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Welcoming words, by the Program Committee

We are very happy to present the program of the next ISHPSSB meeting in Montpellier. As in the previous meetings, you will find in it keynote lectures, organized sessions, individual papers that we have grouped into different sessions, round tables and posters. A new category of activity, “Dialogues”, has been added, and we have put a special emphasis on interdisciplinary sessions.

Preparing this program, we faced a major source of satisfaction, but also of difficulties: the huge number of scholars who intended to attend this meeting, in fact more than 600! We had to abandon our initial project to reduce the number of sessions running in parallel. Nevertheless, we tried to avoid as much as possible that sessions on similar topics take place during the same time slot, but whatever our efforts were, many of you will probably feel frustrated to have to choose between equally interesting lectures. We apologize for that inconvenience: consider that this frustration is the price to pay for the wide attendance! The proximity of the different lecture rooms will probably partially palliate this problem.

Have a nice, friendly and intellectually fruitful meeting!

Michel Morange and Thomas Pradeu, chairs of the Program Committee

Welcoming words, by the Organizing Committee

We are happy to welcome all of you to Montpellier for the ISHPSSB meeting, July 7-12 2013. Montpellier is a Mediterranean city, capital of the Languedoc-Roussillon, a region in the south of France, very close to the sea.

For anyone interested in the history or philosophy of the life sciences, Montpellier is a perfect city, for many reasons. Firstly, it has a long and rich tradition in Medicine and natural history: the Faculty of Medicine, the oldest in France, is also the oldest in activity in the world. It was created in the 12th century and obtained its official status as *Universitas medicorum* in 1220. To philosophers and historians of science and medicine the city is famous, amongst other things, for the "vitalist school", which was born there in the 18th century. The city is home to the oldest botanical garden in France (1593) and one of the oldest in Europe, associated with a famous herbarium. Our welcome cocktail on Sunday will be hosted in this historic place.

Hosting the ISHPSSB meeting in Montpellier not only has resonance for the history of the life sciences. Today this city is the most important European research site for ecological, agronomy and the environmental sciences (over 2300 researchers), with 80 research teams in these disciplines, and a huge diversity of laboratory and other facilities, represented by *Agropolis international,* an association gathering all institutions of the regional scientific community in the domains of agriculture, food, biodiversity and environment (http://www.agropolis.org).

Many of these institutions have supported this conference, and we are grateful to them. Indeed, this conference would not have been possible without the enthusiasm it has raised among the community of researchers here, mostly composed of ecologists, evolutionary biologists and environmental scientists, not to speak of philosophers. Their immediate support for the project was wonderful, and it has allowed all the preparations of the meeting to be conducted in a very friendly atmosphere.

The organizing committee has benefited from the strong support of individuals and institutions both in Montpellier and Paris. Institutional responsibility for the event was entrusted to the Institute of History and Philosophy and Science and Techniques (IHPST, CNRS/Université Pantheon Sorbonne/ENS), a research team with a strong focus on the philosophy and history of biology. The organizing committee also received local support: most of the sessions are located in a building generously lent by University Montpellier 3 Paul-Valéry (human sciences), while the inaugural session and cocktail as well as the plenary sessions, will be in Université Montpellier 1 (medical sciences, law, and economics). *Région Languedoc-Roussillon* and Montpellier City have provided generous funding and resources. Moreover *Agropolis International* has provided generous logistical support, as did the CNRS (*Centre National de la Recherche Scientifique*), to which the IHPST is attached. These local and national supports have greatly facilitated the smooth organisation of the Meeting conditions including a number of what we hope will be pleasant social events. These will include a cocktail at the Botanical garden (immediately after the inaugural session), a drinks party accompanying the poster session (Monday), a public lecture housed by the City of Montpellier (Tuesday evening), and a banquet at *Parc de Grammont* (Thursday). Several visits (botanical garden, the Museum of the Faculty of Medicine, Ecotron) have been organized for those who have booked in advance.

So far, the response has been excellent: we have two reasons to be satisfied:

- More than 600 active participants have registered, from all parts of the world. As such, this is a significant success.

- The program committee has planned a number of sessions in different formats (symposiums, "dialogues", roundtables, contributed papers, and plenary talks). The topics range through a very broad set of themes, from the philosophy of molecular biology to biology education, history of early medicine, the environmental crisis, etc. We are happy that this conference has drawn together such a wide range of interests, representing the overall scope of the Society.

In the margins of the Meeting, we hope that you will be able to appreciate the beautiful setting of a city with such a rich history and, also, the biggest ratio of students in France in any city. Please experience the varieties of *provençal* cuisine, as well as the diversity and sophistication of the local wines, the Languedoc Roussillon is a country of vineyards and the quality of the wines produced here has been steadily increasing in recent years.

Our local organisation team, here, consisting of biology and philosophy scholars and students from Paris and Montpellier, will be happy to help you during the conference and to help you with any query you may have about the Meeting, the City, and your stay in general.

We wish you a very happy, fruitful and friendly ISHPSSB meeting in Montpellier.

Jean Gayon and Philippe Huneman, chairs of the Organizing Committee.

Acknowledgments

ISHPSSB 2013 is supported by:

- *Région Languedoc Roussillon*
- *Ville de Montpellier*
- *Agropolis International* (Montpellier)

- *Centre National de la Recherche Scientifique*
- *Institut Écologie et Environnement (INEE)* du CNRS
- *Institut Universitaire de France*

- *Université Montpellier 1*
- *Université Montpellier 2 — Sciences et Techniques*
- *Université Paul-Valéry Montpellier 3*
- *Université Paris 1 Panthéon-Sorbonne*
- *Université Paris-Sorbonne — Paris IV*

And the following research teams:

- *Centre d'écologie fonctionnelle & évolutive (CEFE),* Montpellier
- *Centre Méditerranéen de l'environnement et de la biodiversité (LaBEx CeMEB),* Montpellier
- *Institut d'Histoire et de Philosophie des Sciences et des Techniques (IHPST),* Paris
- *Institut des sciences de l'évolution (ISEM),* Montpellier
- *Laboratoire Epsylon*, Montpellier
- *Sciences, Normes, Décision (SND),* Paris
- *Sciences, Philosophie, Histoire (SPHERE),* Paris

Committees

Program Committee

- Patrice David (CEFE, Montpellier)
- Michel Morange (Ecole Normale Supérieure & IHPST, Paris) (*co-chair of the program committee*)
- Thomas Pradeu (Paris-Sorbonne University, Paris) (*co-chair of the program committee*)
- María Jesús Santesmases (Computensa Universidad, Madrid),
- Judy John Schloegel (Argonne Laboratory, Chicago)
- Karola Stotz (University of Sydney, Sydney),
- Edna Suárez (UNAM, Mexico),
- Chris Young (Alverno College, Milwaukee)

Organizing Committee

- Brigitte Cabantous (Agropolis International, Montpellier)
- Vincent Devictor (ISEM, Montpellier)
- Jean Gayon (IHPST/Paris I) (*co-chair of the organizing committee*)
- Bernard Hubert (Agropolis International, Montpellier)
- Philippe Huneman (IHPST, Paris) (*co-chair of the organizing committee*)
- Finn Kjellberg (CEFE, Montpellier)
- Annick Lesne (CNRS & Université Pierre et Marie Curie)
- Paul Luu (Agropolis International, Montpellier)
- Virginie Maris (CEFE, Montpellier)
- Francesca Merlin (IHPST, Paris)
- Michel Morange (Ecole Normale Supérieure & IHPST, Paris)
- François Munoz (AMAP, Montpelier)
- Antonine Nicoglou (IHPST, Paris)
- Pascal Nouvel (Université Montpellier 3, Montpellier).
- Thomas Pradeu (Paris-Sorbonne University, Paris)

Introductory speeches (Sunday July 7th)

- Paul Griffiths, president of the ISHPSSB
- For the Région Languedoc-Roussillon: one representative of the Region
- For the University of Montpellier 3: Patrick Gilli, vice-president of the Scientific Board of the University & Pascal Nouvel, Department of Philosophy & Epsilon Team
- For the program committee: Michel Morange and Thomas Pradeu
- For the organizing committee: Jean Gayon and Philippe Huneman

Meetings of the Society

- **General Meeting of the Society: Thursday 11th, 2:30pm-4:30pm, Amphi Giraud**
  All members are strongly encouraged to attend. This is the best way to influence the future of the Society! The Hull and Greene Prizes will be awarded during the general meeting.

- **First Council Meeting: Monday 8th, 1pm-3pm**

- **Second Council Meeting: Thursday 11th, 12:30pm-2:30pm**

- **Student Advisory Workshop, Tuesday 9th, 12:30pm-2:30pm: Navigating Intellectual and Professional Transitions in an Interdisciplinary World**
  Students in the history, philosophy, and social studies of biology face particular opportunities and challenges in engaging with multiple disciplines. Pursuing a PhD and career in these fields can involve major intellectual and professional transitions, e.g., from the context of a pure humanities background to engagement with the life sciences, or from an interdisciplinary PhD program (like HPS or HSS) to professional life in a traditional disciplinary department (like Philosophy, History, or Anthropology). Four panelists will advise students on these transitions and answer questions from the audience.

- **Graduate student meeting, Wednesday 10th, 12:30pm-2:30pm**

Plenary talks

➢ Sunday July 7th, 4pm-5pm (Amphitheater Giraud, University of Montpellier 1):

Maaike van der Lugt (Paris-Diderot University, France)
Beginnings. Medicine and Natural Philosophy in Medieval Montpellier

The medieval university of Montpellier prided itself on being the place where medical science first originated "before any other university in the world". Traditionally, historians have explained the early rise of the medical schools of Montpellier by pointing to the unique geographical location of the city – at the crossroads of cultures – and its openness to trade. More recently, this explanation has met with serious criticism and Montpellier's chronological primacy has also been qualified. Its reputation as a major and innovative centre for medieval medical learning remains, however, beyond dispute. Medieval physicians claimed scientific status for the medical art by developing its theoretical dimension and by linking up their causal models with natural philosophy. The physicians of Montpellier fully subscribed to this "philosophical turn". At the same time, they reflected on ways to reconcile respect for Aristotelian biology with the needs of individual patients and the shifting realities of medical practice.

