying Wesley Salmon’s causal process framework to the case of selection. I show that using this framework does not in fact support the conclusion that natural selection is best seen as a population-level causal phenomenon. The key problem is that when the persisting population is defined as a causal process (per Salmon’s definition), it cannot produce all the necessary internal

DS R515

11:00–12:30

INDIVIDUAL PAPERS

MODELING AND MECHANISMS IN MEDICINE

[How Newtonian was Newtonian medicine?](#)**KIRSTEN WALSH**** (University of Otago, Canada)

With the publication of the *Principia* in 1687, Newton introduced a powerful new methodology. He combined the solid foundation of experiment and observation with the rigour of mathematical reasoning. By the 1690s, the “Newtonian method” had spread beyond mechanics to other branches of natural and even general philosophy. In Scotland, there emerged a “Newtonian medicine”—a starkly mathematical approach to medicine that viewed the human body as a machine, to be explained by geometrical and mechanical principles. This mathematical form of Newtonian medicine all but disappeared in the 1730s, to be replaced by an aethereal Newtonian medicine, based on the queries introduced in the 1717 edition of Newton’s *Opticks*. Focusing on Newtonian theories of disease, I follow this transition from mathematical to aethereal Newtonianism, asking: How Newtonian was Newtonian medicine?

[Extrapolation and its challenges: How explanatory accounts are pieced together from multiple experimental models](#)**TUDOR BAETU** (Universidade do Vale do Rio dos Sinos, Brazil)

Not only clinical research, but also basic science systematically relies on the epistemic practice of extrapolation from surrogate models, to the point that explanatory accounts presented in review papers and biology textbooks are in fact composite pictures reconstituted from data gathered in a variety of distinct experimental setups. This raises two new challenges to previously proposed mechanistic-similarity solutions to the problem of extrapolation, one pertaining to the absence of mechanistic knowledge in the early stages of research and the second to the large number of extrapolations underpinning explanatory accounts. An analysis of the strategies deployed in experimental research supports the conclusion that, while results from validated surrogate models are treated as a legitimate line of evidence supporting claims about target systems, the overall structure of research projects also demonstrates that extrapolative inferences are not considered “definitive” or “sufficient” evidence, but only partially justified hypotheses subjected to further testing. Almost two decades ago, LaFollette and Shanks

mounted a strong case against the use of animal surrogate models in clinical research, on the grounds that extrapolative inferences are useful only as means to generate new hypotheses. In response, Daniel Steel pointed out that there is no sharp divide between the contexts of discovery and justification, arguing that, when properly regimented by validation protocols, extrapolations are a common and reliable method of generating new knowledge. An analysis of the experimental practice of basic science suggests that the truth is somewhere in the middle. Steel is right in claiming that the use of surrogate models is both a common and a reliable scientific method, and that extrapolations from surrogate to target can be justified by means of a variety of theoretical and experimental considerations. I argue that, given the systematic use of extrapolative inferences and the overall absence of strong indicators of relevant similarity in basic science, the justificatory evidence supporting extrapolations is not deemed definitive, as demonstrated by the subsequent efforts deployed to further test knowledge gained by juxtaposing results from different experimental setups. Extrapolations are merely one epistemic tool to be used in conjunction with other methods of investigation, ranging from cross-referencing findings in complementary surrogate models to clinical trials of treatments. Understanding why extrapolation is an acceptable epistemic practice requires thinking beyond the reliability of individual extrapolations, and understanding how extrapolations are used in the context of a much more comprehensive research strategy that combines both a bottom-up process of inferring mechanistic accounts based on experimental data—a process that relies heavily on extrapolations across different experimental setup —, and a subsequent top-down testing of predictions made by these accounts. More specifically, I propose that extrapolations are an acceptable epistemic practice not only in light of model validation attempts, but also because they are part of an overall research strategy ensuring that relatively poorly justified extrapolations in the initial stages of research are tested in later stages of research, and that fallback positions make possible the troubleshooting of faulty extrapolations.

Identity and unity: Challenges for the “immune self”

ANNA FRAMMARTINO WILKS (Acadia University, Canada)

As the self/other dichotomy continues to come under attack by contemporary immunologists, the possibility of a coherent notion of the immune self appears increasingly less plausible. Recent findings from both the ecological perspective (Cohen 2013) and the molecular perspective (Matzinger 2002) offer substantial evidence for the view that “there can be no circumscribed, self-defined entity that is designated – the self” (Tauber 2012). Alternative and diverse models of immunology are currently being developed which aim to accommodate the ample evidence that we now have of the continual and complex interactions between the inner workings of the host organism and the material it encounters in its environment. Consequently, the notion of immune identity has been supplanted by the notion of immune reactivity (Tauber 2012). Moreover the specific kind of reactivity manifested by immunological function indicates that the immune system is a cognitive system. While this paper generally defends the cognitive paradigm of immunology, it rejects one of its central precepts. Specifically, it rejects the view that the non-identity of the immune self implies its lack of unity. My defense of this position is

rooted in the account of cognition of Immanuel Kant, which views the function of unity as the fundamental feature of cognition (Brook 1994). I argue that if the immune self were not able to function as a unity, it would not be able to function as a cognitive system. The reason is that a cognitive system, like any system, involves the synthesis or working together of “many” as “one.” Thus an intelligible account of the cognitive view of immunology may dispense with the notion of the identity of the immune self (Pradeu 2012), but it may not dispense with at least a functional notion of the unity of the immune self.

12:30–15:30

LUNCH BREAK

13:00–15:00

COUNCIL MEETING | Room DS-1955

15:30–19:00

EXCURSIONS IN AND AROUND MONTRÉAL

NOTE: the symbol ** indicates that, at time of publication, the attendance of this presenter has not been confirmed.

Index

A

ABOUHEIF, EHAB	39, 108
ABRAMS, MARSHALL	21, 49, 50
ABRANTES, PAULO	304
ACERBI, ALBERTO	140
AFFIFI, RAMSEY	302
AKLE, DAVID	301
ALLEN, GARLAND	137
ALMEIDA, MARIA STRECHT	210
ALVES NETO, CELSO ANTONIO	115, 116, 313
AMUNDSON, RON	127, 150
ANDERSEN, HOLLY	98, 124
ANDERSON, WES	6
ANDERSON, ERIK	296
ANDREWS, KRISTIN	27, 46
ANKENY, RACHEL A.	107, 307, 309
AOUACHERIA, ABDEL	71
ARCHER, EDWARD	13
ARIEW, ANDRÉ	134
ARNELLOS, ARGYRIS	250
ARNET, EVAN	100
ASSIS, LEANDRO	179
ASSUNÇÃO, LÍVIA	69
ATANASOVA, NINA	297
ATYTALLA, JOHN	202
AUBÉ BEAUDOIN, FÉLIX	260
AUTZEN, BENGT	51, 52

B

BAEDKE, JAN	155
BAETU, TUDOR	98, 325
BAGNOLINI, GUILLAUME	52, 196
BANVILLE, FRÉDÉRIC-ISMAËL	18
BARAHONA, ANA	136
BARKER, MATTHEW	65
BARSANTI-INNES, BRIANNA	179
BARWICH, ANN-SOPHIE	276, 278
BASL, JOHN	166
BAUDISCH, ANNETTE	233
BAUSMAN, WILLIAM	282
BAXTER, JANELLA	316
BEAULAC, GUILLAUME	18
BECHTEL, WILLIAM	43
BEDAU, MARK	12, 97
BEDFORD, HELEN	162, 219
BEIFUSS, MATTHEW	241
BEKE, ALLAN	126
BELLON, RICHARD	145
BENNER, STEVEN	206
BERGANDI, DONATO	166
BERTOLASO, MARTA	24, 25, 63
BETTERMAN, ROBERT	85
BETTY, VASSILIKI	226
BETZLER, RIANA	300
BEZUIDENHOUT, LOUISE	238
BICH, LEONARDO	10
BINNEY, NICHOLAS	107
BIZZO, NELIO	307
BLASCO MÁÑEZ, TERESA	152
BLOCH, CORINNE	213