➢ Tuesday, July 9th, 2:30pm-4:30pm (Amphitheater Giraud, University of Montpellier 1):

Michel Loreau (Station d'Ecologie Expérimentale du CNRS, Moulis, France)
From Populations to Ecosystems: Towards a Unifying Ecological Theory

The vigorous growth of ecology has been accompanied by its gradual fission into several distinct subdisciplines. In particular, community ecology and ecosystem ecology provide two distinct perspectives on complex ecological systems that have complementary strengths and weaknesses. A new ecological synthesis is needed today both to ensure scientific progress and to develop appropriate responses to the global ecological crisis we are entering. Although different unifying approaches have been proposed recently, I champion a theoretical approach that seeks to merge the principles and perspectives of different disciplines. I will show in particular how this approach has made the fast development of the new research field on biodiversity and ecosystem functioning possible and how it is now providing new perspectives on the long-standing diversity-stability debate, thereby contributing to resolving important scientific controversies, making ecology more responsive to societal needs, and transforming ecological theory itself into a more integrative, quantitative and predictive theory.

Isabelle Olivieri (Metapopulations, Conservation et Coevolution, Institut des Sciences de l'Évolution de Montpellier, University of Montpellier 2, France)

Experimental Evolution: What's For?

In this talk, I will first show what is experimental evolution and that it is an expanding field, although it is old and dates back to population cages of Drosophila, almost at the origins of population genetics. I will use examples from bacteria, yeast, plants and arthropods to suggest that it is complementary to other approaches, and shares most caveats of experiments.

Public lecture

(open to everyone, in French)

Tuesday, July 9th, 8pm-10pm
“Jacques 1er d’Aragon” room
(Port Marianne 117, rue des états généraux, 34000 Montpellier)

Bruno Strasser (University of Geneva, Switzerland)

Le déluge informationnel:
Une opportunité pour des sciences expérimentales participatives?

Les sciences contemporaines produisent des données expérimentales à une vitesse croissante, grâce la puissance des ordinateurs et à l'ampleur de leurs réseaux, provoquant un "déluge informationnel". Ce phénomène est généralement présenté comme une menace inédite, ou du moins comme un problème nouveau dont la maitrise serait cruciale pour le progrès de la connaissance scientifique. Toutefois, en considérant l'histoire des sciences on découvre que la question est loin d'être nouvelle. Depuis au moins quatre siècles, les sciences, de l'astronomie à la zoologie, ont été confrontées à leur propres "déluges informationnels". Elles ont trouvé des solutions originales pour y faire face, notamment en mobilisant l'expertise et le travail des amateurs. Ce modèle, très populaire dans les sciences naturalistes, tant en ornithologie qu'en géologie, est aujourd'hui envisagé pour les sciences expérimentales. Il ouvre la possibilité d'une participation d'un large public à la recherche scientifique et l'opportunité d'une démocratisation du savoir.

Dialogues (*alphabetical order*)

Two speakers, having previously written or lectured on the same issue, but having reached different conclusions, are each assigned 25 minutes to present their ideas. They will then debate for 10 minutes, and discuss with the audience for 30 minutes (for a total duration of 90 minutes).

Adaptation and Optimality (Samir Okasha, François Rousset)

Samir Okasha, Department of Philosophy, University of Bristol, UK
Francois Rousset, Institut des Sciences de l'Evolution – Montpellier, CNRS, France

There is a long controversy about the use of optimality reasoning in evolutionary biology. On the one hand, the idea that natural selection will often result in organisms with near-optimal phenotypes is an integral part of the "adaptationist" approach in biology, and is frequently assumed by behavioural ecologists, among others. On the other hand, population geneticists have known since the 1960s that natural selection does not generally lead to maximization of average fitness in a population, and that sub-optimal phenotypes can exist at a population-genetic equilibrium. Part of the problem in this debate is that the notion of "optimization" has not always been understood in the same way by all parties.
Our debate will focus on the meaning, role and proper status of the optimization concept in evolutionary biology.
Chairperson: TBA

Biology in the 21st Century: Hybridization of Experimentalism and Natural History?

Garland Allen, Washington University, USA
Bruno J. Strasser, University of Geneva, Switzerland

The rise of experimentalism and the decline of natural history constitute the historiographic backbone of most generalist histories of biology. Yet contemporary research in experimental biology increasingly relies on practices reminiscent of natural history, such as collecting, comparing, and classifying data of all kind. Furthermore, in addition to model organisms, recent experimental biology encompasses a widening range of species used for comparative purposes. In view of these recent changes, should we revisit our standard narratives about the history of biology? Can we view experimentalism and natural history as forming a new hybrid science? Is the epistemic power of comparative perspectives being rediscovered in experimental biology? Is the approach, which has been so successful in the twentieth century, of relying on a few model organisms drawing to a close? We will explore these questions collectively in a dialogue about the past, present, and future of biology.
Chairperson: TBA

Complex systems, tipping points and early warnings (Sonia Kéfi, Annick Lesne)

What can we tell about an ecosystem's resilience by looking at its dynamics?

Sonia Kéfi, Institut des Sciences de l'Evolution – Montpellier, CNRS, France

With ongoing global change, ecosystems are rapidly changing. Some of them are unexpectedly breaking down, which coincides with losses of species, habitats and ecosystem services. For instance, overgrazing and climate change can suddenly shift drylands into deserts. Because of the potential dramatic ecological and economic consequences of ecosystem shifts, efforts have been devoted to i) understanding the mechanisms underlying those shifts, and ii) devising early warnings that indicate major restructuring of a system symptomatic of an impending shift. I will present an overview of the latest research addressing these two questions in ecology. I will then discuss the challenges related to the validation and applicability of early warnings in real systems.

Understanding transitions in ecosystems: what could bring complex systems science?

Annick Lesne, CNRS & Université Pierre et Marie Curie, France

Ecosystems can be seen as a paradigmatic example of complex systems, insofar as they involve the interaction of heterogeneous elements, at different space and time scales, with emergent features and strong reciprocal couplings between various levels of organization. I will discuss in which respect concepts from statistical physics, dynamical systems and network science may apply – or not – to ecosystems.

Recent investigations of abrupt transitions experienced by ecosystems and the possible way to foresee them from field data analysis will be revisited in this perspective. Several notions originating in the study of bifurcations and dynamical critical phenomena may be relevant: divergence of correlation range and ensuing slowing down of the relaxation of perturbation, scaling laws near a critical transition, e.g. the percolation transition in a fragmented habitat, cascading failures in a network. However, several difficulties prevent from a mere transposition of simple models and associated results. A first one is to bridge the gap between the levels of organization at which data are collected and those at which dramatic perturbations of the dynamics may develop. The dimensional reduction of a spatially extended ecosystem to a few variables to which apply the notions of bifurcations or phase transitions is also a serious hindrance. The exciting challenge is thus to turn sound intuition and attractive metaphors into operational and solidly founded tools.

Chairperson: François Munoz

Recomposing Biological Mechanisms Through Diagrams and Computational Models (around William Bechtel)

A dialogue between William Bechtel and Carl Craver was planned. Unfortunately, Carl Craver could not attend this meeting for personal reasons. In accordance with Bill Bechtel, we decided to maintain this session, as a "conversation" with other experts in the field.

Participants:

- William Bechtel, University of California, San Diego, USA
- Lindley Darden, University of Maryland, USA
- Alan Love, University of Minnesota, USA
- Paul Griffiths, University of Sydney, Australia

Chairperson: Joan Straumanis, U.S. NSF, retired

Round tables (*alphabetical order*)

Back to Darwin's tangled bank: taking ecological sciences seriously in evolutionary biology

Organized by Emanuele Serrelli, Department of Human Sciences, University of Milano Bicocca, and Applied Evolutionary Epistemology Lab, Center for Philosophy of Science, Faculty of Sciences, University of Lisbon, Portugal

Evolutionary biology has simplified too much the ecological world, which is instead a specific object of different sciences and approaches. Macroevolution people (mainly paleontologists) long pointed out the importance of big ecological perturbations for the most significant evolutionary events: the pulse of ecological equilibrium and disruption would dictate the tempo of evolution. Some macro evolutionists have also claimed that ecological dynamics should be what counts at all scales. However, in micro evolutionary studies, inheritance and bits of information have been privileged: we often have "the environment" as a thin background, furthermore grossly summarized and conflated in selective pressures acting on this or that trait. Today, evolutionists are calling for an Extended Evolutionary Synthesis, pointing out, for example, developmental concepts, modifications of population genetic models, or different interpretations of the involved factors. Little reference is made to the progress of ecological sciences that, instead, can be the ground for a really different evolutionary theory, perhaps closer to Darwin's original thought. Ecological sciences can also reformulate concepts that seem familiar, such as function, organization, adaptation, selection, and they can create a new way of telling evolutionary histories. Many studies are already ahead in this direction, implying forced reference to biogeography and ecological contexts and cohabitation. The specific consideration of ecological concepts, such as biodiversity and ecosystem, as well as the epistemological controversies surrounding them, may shed a new light on evolutionary studies. As these ecological concepts are not very clear in the ecological literature itself, they require a conceptual treatment towards more clarity, perhaps towards an ontology of ecology. In this line a lot of work needs to be done, and experts in ecological sciences are probably the ones that will most contribute.
Speakers:

- Greg Cooper, Washington and Lee University, Lexington, VA, USA
- Nei de Freitas Nunes-Neto, UFBA, Federal University of Bahia, Brazil
- Julien Delord, Independent Researcher, Toulouse, France

Chairperson: Emanuele Serrelli

Conceptual transfers and parallelism in evolutionary biology and economics

Organized by Silvia De Monte, Ecology and Evolution lab, Ecole Normale Supérieure & CNRS, France

Since the 1960s, evolutionary biology has made extensive use of economic concepts and methods, as shown by cost-benefit considerations or by the role played by classical game theory in population biology. But the reverse is also true: "evolutionary economics" and "evolutionary game theory" testify for a massive influence of evolutionary biology over economic theory. However, even if the affinity between evolution and economics has been for a long time acknowledged -such that Maynard-Smith introduced evolutionary game theory by invoking an analogy between natural selection and rationality - the very nature of this conceptual affinity, as well as its limits, has never really been systematically questioned.
This roundtable brings together economists, philosophers of biology and of economy and

evolutionary biologists involved in this project of questioning the conceptual transfers and parallelisms between both disciplines. They will analyze several key notions of both fields, and, through a systematic survey of their meaning and uses , determine to what extent they are comparable, identical or, at the contrary, just homonymous. Each participant will introduce and explicate notions from biology (resp. economics), whereas respondents will explain how these notions are used in economics (resp. evolutionary biology), and other participants will emphasize analogies and discrepancies. Some key notions will be scrutinized among the following interrelated ones: fitness/utility, altruism, information, time scales, equilibrium, adaptation, competition, cooperation. Feedback from philosophers, biologists and economists present in the audience, who could present their own take on the concepts under focus, will fuel the discussions.