BLUTE, MARION	106
BOGNON, CÉCILIA	165
BOLDUC, GHYSLAIN	93
BOLKER, JESSICA	19
BONNIN, THOMAS	16
BOOTH, AUSTIN	248
BORCK, CORNELIUS	130
BORRELLO, MARK	69
BOURRAT, PIERRICK	106, 317
BOURRET**, PASCALE	239
BOUTEL, ADRIEN	170
BOUZAT, JUAN L.	215
BOYD, RICHARD	48
BRAIN, ROBERT M.	130
BRADIE, MICHAEL	304
BRANDT, CHRISTINA	199
BREMER, MARTIN	204
BRIGANDT, INGO	43, 99, 100, 122
BROOKS**, DANIEL	242
BROWN, RACHAEL	26, 45, 46
BROWNING, HEATHER	171
BRUMBLE, KIMBERLY	78, 213
BRUNER, JUSTIN	94, 95, 292
BRUNET, TYLER	232
BRUSSE, CARL	95
BRZOZOWSKI**, JERZY	150
BURIAN, RICHARD	226
BUSKELL, ANDREW	140
BUTTOLPH, MICHAEL	54
BZOVY, JUSTIN	238

Index

C

C. DUSSAULT, ANTOINE	87, 106
C. NECO, LUCIA	74
CABLE, KELE	55
CAIANIELLO, SILVIA	24, 25
CALCOTT, BRETT	23
CAMBROSIO, ALBERTO	223, 239
CANIGLIA, GUIDO	25
CAO, ZHIPING	73
CAPORAE, LINNDA	146
CASPER, STEPHEN	279
CHAMPAGNE, FRANCES	205
CHARBONNEAU, MATHIEU	139, 140
CHEN, RUEY-LIN	124, 276
CHIN-YEE, BENJAMIN	181
CHIRIMUUTA, MAZVIITA	142
CHIU, LYNN	256
CHOUKAH, SARAH	197
CLARKE**, CHRISTOPHER	313
CLARKE, ELLEN	106
CLATTERBUCK, HAYLEY	26, 46
CLELAND, CAROL	129, 184, 206
CLOUGH, SHARYN	267
COLLERAN, HEIDI	48
COLLIER, JOHN	172
CONLEY, BRANDON	106
CONRADO, DALIA MELISSA	6
CORIALE, DANIELLE	121
CRAIG, LINDSAY	215
CRAWFORD**, DAVID	76
CREATH, RICHARD	324
CRAVER, CARL F.	124, 143

CRÉMIÈRE, CÉDRIC	237
CROWE, NATHAN	198, 307, 309
CROZIER, GILLIAN	159, 160, 221
CRUZ, LEILA	323
CURNUTTE**, MARGARET	259
CURRIE, ADRIAN	28, 129

D

DAGAEFF, ANNE-CÉCILE	46
DANG, HAIXIN	34
DAOUST, LOUISE	19
DARDEN, LINDLEY	124, 246
DARLU, PIERRE	237
DAVIS, LAURA	174
DE ANDRADE MARTINS, ROBERTO	262
DEBRULER, KIMBERLY	182
DELEHANTY, MEGAN	180
DELISLE, RICHARD	145
DEMAZEUX, STEEVES	218
DEPEW, DAVID	226, 240
DESAUTELS, LANE	99
DESJARDINS, ERIC	86, 129
DESMOND, HUGH	130
DIETRICH, MICHAEL	101, 147
DIFRISCO, JAMES	286
DJEDOVIC, ALEX	258
DONDA, PEDRITA	73
DONOVAN, BRIAN	288
DOOLITTLE, W. FORD	103, 227
DOWNES, STEPHEN	29, 48
DUCHESNEAU, FRANÇOIS	92, 93
DUPRE, JOHN	63, 207

DUSSAULT, ANTOINE	87, 143
DUTREUIL, SÉBASTIEN	70, 143
DURAND, MARION	245

E

ELGIN, MEHMET	231
EL-HANI, CHARBEL	74, 323
ELIOT, CHRISTOPHER	56
ELLIOTT, STEVE	35
ELLIOTT-GRAVES, ALKISTIS	55, 88
ENGELMANN, STEPHEN	241
ERESHEFSKY, MARC	65
ERWIN, DOUGLAS H.	39
ESSER, STEVE	324
ESTAVILLO, CANDELARIA	323
ETXEBERRIA, ARANTZA	30