Speakers:

- Jean-Baptiste André, Laboratoire Ecologie-Evolution, Université UPMC, Paris, France
- Mikael Cozic, Université Paris XII & IHPST, Paris, France
- Johannes Martens, Department of Philosophy, Bristol, UK
- Silvia De Monte, Laboratoire Ecologie-Evolution, Université UPMC, Paris, France
- Bernard Walliser, Paris School of Economics, France

Chairperson: Werner Callebaut, KLI, Vienna, Austria

Doing Science Without Natural Kinds

Organized by Serife Tekin, Edouard Machery, Collin Rice, University of Pittsburgh, USA

It is commonly assumed that in order for a discipline to be scientific it has to involve natural kinds. Roughly, a natural kind is a class about which many scientifically relevant generalizations can be formulated. However, several areas of cognitive science and biological theorizing do not lend themselves to being characterized in terms of natural kinds. This could happen in at least two ways: (1) the domain of inquiry does not contain the kind of modular or discrete organization that makes natural kinds likely to be found, or (2) the kind of scientific inquiry being performed does not require invoking natural kinds.

In this round-table we will investigate these issues through the discussion of various examples of scientific theorizing without natural kinds. First, Serife Tekin will investigate the use of multidimensional models of the self in psychiatry. Second, Collin Rice will analyze the use of optimization models to provide explanations of phenotypic traits in biology and to guide investigations concerning modularity within cognitive science. Finally, Edouard Machery will be looking at the taxometric methods developed by Paul Meehl to distinguish taxa from continuous phenomena in the domain of psychiatry, abnormal psychology, and personality psychology, with a particular focus on his book,Multivariate Taxometric Procedures: Distinguishing Types from Continua(1997, Sage). Analysis of these cases shows how scientific theorizing can proceed independent of natural kinds and where invoking natural kind terms can be expected to be most fruitful.

Speakers:

- Serife Tekin, University of Pittsburgh, USA
- Edouard Machery, University of Pittsburgh, USA
- Collin Rice, University of Pittsburgh, USA

Chairperson: TBA

Eugenics Roundtable: Past and Present

Organized by Rob Wilson, University of Alberta, Canada

This session will feature participants from the double-session on eugenics (see “Sessions”).

Session: Eugenics I & II (Double session. Part I, eugenic traits: Amir Teicher, Rob Wilson, Caroline Lyster. Part II, politics and eugenics: Judy Johns Schloegel, Aida Roige Mas, Gordon McOuat) and others who are interested in a more extended discussion both of themes that arise in those sessions and broader issues concerning eugenics and ISH-related work linking past and present.
Speakers:

- Amir Teicher, Tel Aviv University, Israel
- Rob Wilson, University of Alberta, Canada
- Caroline Lyster, McGill University, Canada
- Judy Johns Schloegel, independent scholar
- Gordon McOuat, University of King's College/Dalhousie University, UK

Chairperson: Matthew Smithdeal, University of British Columbia, Canada

Evolution's narratives: from competition to interaction

Organized by Nathalie Gontier, Applied Evolutionary Epistemology Lab, Center for Philosophy of Science, Faculty of Science, University of Lisbon, Portugal

In recent years, we've seen the language of evolution switch metaphors. With the rise of selection theory, only the fit survived. Nature was considered Red in Tooth and Claw, genes were selfish survival machines that ride temporary vehicles, every type of behavior portrayed by an organism was measured in terms of cost-benefit equations, competition, and free-riders. Today, research in ecology, symbiosis and symbiogenesis is providing new narratives, and what unites all of them is the study of interactions. Models are shifting from trees to networks. We have come a long way from studying individual organisms or species as monolithic wholes that are weeded out in an active homogeneous environment: relationships and processes run through and across every level of biological organization. Ecology and biogeography are integrating research on climate and environmental change as important causal factors in life's evolutionary history. Microbiology accumulates evidence of massive horizontal gene transfer in cohabiting organisms. Symbioses are changing how we understand individuality: an organism becomes what it is through the interactions it has with its environment, and the symbiotic associations it has with the various life forms that surround it. Sociocultural sciences offer clear counterparts. Anthropologists and linguists are now able to quantify the various types of horizontal transmissions involved in processes such as language borrowing and culture contact. And the social, cognitive and technological sciences are using metaphors of hybridization to study the various interactions that are associated with embodied cognition, situated knowledge, the extended mind. Do these changes reveal that we are we at the brink of a new paradigm shift? What are the consequences for the biological and the sociocultural sciences? And what important roles can philosophers of science play in this new era?
Speakers:

- Jan Sapp, York University, Toronto, Canada
- Michael Bradie, Bowling Green State University, Bowling Green, OH, USA
- Charbel Niño El-Hani, UFBA, Federal University of Bahia, Brazil

Chairperson: Nathalie Gontier, Applied Evolutionary Epistemology Lab, Center for Philosophy of Science, Faculty of Science, University of Lisbon

Evolutionary transitions as social contracts?

Organized by Marion Blute, Department of Sociology, University of Toronto, Canada & Alejandro Rosas, Department of Sociology, University of Toronto, Canada

There is an emerging view that "fraternal" transitions based on economies of scale are better understood than “egalitarian” ones based on complementary functions. The purpose of this roundtable is to discuss the latter.

Speakers:

- Marion Blute, Department of Sociology, University of Toronto, Canada
- Daniel Brooks, Department of Ecology & Evolutionary Biology, University of Toronto., Canada
- Alejandro Rosas, Department of Philosophy, National University of Colombia, Colombia
- Eörs Szathmáry, Department of Plant Systematics, Ecology and Theoretical Biology, Biological Institute, Eötvös University, Hungary
- Richard A. Watson, Electronics & Computer Science (ECI), Faculty of Physical and Applied Sciences, University of Southampton, UK

Chairperson: Peter Godfrey-Smith, Philosophy Programme, City University of New York, USA

From Groups to Individuals: Evolution and Emerging Individuality

Organized by Frédéric Bouchard, Département de philosophie, Université de Montréal & CIRST, Montréal, Canada

Our intuitive assumption that only organisms are the real individuals in the natural world is at odds with developments in cell biology, ecology, genetics, evolutionary biology, and other fields. Although organisms have served for centuries as nature's paradigmatic individuals, science suggests that organisms are only one of the many ways in which the natural world could be organized. When living beings work together - as in ant colonies, beehives, and bacteria-metazoan symbiosis - new collective individuals can emerge. MIT Press has recently released a volume on this topic (edited by Frédéric Bouchard and Philippe Huneman). This round table brings together many of the contributors to this volume to discuss some of the questions that arise from this pressing issue. Informed by their research on symbiosis, insect societies and evolutionary transitions, participants of the roundtable will discuss individuality and its relationship to evolution and the specific concept of organism; the tension between group evolution and individual adaptation; and the structure of collective individuals and the extent to which they can be defined by the same concept of individuality.We aim at confronting conflicting view points on issues such as the role of kin selection, the legitimacy of a specific concept of organism, and the gradual or discrete character of the concept of biological individuality.

Speakers:

- Frédéric Bouchard, Department of Philosophy, University of Montreal, Canada
- Ellen Clarke , All Souls College, University of Oxford, UK
- Charles J. Goodnight, Department of Biology, University of Vermont, USA
- Matt Haber, Department of Philosophy, University of Utah, USA
- Philippe Huneman, IHPST, CNRS, France
- Thomas Pradeu, Paris-Sorbonne University, France
- Minus van Baalen, UMR Écologie et évolution, CNRS, France
- Scott Turner, Department of Biology, State University of New York College of Environmental Science and Forestry, USA

Chairperson: Silvia de Monte, Biologie, École Normale Supérieure, UMR Écologie et evolution CNRS, France

HPS Informatics Demonstrations

Organized by Jane Maienschein, Arizona State University, USA

We propose to provide a training session for use of open source tools for digital HPS work. These include visualization and other ways of taking HPS data and scholarship in a repository and making them accessible, visible, and usable for a variety of purposes. With the right tools, it is possible to ask new questions and discover new patterns, as well as to carry out computational approaches to HPS research.

We will provide basic introductions to the idea, demonstrate how an HPS repository works, and invite other examples. We are in the process of developing a shared repository for digital HPS tools and will also discuss that project. The session draws on the expertise of the international Digital HPS Consortium.

Information, how meaningful it is?

Organized by Livio Riboli-Sasco, Université Pierre et Marie Curie - Paris 6, France
Minus Van Baalen, Université Pierre et Marie Curie - Paris 6, France
& Arnaud Pocheville, Laboratory Ecology & Evolution, UMR7625, Ecole Normale Supérieure, France

This round table will focus on the concept of information in biology. While addressing a concept which clearly lacks a common definition, we will have in mind to keep a clear focus on two current research approaches. First of all we will discuss how extended inheritance approaches (cf. Danchin 2011) have recently invited the community to rethink information. While inheritance is diversified, the primacy of information in inheritance is questionned. This extension of inheritance also stresses the importance to take care of the "processes" that handle information, and not only of the "contents". These processes contribute to shape inheritance pathways, and thus, eventually may affect the global evolution of biological systems.

Second, we will discuss the possibility to export outside of biology concepts and models that have been built within the field of biology to describe information. These models and concepts could be used to analyze the evolution of scientific research, to build phylogenies of concepts, to identify "major transitions" in research practices. This could help us to propose new ways to train future scientists. Exporting methodologies used to analyze evolutionary trends affecting both contents and processes provides an opportunity for mutual enrichment between the study of biological information and culture. This will strengthen our creativity in questioning information.

Both approaches are interesting to bring together at the same round table as they share a very open vision of evolutionary processes. In biological systems, inheritance could be extended, in human knowledge, evolutionary models may apply. A common information concept would strengthen this bound.

Speakers:

- Minus Van Baalen, Université Pierre et Marie Curie, France
- Livio Riboli-Sasco, Science Po Paris, Atelier des Jours à Venir, France

Chairperson: Arnaud Pocheville, IHPST, Paris, France.

Patenting Life: genes and generations

Organized by Berris Charnley, Griffith University, Australia

Patenting life has returned to the spotlight with two ongoing US Supreme Court cases on the subject. What was apparently settled law has been thrown into new uncertainty. The consensus has been that modifying, isolating or synthesising a life form constitutes a transformative act turning natural phenomena into patentable human artefacts deserving an increasingly absolute form of monopoly protection. Of course an arguable case can be made for expanding patentable subject matter in the ways that have become the norm. But such a case does not deserve to be taken for granted and the present legal challenges are thus both timely and necessary. The first case (Bowman vs. Monsanto) can be considered to re-open the necessary debate about the inherent patentability of 'inventions' capable of replicating themselves, though it does not strictly address the question. One would at least hope to see a necessary assessment of what it means to 'make' an invention, when said invention is a gene, seed or plant. The second case, AMP v Myriad, will refocus attention the established legal interpretation, based on a problematic reading of a century of case law, that the isolation of DNA may constitute the creation of a new patentable 'thing' regardless of whether the sequence of the patented DNA has been altered. This round table will bring together leading law experts with historians, sociologists and philosophers of biology to question what a wider, and indeed, more global, view can add to current debates over the use of patents to protect biological objects.

Speakers:

- Robert Cook-Deegan (Duke)
- Graham Dutfield (University of Leeds)
- Jean-Paul Gaudillière (CERMES3)
- Amanda Odell-West (University of Manchester)
- Bronwyn Parry (King’s College London)
- Robin Scheffler (Yale)
- Ravi Srinivas (RIS, India)
- Kara Swanson (Northeastern University)
- Antony Taubman (WTO)

Chairperson: Berris Charnley (Griffith University)

Philosophy of Biology and Biology Education

Organized by Kostas Kampourakis, University of Geneva, Switzerland

While philosophers of biology have achieved a thorough understanding of the methods and conceptual structure of biology, there still is lively debate about many issues. This round table addresses the question how these results of the work of philosophers of biology – both the understanding that has been achieved of how biology works and the various perspectives taken in the ongoing controversies – can be brought to bear on biology education in schools and universities. The questions guiding the round table are: What sorts of contributions can philosophy of biology make to improve biology teaching? How can the expertise of philosophers of biology be translated into material that teachers and researchers in science education will be able to use? The panelists will discuss a number of core topics from philosophy of biology as concrete examples of ways in which philosophy of biology can contribute to biology education, including: evolution, intelligent design, non-genetic inheritance, evolutionary developmental biology, Mendelian genetics, gene concepts, and biomedical ethics. After these examples have been presented, the panelists will critically assess them in interaction with the audience, with a view of providing pedagogically sensitive philosophers, historians, sociologists and other students of biology with new impulses for making their work more socially relevant.

Speakers:

- Ingo Brigandt, University of Alberta, Canada
- Richard Burian, Virginia Polytechnic Institute and State University, USA
- David Depew, University of Iowa, USA
- Annie Jamieson, University of Leeds, UK

- Alan Love, University of Minnesota, USA
- Anya Plutynski, University of Utah, USA
- Michael Ruse, Florida State University, USA
- Tobias Uller, University of Oxford, UK
- Kostas Kampourakis, University of Geneva, Switzerland

Chairperson: Thomas Reydon, Leibniz Universität Hanover, Germany

Plant Science: Its Role In Biology

Organized Sabina Leonelli, University of Exeter, UK

Plant science is too often a ‘forgotten' field within the history, philosophy and social studies of science. This is puzzling, given its immense contributions to the history of genetics, ecology and cell biology, among other fields; the crucial role played by plant scientists in contemporary systems biology and data-intensive research; and the importance of ongoing plant research towards addressing the key social and economic challenges of our time, such as food security, bioenergy and climate change. Among the possible reasons for the relative invisibility of plants within biology are the difficult relations between 'basic' and 'applied' plant science (and particularly molecular approaches carried out in the lab versus field-based investigations closely aligned with agricultural practices); the scarcity of funding and media attention in comparison to biomedical research; and the lack of co-ordination between scholars interested in this field (the digital platform History, Philosophy and Sociology of Plant Science is trying to address this in the UK, though it lacks long-term funding). This session brings together plant scientists, philosophers and historians to identify and discuss past and current contributions of plant science to biology; reflect on the reasons for the relative lack of visibility of these contributions; and explore ways to deepen current understandings of the role of plant science in biology, and encourage public and scholarly interest in plants. The session will feature short addresses by panel members and an open discussion in which we hope many of our fellow ISHPSSB members will participate.

Speakers:

- Jean-Francois Briat, Centre National de la Recherche Scientifique, Biochimie et Physiologie Moléculaire des Plantes, Montpellier, France
- Berris Charnley, Griffith University, Australia
- Bertrand Muller, Ecophysiologie des Plantes sous Stress Environnementaux (LEPSE), UMR INRA-SUPAGRO, Institut de Biologie Intégrative des Plantes, Montpellier, France
- Staffan Müller-Wille, University of Exeter, UK
- Francisco Vergara-Silva, Universidad Nacional Autónoma de México, Mexico
- Vassiliki Betty Smocovitis, Departments of Biology and History, University of Florida, USA

Chairperson: Leonelli Sabina, University of Exeter, UK

Responses to *Principles of Evolutionary Medicine*: an Interdisciplinary Round Table

Organized by Pierre-Olivier Méthot, Institute for the History of Medicine and Health, University of Geneva, Switzerland
& Paul Griffiths, University of Sydney, Australia

Evolutionary medicine has not yet had the transformative impact on medicine envisaged by its founders, and philosophers of science have questioned its heuristic value for biomedical research. However, there is a growing interest for evolutionary explanations of health and disease among biomedical researchers. *Principles of Evolutionary Medicine* (Gluckman, Beedle, and Hanson, 2009) represents a major step forward in the debate as it places recent developments in evolutionary developmental biology, epigenetics, and genomic at the heart of evolutionary medicine, although it still sees a large role for the reconstruction of evolutionary history in deriving medical hypotheses. Furthermore, while in classic Darwinian medicine there is a mismatch between modern environments and the ancient "environment of evolutionary adaptedness", *Principles of Evolutionary Medicine* changes the meaning of the concept of "mismatch". Though the earlier sense persists in Gluckman's work, the mismatch concept it introduces operates on an ontogenetic timescale, not a phylogenetic timescale, and relates to mechanisms generating phenotypic plasticity and robustness at the individual level of adaptation. The proposed Round Table will bring together the authors of *Principles of Evolutionary Medicine* and philosophers of science to discuss conceptual and methodological issues arising from the book, including: How does the concept of mismatch work to generate insights into human health and disease? Can life history theory lead to significant and testable predictions of an organism' responses to changing environments? Does evolutionary biology provide a theoretical framework to medicine or a "tool-kit", and is such framework necessary to understand changes in health and disease?

Speakers:

- Peter Gluckman, Liggins Institute, University of Auckland, New Zealand
- Mark Hanson, Faculty of Medicine, University of Southampton, UK
- John Matthewson, School of Humanities, University of New Zealand, New Zealand
- Pierre-Olivier Méthot, Institute for the History of Medicine and Health, Geneva University, Switzerland
- Dominic Murphy, University of Sydney, Australia
- Kenneth Schaffner, Department of History and Philosophy of Science, University of Pittsburgh, USA

Chairperson: Paul Griffiths, University of Sydney, Australia

Roundtable on Elliott Sober's book *Did Darwin write the Origin Backwards, and other philosophical essays on Darwin's theory*

Organized by Elliott Sober, Philosophy Department, University of Wisconsin Madison, USA

Elliott Sober's 2011 book has four chapters and a postscript. The first chapter is about the relationship of common ancestry and natural selection in Darwin's theory. The second chapter concerns Darwin's views on group selection. The third chapter is about theorizing about sex ratio -- before Darwin, by Darwin, and after Darwin. The fourth chapter concerns the relationship of Darwin's theory to naturalism (both methodological and metaphysical). The postscript has three parts: (i) on the use of parsimony to reconstruct ancestral characgter states

in a phylogenetic tree, (ii) on realism versus conventionaism concerning units of selection, and (iii) on the reality of the probabilities used in evolutionary theory.
This roundtable will take the form of comments on the book from:

- Jean Gayon (Paris)
- Tim Lewens (Cambridge)
- Samir Okasha, (Bristol)
- Reply: Elliot Sober (Wisconsin)

Chairperson: TBA

Will the distinction between medicine and enhancement be soon obsolete?