F

F. JAPYASSÚ, F. JAPYASSÚ	74
FABRIS, FLAVIA	249
FAGAN, MELINDA	42, 116
FAGOTTO, FRANCOIS	85
FANG, WEI	78
FARIA BERÇOT, FILIPE	191
FAZELPOUR, SINA	224
FEHR, CARLA	99, 122
FELISBERTO, ALAN DANTAS S.	69
FELTZ, BERNARD	154
FENTON, ANDREW	283
FIELDS, ARCHIE	311
FILLER, JOSHUA	284
FINKELMAN, LEONARD	150

Index

FIRESTEIN, STUART	277	GONZÁLEZ RECIO, JOSÉ LUIS	220	HERNÁNDEZ CHÁVEZ, PAOLA	107
FISHER, MAYA	156	GONZALEZ-CABRERA**, IVAN	209	HEUNEMANN, JULIA	204
FISLER, MARIE	237	GONZALEZ-GRANDON**, XIMENA	152	HEY, SPENCER	179
FITZPATRICK, SIMON	27, 46	GOUVEA, DEVIN	318	HICKS, DANIEL	322
FLEMING**, LEONORE	324	GRAHAM, GABRIELLE	320	HIEKEL, SUSANNE	243
FORBER, PATRICK	109	GRAUVOGEL, KATE	20	HILMER, BRIGITTE	144
FOSSHEIM, HALLVARD	187	GREEN, SARA	42, 44	HINTERBERGER, AMY	101
FOWLER, JAMES	239	GREGG, BENJAMIN	265	HOCHMAN, ADAM	67, 187
FRANKLIN-HALL, LAURA	40, 41, 101	GREGORY, T. RYAN	103	HOCHSTEIN, ERIC	141, 142
FRASER, BEN	292, 293	GRIESEMER, JAMES	146	HOGAN, ANDREW	280
FRIESEN, STEPHEN	32, 214	GRIFFIN, GILLY	221	HOLLIN, GREGORY	217, 297
FRIESEN, PHOEBE	194	GRIFFITH, ELIZABETH	185, 206	HOLMAN, BENNETT	8
FUJIMORI, HAJIME	8	GRIFFITHS, PAUL	24	HOLMES, MATTHEW	315
FULDA, FERMIN	246	GROSS, JEAN-FELIX	8, 9	HONENBERGER, PHILLIP	32, 291
		GROSS, FRIDOLIN	261	HONIGSBAUM, MARK	117, 118
G		GUERRERO MC MANUS, FABRIZIO	13, 155	HOPSTER, JEROEN	295
GALE, GEORGE	321	GUEVARA-ARISTIZABAL, JUAN	303	HOQUET, THIERRY	145
GAMBAROTTO, ANDREA	164	GURTLER, BRIDGET	157	HOUF, JESSICA	163
GARCÍA, RUTH	220	GUTTINGER, STEPHAN	207	HUBER, MAXIMILIAN	232
GARSON, JUSTIN	15			HUNDLEBY, CATHERINE	203
GARVEY, COLIN	169	H		HUNEMAN, PHILIPPE	60, 71
GAULT, DYLAN	161, 300	HABER, MATT	48, 115	HUTCHESON, EMILY	16
GAYON, JEAN	207, 226	HALBERG, CLAUSS	52	HUTCHINS, BARNABY	255
GERMAIN, PIERRE-LUC	155, 261	HALINA, MARTA	45, 46	HUTTEGGER, SIMON	95, 110
GERSON, ELIHU	192, 193	HALL, NANCY	138		
GIAIMO, STEFANO	233	HANLEY, BRIAN	172	I	
GILBERT, SCOTT	108	HARDING, SANDRA	68	IJÄS, TERO	212
GILMORE-SZOTT, ELEANOR	176	HAVSTAD, JOYCE	179	INGLEHART, ASHLEY	188
GIRAUD, EVA	217	HEALEY, JENNA	158	INKPEN, J. ANDREW	28
GISSIS, SNAIT B.	131	HEAMS, THOMAS	299	IOANNIDIS, STAVROS	242
GLENNAN, STUART	98	HELLSTRÖM, NILS PETTER	237	ISHIDA, TOMOKO	154
GODMAN, MARION	17	HENRIQUEZ GARRIDO, RUY JOSE	13	ISHIDA, YOICHI	243
		HEREDIA, DIANA	263		