Organized by Sylvie Allouche, Center for Ethics in Medicine, University of Bristol, UK & Pascal Nouvel, Université de Montpellier 3, France

Given the advances of medical technologies, doctors are faced with an increasing demand to use them for purposes that go beyond what has been traditionally conceived as proper medicine, that is cure and care. For the past twenty years, awareness of this phenomenon has emerged and developed, and various attempts have been made to understand its scope and consequences. Some European philosophers have argued for the necessity of a neologism based on the Greek roots "anthropos" and "techne" to address and understand these changes in medical practice. Jérôme Goffette (2006) for example has introduced the term "anthropotechnie" defined as "the art or technique of extra-medical transformation of human beings by intervention in and on their bodies". He does not mean however that medicine and anthropotechnie are completely separate: the same person can be both a doctor and an anthropotechnician. But Goffette argues that the difference of goals entails a difference of practices, especially regarding the conduct of consultation. In the Anglo-Saxon world, these questions have crystallised around the notion of "human enhancement". The argument often put forward by their proponents is that there is a clear continuity between medicine and enhancement, and therefore no reason to fear the development of the latter. A third position, even more radical, would be that technological progress will actually make the very distinction between medicine and enhancement increasingly pointless, as the medicine of the future will take care of human beings in all their needs and aspirations without worrying whether this is by providing care or enhancement. The purpose of the round table is to discuss this claim.
Speakers:

- Pascal Nouvel, Université de Montpellier 3, France
- Darian Meacham, University of West England, UK

Chairperson: Sylvie Allouche, University of Bristol, UK

Posters (*alphabetical order*)

A Case Study for the Multifaceted Concept of the Gene: the Anarchistic honey bee Project
Ronai Isobel, The University of Sydney, Australia

'The gene' provides an extremely important framework for biological research, however, there is no singular conception of the gene. The identity of each gene concept is shaped by different research practices in Biology. To explore how biologists conceptualise the gene I undertook an analysis of scientific research practice using interviews with biologists at the University of Sydney. I also examined their published research output in a long term behavioural genetic study: the Anarchistic honey bee Project.

The current assumption in the literature is that the research context within which a particular biologist works is what leads them to hold a particular, and singular, concept of the gene. However, my illuminating case study demonstrated that biologists can readily shift between different research contexts and therefore an individual biologist can, and does, utilise varying concepts of the gene in different research contexts. Furthermore, a rich and complex connection must exist between all the different concepts of the gene, otherwise movement between gene concepts would not be possible.

It could be thought that as a multifaceted concept, the gene could easily engender chaos and miscommunication within biological discourse, however, semantic flexibility is competently practiced by biologists. They readily utilise different conceptions of the gene and deploy the concept appropriate for each research context. This results in the meaning of this central concept being implicit and dynamic. How biologists effectively communicate about the concept of the gene is something to be explored in my future research.

An organizational account of the genome function
Muro Elsa, University of Navarra, Spain

Post-genomic research has modified our understanding of how genome structure supports genome function, challenging the modern concept of the gene as a structural and static unit. New definitions of the gene have been proposed conceiving of the gene as a functional and dynamical unit.

In this poster I summarize some of these “dynamical gene concepts”, such as Griffiths and Neumann-Held´s concept of “gene as a process”, Keller and Harel´s concept of “genetic functor” and Griffiths and Stotz´s concept of genes as “things an organism can do with its genome”. There are two crucial consequences of these definitions: i) the same part of the genome can be a gene at a particular space and time, and a different gene at other particular space and time; ii) there is a circular causal regime governing genes.

I suggest to revise those dynamical gene concepts by conceptualizing the genome function through an organizational perspective, rather than from the earlier perspectives proposed (selected-effects and causal-role accounts). The reasons are that on the one hand, a circular causal regime is essential in an organizational theory of biological functions; and, on the other hand, this theory is very close to a process metaphysics. I apply Schlosser´s organizational account (1998) because his definition of functions includes temporal indices and can deal smoothly with the multi-functionality of traits, so that it emphasizes the independence of functions from structures.

Case Study – Importance of bioethics in determining whether or not to promote the governmental R&D programs in Korea
Han Min-Kyu, Dongwon Industries, South Korea

In Korea, whether the large-scale governmental R&D program planning is promoted or not is determined thorough "Preliminary Feasibility Study" that is an institutional system of Korea for investigating the feasibility of governmental R&D program planning for more than 50 billion won (about 50 million U.S. dollars) beforehand. The validity of technical point of views is an important aspect in the preliminary feasibility study as well as policy and economic point of view, and these three point of views have an influence to make a decide the program's validity to promote.

There are more than 10 governmental programs receives a preliminary feasibility study each year, the bioethics issues have been raised in on of them. In 2010, a program for prevention research to invest total 280.0 billion won (about 280 million U.S. dollars) for 10 years has been planned and had received a preliminary feasibility study. As a result this program was not accepted the validity of the promotion, because it did not include the contents of the relevant bioethics despite the its main contents to build a biobank to target a human sample of the scale of millions as well as other issues not explained in the three point of views. In this report, I would like to introduce the overview of the preliminary feasibility study in Korea and the bioethics issues affected to determine the validity of the promotion of this program.

Dialectics and neo-Lamarckism defended
Muñoz-Rubio Julio, Universidad Nacional Autónoma de México, Mexico

In this paper, I highlight and support the elements of the Neo-Lamarckian vindications of Eva Jablonka, Marion Lamb and collaborators, applying a pro-dialectical interpretation of evolution. Jablonka *et al*. present the organism as an entity endowed with an activity, in which niches and conditions of life are continuously built. They support an evolutionary model of complex spacetime transitions, refuting the reductionist systems constituted of simple linear information transmission. The integration of genetic, epigenetic, behavioral and cultural levels in evolutionary phenomena, shows a dynamics, in which *synthesis* and *becoming* processes can be explained by means of the Hegelian-Marxian-Engelsian concept of *Aufhebung*. It is a matter of concrete moments of the unity of the opposed, producing the conditions for their own overcoming. Such transitions constitute the essence of constant movements or transgressions of the *Limits* present in the different units of living systems .*Limit* understood as anything that establishes and contains what lies beyond and therefore, constitute themselves as condition of their self-negation.

The integration of the aforementioned levels of evolution, as explained by Jablonka *et al*., means a comprehension of evolutionary process as mediated by the interpenetration of the parts and the wholes. Besides a back and forth movement of certain emergent properties as processes of quantitative-qualitative changes, and negations and self-negations, is shown.

Finally, the dialectical approaches used by Hegel in *Science of Logic*, and by Marx in *Grundrisseare* postulated as efficient tools for the study of these innovative neo-Lamarckian interpretations.

Designing generic dynamic landscapes
Franceschelli Sara, Institut Desanti, ENS de Lyon, France

From the theory of evolution to embryology and statistical physics, the "landscape" metaphor - qualified as "adaptive", "epigenetic", or "energetic", depending on the domains under consideration - presents a characteristic shape defined by peaks, pits, and cols. These figures played and play an important role in the development of biology, from population genetics and evolutionary theory to embryology and epigenetics, and still deserve theoretical interest (Gavrilets 2004, Pigliucci & Kaplan 2006, Ao 2009, Bazzani et alii 2011). What are the nature and the evolution of equilibria of the landscape? How are its stability and robustness characterised? What is the effect on a landscape of different kinds of perturbations? At what spatiotemporal scale is it suitable to situate such analyses and investigations? What are the variables that are represented by the landscape?

This set of questions has motivated a performative design research program in a school of applied arts EnsAD (Paris). This design experience, switching from the representation to the performance, points not to the design of a single object, but of classes of objects through the design of generative process. Focusing on the generic dynamical properties of landscapes to be instantiated by the behaviour of designed devices, we thus worked on a pragmatics of landscapes. Through some videos I will depict the morphodynamical behaviours of some dynamic devices and illustrate our approach, based on a spatial translation of questions that emerged during workshops involving researchers, designers, and applied art students.

Does Alex have a theory of mind?

Chang Shereen, University of Pennsylvania, USA

Theory of mind, often thought to be the central characteristic of personhood, is the ability to attribute mental states to others (Premack and Woodruff 1978). Standard tests for it in humans involve false belief tasks, which rely on verbal responses to establish that the subject has a theory of mind. However, it is difficult to determine that nonhumans have theory of mind when they are not linguistic. Nonverbal tests of theory of mind are vulnerable to methodological problems, with challengers arguing that positive experimental results are better explained by positing that the nonhuman subject merely makes predictions based on behavioral associations rather than mental state attributions (Povinelli and Vonk 2003).

Consider Alex, an African grey parrot with 30 years training in the appropriate use of English labels for objects, categories, and concepts (Pepperberg 2009). Pepperberg reports an incident during testing when Alex manipulates her into asking him a different question so that he may demonstrate his spontaneous transfer of the concept "none" from one context to another. I argue that the best interpretation of Alex's behavior is that he has a theory of mind. I suggest that, by studying Pepperberg's model of social learning and the linguistic communication of nonhumans like Alex, we can learn much about the relation between language, sociality and theory of mind.

Historical look at the evolution of the species concept from Antiquity to the 19th century

Lacombe Rémi, Université Paul Valéry - Montpellier III, France

Faced with the incredible diversity of organisms in the biosphere, our knowledge is in a difficult position; To know the living, one of the frequently ways is the classification, which identifies, ranks and classifies living beings into categories to establish clearly the reports (physiological, kinship, biotope...) bringing them closer or separating them. But think of the living by categories implies that it takes a final category is the smallest unit classificatory and called the species. But is the concept of species really conclusive? Doesn't it require rather special flexibility because of its place in the classifications?

Giving some openings to begin answering these questions, I propose to browse through the history of the concept of species and through the great thoughts which have reinvested it, for showing its importance in biology, ethics and metaphysics.