Index

J		L		LOUSON, ELEANOR	171
JACKSON, JOHN	240	LAI, BO-CHI G.	38	LOVE, ALAN	61, 85, 274
JABLONKA, EVA	183, 205	LAIMANN, JESSICA	151	LU, QIAOYING	317
JODOIN, LAURENT	252	LALONDE, JOSH	262	M	
JOHNS SCHLOEGEL, JUDY	219	LAMB, SUSAN	235	MACHADO LEITE, CLARISSA	323
JOSÉ LUIS, VERA	200	LAMM**, EHUD	319	MAGNUS, P.D.	65
JUSTUS, JAMES	322	LANCASTER, CHERYL	189	MAIENSCHEIN, JANE	125, 147
		LAPLANE, LUCIE	126	MAIOCCHI**, MASSIMO	146
K		LAUBICHLER, MANFRED	25, 39	MAISA JENSEN, GERDA	191
KAHAN, DAN	64	LEAN, CHRISTOPHER	55, 56	MALATERRE, CHRISTOPHE	184, 186, 206
KALKMAN, DAVID	95, 265	LEAN, OLIVER	263	MANSFIELD, BECKY	205
KAPLAN, JONATHAN	68, 161, 162	LECOINTRE, GUILLAUME	237	MARISCAL, CARLOS	28, 130
KÄSTNER, LENA	124	LEEMING, BILL	136	MARLOR, CHANTELLE	310
KEATING, PETER	223, 239	LEFÈVRE, VICTOR	106	MARSHALL, KATIE	87
KEIJZER, FRED	153	LEFKADITOU, AGELIKI	187	MARTENS, JOHANNES	177
KELLY, MIKE	107	LENNOX, JAMES	272	MARTIN, AUGUST	39
KENDIG, CATHERINE	314	LEONELLI, SABINA	193, 307, 309	MARTIN, JOSEPH D.	146
KERSTEN, LUKE	174	LEVINE, ALEX	320	MARTINS, LILIAN AL-CHUEYR PEREIRA	111
KETCHAM, SAMUEL	283	LEWIS, CORY	285	MATLIN, KARL	125, 147, 148
KILLIN, ANTON	304	LI, XIANGYI	233	MATSUMOTO, SHUNKICHI	124, 274, 275
KIM, KYURI	258	LIANG, WENBO	8	MATTHEN, MOHAN	134
KIRK, ROB	307, 308	LIDGARD, SCOTT	120	MATTHEWS, LUCAS	77, 233
KOKKONEN, TOMI	176	LINQUIST, STEFAN	102, 103	MATTHEWSON, JOHN	40, 41
KOLMES, SARA	85	LIU, KATHERINE	62	MATTHIESSEN, DANA	249
KOVAKA, KAREN	34	LIU, DANIEL	229	MCCONWELL, ALISON	36
KRICKEL, BEATE	212	LIVINGSTONE SMITH, DAVID	128, 150	MCLOONE, BRIAN	33
KROKER, KENTON	280	LLOYD, ELISABETH	100	MCSHEA, DAN	130
KRONFELDNER, MARIA	127, 128, 148, 150	LOCK, MARGARET	205	MEANEY, MICHAEL	183
KRUEGER, JAMES	290	LOPES DE SOUZA, ROSA ANDREA	191	MEIRMANS, STEPHANIE	310
KYLLINGSTAD, JON RØYNE	67, 187	LOPEZ-PALETA, MIGUEL	221	MELONI, MAURIZIO	183, 205
		LORING, PHIL	187	MEKIOS, CONSTANTINOS	251