Our journey begins in Antiquity with a thought about the eidos shared between Plato and Aristotle, and then we'll see in a second time this debate's legacy to the Middle Age with the emergence of a new science, natural theology, directly influenced by the writings of St. Thomas Aquinas. A third time will be devoted to the impact of these thoughts on Charles Darwin and his predecessors who, despite their contributions and experiences, have not managed to overcome the paradigm of the concept of species as a result of the scala naturae (or scale of beings). Once completed this journey, I invite you to reflect on the discussion instead we give today to this concept.

History of science in the high school: Lazzaro Spallanzani´s experiments in animal reproduction

Pereira Miler, University of São Paulo, Brazil
Prestes Maria Elice, University of São Paulo, Brazil

The History of Science, in last decades, is pointed by specialized literature as an appropriate pedagogical resource to teach current scientific content and to approach aspects of the Nature of Science in class. This work treats the History of Science as a tool for students discussions about the construction of scientific knowledge. The goal is to work the concept of animal reproduction focusing the study of the development of experimental method in investigation of living beings. The historic episode chosen, the study of amphibian reproduction accomplished by Lazzaro Spallanzani (1729-1799), will allow us to explore among students specially the difference between observation and theory and the relations between them. Such metascientific aspect is important to promote a critique to the empirical-inductivist notion, which is still preponderant in the teaching of Science. This historical episode will be worked through a Teaching Learning Sequence, as discussed by M. Méheut and will be constituted by eight classes planned according to an investigation-teaching strategy. The Teaching Learning Sequence will be applied in a public high school of São Paulo city, Brazil. Amongst, didactic material to be used in sequence are support texts to students, drafted based in History of Science research methodology, from primary sources analized in its context, and simulation of experiments in virtual environment. The Teaching Learning Sequence application will be registered and evaluated by data triangulation, using different research instruments and qualitative analysis. The results may indicate new possibilities of using History of Science in scientific education.

How does epigenetics influence our view on evolution?

Laitinen Roosa, University of Helsinki, Finland

Evolution is explained through natural selection on adaptive inheritable traits. Traditionally, the material that is carried from one generation to the next and provides the phenotypic variation that can be under selection is associated with genes and DNA. However, there is also phenotypic variation that is not explained by differences in DNA sequences but by modifications which change gene expression and influence the phenotype without changing the DNA. These are called epigenetic modifications and include processes such as DNA methylation, histone modification and small and long non-coding RNAs. Recently, it was found that epigenetic modifications do not only influence the phenotype of organisms but that they are also inherited from one generation to the next and are also under selection. Whereas the changes in DNA are stable, the epigenetic changes are less stable but faster. While on the one hand epigenetic modifications depend on the underlying genes, on the other hand they affect gene action. However, it is still largely unknown how the interplay between the epigenetic modifications and genes could influence adaptation and evolution. In this poster I will discuss how epigenetic marks, in the light of current knowledge, influence our current view on inheritance and evolution.

Is domestic fowl a ‘genetic tool’ Gallus gallus as a model organism

Lopez Paleta Miguel , Doctorado en Filosofía de la Ciencia (UNAM), Mexico

Domestic fowl (*Gallus gallus*) is one of the most widely used organisms in the history of biological research. It has been involved in major biological disputes and it is a conspicuous character in the establishment of long-term biological concepts. However, nowadays, some biologists claim that chicken has been excluded from some fields of research associated to molecular and genomic approaches.

Apparently, this is due to a diminished performance when Gallus gallus is used as a “genetic tool". This means that although domestic fowl is a useful model within some research fields such as developmental biology, some molecular protocols and applications are not readily employed in this bird. Moreover, as opposed to many other members of the exclusive group of "model organisms", chicken does not seem to have a meticulous genetic standardization and there is not a single exclusive standard strain used in every laboratory interested in chicken biology.

This paper discuss that nevertheless Gallus gallus has two epistemic features which make it a "model organism". Namely, it has a broad representational scope and a defined epistemic target. Therefore, domestic fowl is an adequate model for some enquiries about the vertebrate development and, within these research fields, biologists have made improvements in their protocols that (some researchers claim) make domestic fowl a proper "genetic tool".

Levels of biological organization in the holobiont

Yang Shijian, Xiamen University, China

Holobionts are the symbiotic complex formed by a multicellular animal/plant organism and the microbial community living inside its body. There are thus two types of symbiotic relationships: holobiont symbioses (e.g. cow-rumen flora symbiosis, or Squid-V. fischeri symbiosis) and nonholobiont symbioses (e.g. cleaner fishes and client fishes).

Can holobionts be units of evolution? Some philosophers have argued no --- host organisms form Darwinian populations, while symbionts form another Darwinian population. Understood this way, holobionts cannot form a unit of evolution. However, I will argue that this fails to take into account of the levels of biological organization in the holobiont. Two levels, the organism level and the cellular level, can be distinguished. On the cellular level, symbionts do constitute Darwinian populations, but on the organism level, symbionts should be better viewed as constituting a part of an organ of the holobiont, and it is reasonable to view a holobiont as a unit of evolution.

Revolutionary, evolutionary or mangled science: Dietschy's development of the tritiated water technique for measuring cholesterogenesis as a case study

Haave Neil & Bannister Jill, University of Alberta, Canada

The philosophies of Kuhn, Hull and Pickering consider the nature of science from different vantage points. Kuhn viewed science as operating for periods of time in which scientists worked within a paradigm - an accepted norm of practice - that were punctuated by revolutions in which old paradigms are entirely replaced by new paradigms. In contrast, David Hull considered science to progress in an evolutionary manner where conceptual lineages can be traced from communities of practice through their students and are dependent upon the establishment of professional relationships. What sets both Kuhn and Hull apart from more traditional understandings of the nature of science which considered only rational factors, is that they both acknowledge the role of human behaviour admitting that science can, at times, have irrational influences. Pickering's philosophy of science also considers the role of theory and social influence, but adds the technical component asserting that the interplay that occurs between instruments and scientists can have a profound impact on the development of our understanding of nature. Our analysis of the published works of Dietschy suggests that, in this case, a dance of agency existed in the development of using tritiated water to measure rates of cholesterol synthesis during the 1970s and 80s. Although Dietschy's new method of measuring cholesterogenesis produced accurate reliable results, the accepted norm of practice did not change. The use of radiolabelled carbon substrates continued alongside the use of tritiated water; a result due to the technical difficulties of using large amounts of radioactivity.

Survival determinism in situ: an evolutionary perspective on disease etiologies

Krsmanovic Pavle, German Cancer Research Center, Germany

In the history of biomedical studies research has been primarily focused on the processes that played a role in initiation and progression of some diseases. In an attempt to mimic these processes as closely as possible the strategy of biomedical researchers has been to try to reproduce the same sequence of the events on an experimental model system. An ample amount of data that has been thereby produced strongly supports the direct links between the effects of the disease-causing events and the origin of the respective diseases.

In an effort to put the origin of many diseases in a broader biological as well as philosophical context a novel concept has been put forward. The process in question was termed survival determinism and it refers to an ancient mechanism of unicellular organisms designed to secure their survival under novel or rapidly changing environmental conditions. On the one hand targeted survival determinism was primarily discussed in the context of rapid environmental change and/or some genetic defects. Thereby the diseases caused by such changes or defects would be seen as relicts of the ancient evolutionary mechanisms. On the other hand, stochastic survival determinism was indicated as the major process behind the generation of genetic and genomic variability under conditions of drastic and rapid environmental changes. The mechanism was initially discussed in analogy to the processes observed to take place in cancer cells.

The Island as object of ecological studies: a proposal for biology teaching

Brando Fernanda, Universidade de São Paulo, Brasil
Caldeira Ana, Universidade Estadual Paulista Júlio de Mesquita Filho, Brazil

The aim of this work is to present studies that explore the "island" as investigation background, and adopt Peirce's philosophical system to treat determined concepts in biology teaching. The environmental choices as study objects within specific literature offer wide possibilities. The diversity of terrestrial, aquatic organisms, and even original native flora in urban areas, were inspiring environments for the elaboration of central ecology concepts in certain historical conditions. *Islands* have been favored in theoretical discussions that especially are concerned to populations sharing local resources, and the colonization and extinction pattern of local species. An example of such studies has occurred in Krakatau, Indonesia, which suffered a volcanic eruption in 1883, destroying local fauna and flora. The recolonization process has been extensively observed, registered, and reported. In view of that, the discussion concerning ecological studies developed in islands shall occur from original works, as well as secondary sources, that privilege this type of landscape. The Semiotics of Charles Sanders Peirce (1839-1914) shall anchor a proposal that makes use of History of Biology as an instrument for biology teaching.

The Non-Mendelian Revolution: A Conceptual Reinterpretation of the Genetic Revolution

Tanghe Koen, UGent faculteit letteren en wijsbegeerte, Belgium

In 1989, Peter J. Bowler called the Mendelian revolution a revolution of major conceptual proportions. It was one which, he said, might ultimately even have to be regarded as at least as important a transformation in our ideas about life as ‘the Darwinian debate’, even though its effects are not as immediately visible as those of that debate. The genetic revolution has, indeed, like other major scientific revolutions, been accompanied by an important paradigm-shift. The main reason why, in sharp contrast to those other revolutions, it is still not identified with that profound change in our thinking, is simple: the full effects of the genetic paradigm-shift indeed only became clearly visible long after it started in the 19th Century. The new, genecentric interpretation of life was, to be precise, explicitated and, to a certain extent, elaborated in 1976, in the second most popular science book of the 20th Century: *The Selfish*

Gene. It revolves around the simple but profound and radical idea that somas are mere survival machines of genes. This doctoral thesis not only charts the genecentric paradigm-shift, but also explains why the new interpretation of life was only explicitated in 1976. Last but not least, it argues that a reinterpretation of the history of genetics in terms of this paradigm-shift is heuristically interesting in that it sheds new and clarifying light on a large number of historical and contemporary issues, ranging from Gregor Mendel's experiments and their 'rediscovery' in 1900, Lamarckism, Darwin's theory of evolution and the nature/nurture debate, to the discovery of DNA, the emotion revolution and the selfish gene theory itself. Some long-debated, profound questions will never be resolved, as long as we don't learn to think about the genetic revolution in terms of the genecentric paradigm-shift that made it possible.

The use and abuse of neurosciences in economics: the neuromarketing

Garvia Cristian, Université de Provence – Aix-Marseille, France

Neuromarketing is a young field of research from economics that studies consumer behavior in order to encourage him to buy a product. In theory, if a seller can know for what consumer are looking for, he will optimize the profit of sales and, at same time, buyers will be pleased. More and more advertising agency's uses neurobiological tools to understand consumer's choices: the neuromarketing is possible since neurobiology can "read our minds scientifically".
However, we considerate that neuromarketing is not a real science but a tool for advertisers, using the neuroimaging techniques and test initially conceived for neurobiology or psychology and neuroeconomics. In fact, we can think that neuromarketing is closely related to neurosciences but actually we can find only one thing in common: the use of concrete tools as EEG, MRI, fMRI and others.
We want to demonstrate that neuromarketing is not a real science, but the perception of consumers and economics researchers about their efficiency and scientific value are probably disproportionate. Even if we can know for example what song, smell or color are the most powerful to attract the consumer, there are too many other factors to consider to explain a decision.
In other hand, despite the authentic efficiency of neuromarketing, we want to demonstrate too that we can find a real and important ethical debate if we considerate the aim of these studies, clearly conceived to manipulate and to compel consumers to buy compulsively.

When seeing incorporates the outcomes of doing: Epistemological background and issues of the concept of affordance

Camus Thomas, Brouillet Thibaut & Vagnot Caroline, all at Dynamique des capacités humaines et des conduites de santé (EPSYLON), Université Paul Valéry - Montpellier III, Montpellier, France

How perception incorporates the consequences of our actions? This central question in psychology and in philosophy of science has hardly resolved. In this study, we aim at investigating the impact of contingent action effects on object perception. In contrast to what is commonly accepted, we hypothesize that the way we interact with objects depends on our personal history with these objects rather than on their intrinsic motor properties. To test this, we built an original experiment within a theoretical frame that includes the impact of action and its consequences as a major component of cognition. Our results reveal that an "affordance effect" is at play. The affordance is, according to Gibson (1977, 1979), everything in our environment that permits a certain kind of behaviour to take place. Obviously, such a vague definition would need to be better specified to allow a specific experimental approach of this concept to take place. On the other hand, the precisions concerning this concept will definitely guide the way we try to investigate what lies under it. To solve this dilemma, we propose to introduce some philosophical tools that, according to us, furnish a coherent background and some issues to clarify the concept of affordance and its consequences. We thus propose to re-interpret the theoretical aspects of our experiment within the context of Dewey's naturalistic metaphysic (1896, 1916, 1929), showing that understanding the cognitive performances of an individual shouldn't need to postulate the existence of separate entities. Then, we will discuss our results in light of some more recent works of Chemero (2009) and his Radical Embodied Cognition theory.

When species delineation challenges conservation policies: the case of a flagship carnivorous pitcher plant

Di Giusto Bruno, Ming Chuan University, Taiwan

Bonhomme Vincent, BotAnique et BioinforMatique de l'Architecture des Plantes, CNRS, France

The failure in agreeing on a clear species concept raises issues in conservation. Grouping different varieties under a same species name may result into having a false impression of abundance and overlooking the need of protection for rarer types. In Brunei, the recent destruction of a study site led us to reconsider the taxonomical status of sparse forms of the pitcher plant *Nepenthes rafflesiana*. Abundant in Peninsular Malaysia, Sumatra and Borneo, this carnivorous species - classified as most *Nepenthes* under the Annex II of CITES - presents several original varieties restricted to Borneo. We combined morphological and ecological studies to compare the taxonomic status of 3 forms of this species: *typica*, *gigantea* and *elongata*; the latter has been recently classified as a new species, *Nepenthes baramensis*, for its symbiosis with woolen bats. Our findings showed that *typica* and *elongata* use different chemical pathways to attract insects, resulting in different visitor and prey spectra. Furthermore, morphological analysis showed that the three varieties differed in their development and their use or not of wax to retain their prey. Finally, distinct flowering peaks suggest the presence of limitations to pollen exchange. These distinct traits support the taxonomic change for *N. baramensis* and the need of revising the classification or, at least, the conservation status for other forms such as the rare *gigantea*. Developing combined morphological and ecological studies could help to decrease the risks of biodiversity loss and local extinction, especially for forms with highly fragmented distribution.

Sessions (*alphabetical order*)

Abstracting from the Living: Characters and Classifications in the Life Sciences

From Merkmal to Marker. The taxonomic origin of the genetic character concept
Meunier Robert, Berlin Institute for Cultural Inquiry, Germany

Historians of genetics have long pointed out the continuity between taxonomists´ concerns with the constancy of types and experimental studies of heredity, such as Mendel´s or Johannsen´s. Instead of focussing on the species concept or the question of the constancy of types directly, I wish to reconstruct this relation on the level of the respective character concepts underlying these discourses and the practices by which characters are individuated. Concerning the continuity of the character concept, it can be said that characters were used to classify the offspring of organisms in hybridization as well as in pure line breeding experiments. Only through indicating class membership of the individual organism genetic characters could finally indicate constituents of the gametes that gave rise to the offspring. But there were also significant differences between classification in taxonomy and in studies of heredity. While taxonomy attempts to exclude inter-species variation, genetics deals exactly with this variability. In consequence, taxonomy employs a character concept that rests on reliable observability, whereas genetics operates with a concept of characters that need to be inferred. In Mendel, for instance, whether the expression of a character, such as color, is constant, or dominant hybrid, and in Johannsen, whether the expression of a character, such as size, constitutes a short form of the large class or a large form of the small class, can not be observed, but has to be inferred from observing the offspring of the organism exhibiting a character.

Enriching and observing: Microbial species as practices
Grote Mathias, Technische Universität Berlin, Germany

Microbial taxonomy is considered an utter mess throughout most of the 20th century, with a broadly accepted phylogenetic classification emerging only on the basis of rRNA sequences in the 1980s.

Here, I argue that in contrast to numerous re-classifications, conceptual changes, and the molecular genetic “revolution”, the laboratory practices used for the identification and classification of an exemplary microbe (*Halobacterium*) have remained surprisingly stable for almost a century. Since the late 1890s, enrichment culture has been crucial to obtain microbial material to be analyzed morphologically, physiologically or biochemically. Thus, not only concepts of microbial species, but the entire laboratory existence of the organisms hinged on the technological ideal of a pure culture. In the case under examination here, the simple visual index of colony colour has been central to identify the microbes, as compared to more sophisticated characters. Also, analysis remained entirely on the level of the phenotype until c. 1980.

Clearly, the reliance on laboratory culturing and the scarcity of stable, distinct characters of microbes have impacted on their identification and classification. Yet, it is interesting to note that whereas the resulting determinative, non-phylogenetic classifications might have been unsatisfactory from a general biological point of view, they have at least in this case remained relatively stable on the level of practices involved. Under these premises, I will also analyze the interrelations of isolation, culturing, identification and classification. Against the background of today's molecular genetic practices of classification, this case study allows to discern a way of conceiving of the microbial world that has been prevailing until very recently.

Identifying Medically Relevant Variation to Re-Classify Disease: Linkage Analysis of Neurodegenerative Disorders in the 1980's

Keuck Lara, Institut für Philosophie der Humboldt-Universität zu Berlin, Germany

Mapping technologies have been widely used in evolutionary biology and biological anthropology, but also human geneticists have relied on them to identify hereditary modes of disease contagion, and to correlate diseases like haemophilia with other biological properties such as male sex. The increased use of molecular methods in the second half of the last century, e.g. the identification of restriction fragment length polymorphisms, lead to new hopes to successfully use linkage analysis in research on seemingly hereditary neurodegenerative disorders such as Huntington's disease or Alzheimer's disease.

In my talk, I want to take a closer look at the ways in which the disease definitions of these neurodegenerative disorders have been amended so as to provide suitable objects of analysis, and, in turn, how the results of linkage analysis research have stabilised or de-stabilised existing disease classifications. Classifications are understood as definitions of disease, which allow for ordering individual disease phenomena into groups according to a selection of classifiable characteristics.

My talk addresses such selections by analysing how experimental practices of linkage analysis and conceptual work regarding the search for good classifications of the named neurodegenerative disorders were intertwined, that is to say, how the diseases were treated as both, markers and yet-to-be-ordered-phenomena. Against this background, it shall be discussed how human geneticists dealt with the heterogeneity of disease phenomena, for instance by sub-typing patient populations, by re-framing clinical hallmarks, and by negotiating which individuating properties could be disregarded for the sake of building general, medically relevant categories.

A comparative history of evolutionary theories in the mid 20th century

Evolutionary theories in Portugal during the dictatorial regime (1933-1974) – Portuguese zoologists' differentiated stances towards evolution

Fonseca Pedro, Pereira Ana, Pita João, all at University of Coimbra, Portugal

The presentation provides a critical evaluation of the most popular evolutionary theories in Portugal during the conservative dictatorial regime known as the *Estado Novo* (1933-1974). Neo- Darwinism, Neo-Lamarckism and Theistic Evolution are the main evolutionary theories considered. Due to the length of the presentation, we will narrow our scope to the analyses of the scientific production of some of the country's most influential zoologists, either conducting and supervising research at Portuguese universities, such as João Gualberto de Barros e Cunha (1865-1950) (University of Coimbra), Amílcar de Magalhães Mateus (1911-1996) (University of Oporto) and Germano da Fonseca Sacarrão (1914-1992) (University of Lisbon), or at other relevant scientific institutions, such as Alberto Candeias (1891-1972) (Estação de Biologia Marítima). In order to guarantee a better contextualization of our subject, a brief historical survey of evolutionary theories in Portugal before 1933 will be presented. We then address in greater detail the following three topics: (1) the stances of the cited Portuguese zoologists towards different evolutionary theories, especially in their dissertation thesis and popular science works; (2) the influence of different evolutionary theories on their scientific research (and the scientific research of their disciples); (3) the differentiated treatment of different evolutionary theories in secondary and high school textbooks of their authorship and co-authorship. In another presentation, within the same session, we will also be analysing the scientific production of some of the country's most influential botanists during the same period.