Index

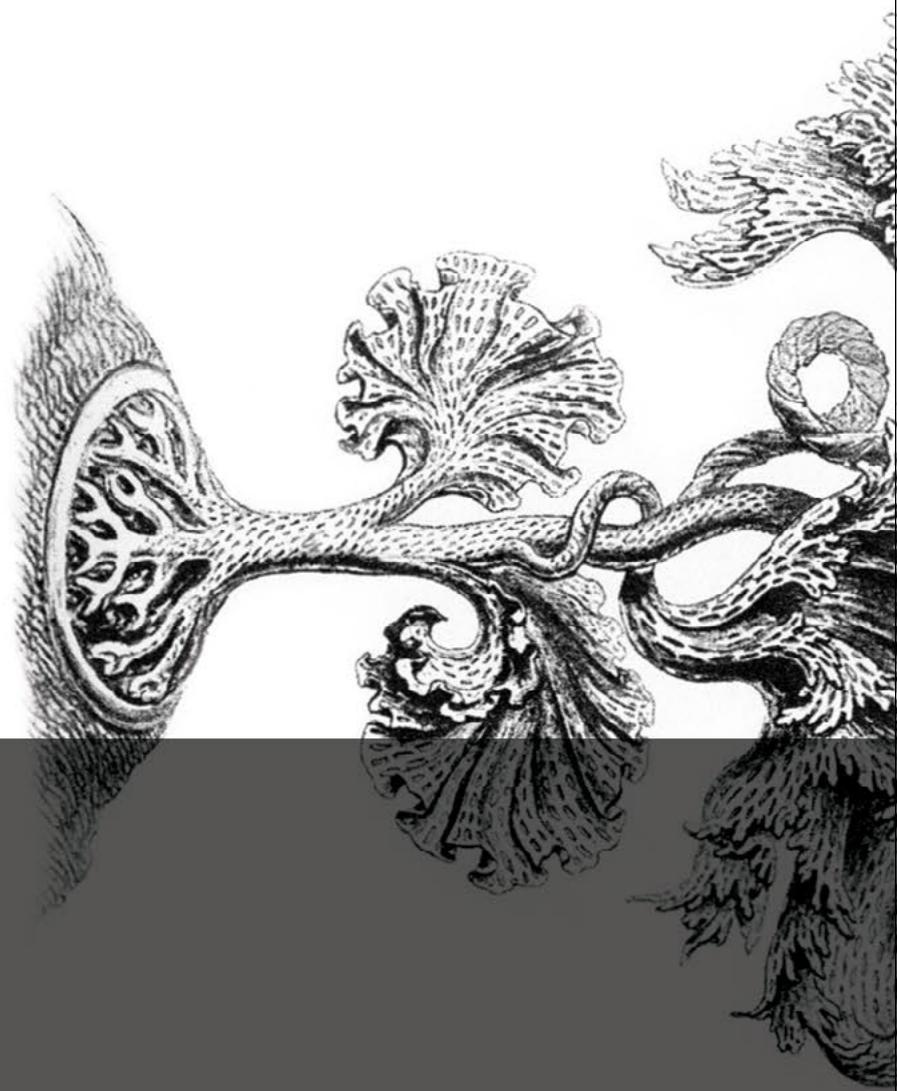
MERCADO-REYES, AGUSTÍN	37, 89	N	PARRAVICINI, ANDREA	11, 209		
MERLIN, FRANCESCA	46, 81, 82	NELSON, NICOLE	104	PEARCE, TREVOR	229	
MESOUDI, ALEX	140	NEWMAN, STUART	271	PEARSON, CHRISTOPHER	312	
MÉTHOT, PIERRE-OLIVIER	117, 118	NICHOLSON, DANIEL	207	PELUFFO, ALEXANDRE	82, 83	
METZ, EMLÉN	64	NICOGLU, ANTONINE	81, 82, 207	PENCE, CHARLES	21	
MEUNIER, ROBERT	14	NIKLAS, KARL	85	PEREZ-RUIZ, ALBA LETICIA	267	
MEYNELL, LETITIA	123	NOUVEL, PASCAL	52, 53, 196	PERIÉ, LEÏLA	46	
MILLER, SHAWN	174	NOVICK, AARON	91	PERRET, NICOLE	11	
MILLER, MARK	225	NUNES-NETO, NEI	6, 143	PETERSON, ANNE	271, 273	
MILLSTEIN, ROBERTA L.	57	NYHART, LYNN	120, 121	PFEIFER, JESSICA	261	
MITCHELL, SANDRA D.	24	O	PIOTROWSKA, MONIKA	106		
MIZZONI, JOHN	5	O'CONNOR, CAILIN	95, 109, 131, 132	PLUTYNSKI, ANYA	62, 63	
MOFFATT, ANDREW	254	O'MALLEY, MAUREEN	112, 113	POCHEVILLE, ARNAUD	23	
MOHSENI, AYDIN	285	O'NEILL, ELIZABETH	295	PONTAROTTI, GAËLLE	31, 46	
MOLTER, DANIEL	247	OAKES, JASON	192	POREAU, BRICE	282	
MONNER, SHARI	76	ODENBAUGH, JAY	28, 29, 48	POTOCHNIK, ANGELA	133	
MONTÉVIL, MAEL	10, 57, 58, 59	OKSANEN, MARKKU	268	PRADEU, THOMAS	108	
MORANGE, MICHEL	101, 226	ÖLÇEK, DENIZ	5, 74	PRESTES, MARIA ELICE BRZEZINSKI	256, 307	
MORENO, ALVARO	10, 143	OLSZYNKO-GRYN, JESSE	157	PRÉVOT, KARINE	108	
MORIMOTO, RYOTA	285	OPINEL, ANNICK	161, 162, 219	PUTOIS, OLIVIER	81, 83	
MORIN, OLIVIER	208	OPITZ, DONALD	89, 90	Q		
MORIN-CHASSÉ, ALEXANDRE	239	ORLAND, BARBARA	144	QUINN, ALETA	91, 92	
MORRIS, RICK	306	OSEGUERA GAMBA, JORGE	240	R		
MOSS**, LENNY	270	OKSANEN, MARKKU	268	RACINE, VALÉRIE	39	
MOSSIO, MATTEO	10, 57	OSMANOGLU, KAMURAN	316	RACOVSKI, THIBAUT	59, 61	
MUKA, SAMANTHA	173	OTSUKA, JUN	7	RADICK, GREGORY	46, 186, 288, 289	
MÜLLER-WILLE, STAFFAN	46	P	PANCALDI, GIULIANO	303	RAINER, GEORGIA RAE	315
MUSZYNSKI, ERIC	202	PANOFSKY, AARON	105	RAMSDEN, EDMUND	307, 308	
		PARK, BUHM SOON	258	RANSOM, MADELEINE	223, 224	
		PAROLINI, GIUDITTA	137	RAU, GERALD	178	

Index

RAYMER, EMILIE	306	S	SMALDINO, PAUL	49	
REBOLLEDA GOMEZ**, MARIA	302	SAIDEL, ERIC	245, 247	SMEAD, RORY	132
REDFIELD, ROSIE	288	SÁNCHEZ ARTEAGA, JUAN MANUEL	69	SMITH, KELLY	96, 97, 130
REILLY, BENJAMIN	49	SANSOM, ROGER	7	SMITH, SUBRENA	216
REX, ROGER	304	SANTANA, CARLOS	167	SMITHDEAL, MATTHEW	18
REYDON, THOMAS	65	SANTOS, CINTIA GRAZIELA	72	SOBER, ELLIOTT	51
REYNOLDS, ANDREW	147	SAPP, JAN	126	SOKOLOWSKA, EWELINA	201
REZNIK, JANE	65	SARKAR, SAHOTRA	101, 270	SONNENSCHNEIN, CARLOS	58, 59
RIBOLI-SASCO, LIVIO	46, 82	SARTO-JACKSON, ISABELLA	277	SOTO, ANA	57, 58, 59
RICE, COLLIN	133, 134	SATO, NAOKI	183	STAMETS, GEORGE	84
RICHARDS, RICHARD	145	SCHÄRLI, MARIO	145	STANEV**, ROGER	20
RICHARDS, ROBERT	186	SCHICKORE, JUTTA	137, 139	STEEL, MIKE	51
RICHARDSON, SARAH	101, 183	SCHULTE-HOSTEDDE, ALBRECHT	159	STEIGERWALD, JOAN	90
RICHMOND, MARSHA	110, 111, 135	SCHULZ, ARMIN	153	STEINER, CHRISTIAN	144
RIEPPPEL, OLIVIER	179	SCHÜRCH, CATERINA	211	STEINER, KATHARINA	236
ROBERTS, EVE	312	SCOTT-PHILLIPS, THOM	131, 169	STEPHENSON, RICHARD JAVIER	38
ROE, SARAH	36	SEGER, LAURA	218	STERELNY, KIM	292
ROE, NIALL	230	SENCAN, SINAN	287	STERNER, BECKETT	151
ROGERS, ERIC	244	SEPKOSKI, DAVID	186	STEVENS, HALLAM	101
ROHWER, YASHA	214	SERBAN**, MARIA	234	STISO, CHRISTINA	317
ROMERO SANCHEZ, VICTOR	298	SERVANT-FINE, THIBAUT	210	STOTZ, KAROLA	23
ROSARIO, ESTHER	260	SHAN, YAFENG	54	STUART, YOEL	28
ROSS, LAUREN	37	SHAPIRO, ADAM	254	SUÁREZ PASCAL, DAVID	97
ROUSSEAU-MERMANS, SOPHIA	106	SHERMA, KRITI	287	SUÁREZ-DÍAZ, EDNA	135, 187
ROUX, ETIENNE	106	SHELDON, MYRNA PEREZ	112	SUMAN, FRANCESCO	200
RUBIN, HANNAH	94, 95, 109	SIPI, HELENA	269	SUZUKI, DAICHI	274
RUIZ-MIRAZO, KEPA	31	SIMPSON, SHAWN	177	SWENSON, SARAH	264
RUIZ-TRILLO, IÑAKI	113	SINCLAIR, BRENT	87	SWIATCZAK, BARTLOMIEJ	119
RUSE, MICHAEL	186	SKILLINGS, DEREK	15, 40, 42	SZYF**, MOSHE	183
		SKOLNICK WEISBERG, DEENA	65		
		SLATER, MATTHEW	65		
		SLAYTON, MATTHEW	216		

Index

T		V		Y	
TABB, KATHRYN	194	VIGNOLA-GAGNÉ, ETIENNE	223, 239	YAÑEZ, BERNARDO	200
TABERY, JAMES	104	VILLA, FRANÇOIS	207	YANG, SHIJIAN	73
TAKACS**, PETER	33	VILLELA, MA. ALICIA	253	YEH, HSIAO-FAN	124
TANAKA, SENJI	274	VLERICK, MICHAEL	12	YILMAZ, ÖZLEM	250
TANGHE, KOEN	84	VON STEIN, ALEX	311	YOSHIDA, YOSHINARI	182
TAVARES DA SILVA, TATIANA	307	W		Z	
TAYLOR, PETER	105	WAGNER, ELLIOTT	96	ZARPENTINE, CHRIS	173
TAYLOR, JORDAN	189	WAGNER, GUNTER	39, 226	ZINSER, JASON	34
TEKIN, SERIFE	175	WALSH, DENIS	134, 272	ZOU, YAWEN	255
TESSIER, PEGGY	199	WALSH**, KIRSTEN	325		
TESTA, GIUSEPPE	205	WASHINGTON, NATALIA	68, 194, 195		
THEILHABER, GUSTAVE	71	WASMUTH, SALLY	289, 291		
THOMAS, MARION	93	WEAVER, SARA	123		
THOMASCHKE, DIRK	222	WEINSTEIN, DEBBIE	130		
TICEHURST, KATHRYN	235	WEISBERG, MICHAEL	64, 65		
TOEPFER, GEORG	165	WEITZMAN, JONATHAN	207		
TORRENS, ERICA	253, 301	WHITEHOUSE**, SIMON	281		
TRAULSEN, ARNE	233	WIDEMAN, JEREMY	114		
TURNER, DEREK	129, 269	WILKS, ANNA FRAMMARTINO	326		
U		WILSON, ROBERT A.	127, 148, 149, 150, 227		
UMEREZ, JON	9, 30	WIMSATT, WILLIAM C.	85, 147		
UTAKER, ARILD	53	WINSOR, MARY P.	91		
V		WINTHER, RASMUS G.	252, 307, 308		
VALADEZ BLANCO, OCTAVIO	252	WITTEVEEN, JOERI	305		
VALLÉS, SEAN	156	WOLBRING, GREGOR	149, 150		
VAUGHN, ANNA	178	WOLFE, CHARLES	163, 257		
VELASCO, JOEL	20, 22, 51	WRIGHT, JAKE	318		
VERGARA-SILVA, FRANCISCO	75	WU, JOSEPH	248		
VERNON, KENNETH BLAKE	29, 48, 77				



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