Falls and rises of evolutionary theories during Franco's regime (1939-1975)
Florensa Clara, Universitat Autònoma de Barcelona, Spain

When Franco arrived to power in 1939 soon relied greatly upon Catholic sectors of Spanish society. This meant creationism back to schools and universities. Evolutionism disappeared from the public sphere until the mid 20th century. At that moment, a group of Spanish paleontologists presented an evolutionism that fitted well with Francoist catholic ideology and was allowed to appear in the press, to be taught in seminars, schools and even to future journalists. This was a finalistic-theistic evolutionism and its supporters argued that it had nothing at odds with Catholic dogma. They used scientific arguments and paleontological evidence to prove it. In the 60's, a will of openness and modernity of the regime coincided with some crucial discoveries in genetics which involved Spanish scientists. Then, Neo-Darwinian evolutionism was reintroduced in the media with a new appearance provided by the new vocabulary of genetics. It reappeared clean of old controversies.

In this talk I would like to present the theories of evolution that where discussed during Franco regime in the public sphere. To contextualize I will rely on the few existing research done on the period about evolutionism in education and scientific work. Then I will present my own research on the theories of evolution in the public sphere to show how the rise and fall of certain evolutionary theories followed political changes during Franco's regime.

Microevolution on microscales: shifting views of the temporal and spatial scales of evolution in British genecology
Peirson Erick, Arizona State University, USA

Among plant ecologists interested in intraspecific variation -- especially those involved in the interdisciplinary field of experimental taxonomy, or genecology -- working in Britain in the decades following WWII, the answers to two closely related questions were in flux: First, on how small of a spatial scale can populations of organisms diverge in their evolutionary trajectories, becoming adapted by natural selection to their local environments? And second, just how rapidly can such adaptive evolution occur? By the middle of the 1960s, many ecologists had come to believe that adaptive evolution could occur on temporal and spatial scales commensurate with ecological processes such as succession. This conceptual shift has been implicated as a central factor in the emergence of the field of evolutionary population ecology in the 1960s.

So what accounts for this shift in thinking about the temporal and spatial scales on which divergence and adaptive evolution can occur, and what were the consequences? I will use the ideas and research activities of plant ecologist Anthony David Bradshaw (1926 - 2008) during the 1940s- 1960s as a lens into the shifting conceptual and methodological framework of postwar British experimental taxonomy (or genecology). Drawing on archival sources, I will describe how Bradshaw's ideas about the temporal and spatial scales of adaptive evolution changed, enabling a reconceptualization of the evolutionary significance of phenotypic plasticity (the ability of individual organisms to respond morphologically, physiologically, or behaviorally to changes in environment). Using methods from digital and computational HPS, I will situate Bradshaw within the shifting landscape of British agricultural research, and consider what this might imply about the complex relationships between agriculture, ecology, and evolutionary theory in Britain in the middle of the 20th century.

Anger: new insights on a very old notion (*Interdisciplinary session*)

Anger and genes: a philosophical inquiry
Nouvel Pascal, Université Paul Valéry - Montpellier III, France

In the course of the history of western philosophy, the discussion on the causes and the consequences of anger have been one of the most substantial ethical topics. Homer's Ilyad is a narration about the deleterious consequences of anger for “mortals “. It aims at illustrating the fact that controling anger, once it has begin to burst, is almost impossible. Anger was considered, all along the antiquity, specially by the stoics, as the most notorious (and destructive) passion and, as such, as a paradigm of all other passions. More recently, Darwin, in his book *The expression of emotions in man and animal* (1872) did consider anger as an emotion the roots of which can be traced back in animal species related to man (mostly primates and mammals). Following these insigths, modern biology and genetics together with psychological studies have build a new picture of anger in which genes, cerebral areas and psychological influences of various sorts play a major role. These new explanations, however, deserves a conceptual investigation since it appears that they encapsulate philosophical notions that are rarely discussed as such. In this lecture, we will propose such an investigation and apply it on a recent (2009) publication, the authors of which claim to have identify a gene that is correlated with anger traits in the personnality of certain individuals (they might have come to call the gene “*achille*” if it did not already had a name).

Anger in vitalist thought: Jacques Lordat and the question of passions

Lavabre Thierry, Université Montpellier I Faculty of Medicine, France

Among the vitalisms, the school of Montpellier, following Paul-Joseph Barthez (1734-1806), proposed a theoretical approach of life : given that all vital manifestations are caused by a *Vital principle*, unknown in its nature but suitable for the elaboration of a specific science, the *Science de l'Homme*, this “philosophical“ vitalism is a kind of logical construction, of abstract calculation. Barthez's heir, Jacques Lordat (1773-1870), extended this point of view by the elaboration of a medical Anthropology: man being composed of soul, vital principle and material elements, what matters is the relation between these three components. Lordat applied this approach in different fields, using a combination of clinical, physiological, literary, philosophical or artistic data: “aphasiology” (language disorders), anesthesiology...
In his *Physiological theory of human passions* (*Théorie physiologique des passions humaines*), published in 1853, Lordat defined passions as an unusual and temporary mode of the human complex (as defined above), associating a pathetic idea in soul and an abnormal local sensation derived from the Vital principle, the initial cause being possibly located in both. As usual, Lordat ascertained this definition by arguments obtained from the different fields of human knowledge, providing a very original insight for his time. Far from a strictly experimental point of view, his logical theory appears simultaneously as anachronic and open to subsequent developments.

Anger and personality test: A psychological investigation

Blanc Nathalie, Université Paul Valéry - Montpellier III, France

To understand how individuals interact with their environment, it is now well admitted that their cognitive abilities but also their emotions have to be taken into account. The relation between emotion and cognition has already been investigated and provides interesting results. For instance, Havas, Glenberg and Rinck (2007) induced participants to either smile or frown while judging the emotional valence of sentences. They observed that individuals in the smiling condition were faster to make judgments about positive sentences, while frowners were faster with negative sentences. In summary, as predicted, smiling or frowning influences individuals' emotional state, which in turn influences cognitive processing abilities. In line with this kind of studies, Wingrove and Bond (2005) assumed that personality trait should be taken into account when studying higher-order skills like reading comprehension. They hypothesized that trait anger could be associated with general faster processing of sentences describing angry-provoking situations. One personality test was used to assess individuals' trait anger. The results showed that those who have angrier dispositions as indicated by their score to the personality test, tended to read narratives dealing with anger-provoking situations more rapidly. Overall, individuals with trait anger showed a processing advantage for angry reaction relative to alternative reactions. In a recent paper entitled "the biological basis of anger", Reuter et al. (2009) found a significant association between one gene and trait anger. Taken together, these two sets of studies offer promising perspective for future research with the general objective to combine genetic and psychological approach of human.

Animal Models in Neurobiology (submitted papers)

History of biological researches on memory

Lade Quentin, Sphere, Université Paris Diderot - Paris 7, France

This paper deals with the main biological researches on memory in the postwar era through the history of three experimental systems developed with three animal models. At first, aplysia, a sea-slug domesticated in marine research stations in the late 30's, served as a boundary-object between neurophysiology, experimental psychology and learning studies. Because of its simplicity, it provided the biological model of the seminal work on the neural supports of memory of Nobel Prize winner Eric Kandel. Hermissenda, another sea-slug studied by Daniel Alkon, was very close to Kandel's model and its most direct competitor. Finally, the chick presented an alternative model, derived from ethology, and enabling more integrative approaches of mnemonic processes, heavily advocated by Steven Rose. I will discuss how these animals, constructed as competing embodiments of mnemonic functions, were a part of broader arrangements which encompass representations of memory, sciences and then human beings. It draws three different styles of biological thought which influenced the first biological understanding of memory in the context of nascent neuroscience.

Animal Models as Experimental Model Systems

Atanasova Nina, University of Cincinnati, USA

I argue that animal models in neurobiology are best characterized as experimental model systems that include but are not exhausted by live non-human animals or parts thereof. As such animal models in neurobiology should be conceptualized in relation to the notions of model organism and experimental organism. Nevertheless, following Gayon (2006) and Ankeny and Leonelli (2011), I argue that these notions should be distinguished from one another because, regardless of the similarities they share, they represent different research tools. I stress that the predominant concept in the context of experimental neurobiology isanimal modeland show that neurobiological animal models function as a type of experimental tool that differs in relevant respects from model organisms as they are used in genetics, for example. For this purpose, I study the discussion of model organisms within the philosophy of biology and the life sciences. I analyze the relationship between the notions of model organism, experimental organism, and neurobiological animal model. I conclude that animal models in neurobiology are experimental model systems of the type described by Rheinberger (1992) and Weber (2005). I then compare the notion of experimental model system to that of experimental paradigm (as used by Sullivan 2010) and argue that the former better captures the historical developments of the use of animal models in experimental neurobiology. To exemplify this point, I refer to the developments in the applications and the modifications of the Morris water maze test as an instrument for modeling human learning and memory in rodents.

Humanizing Animals: The Selection and Justification of the Prairie Vole as an Animal Model for Autism Spectrum Disorders

Zautra Nicholas, Arizona State University, USA
Robert Jason, Arizona State University, USA

Against the historical preference for a small set of animal models in neuroscience, some scientists and science scholars have advocated focusing on better-chosen animals for understanding the development and evolution of brains than rats and Rhesus macaques. Where the aim of the research is to shed light on human brain disorders in particular - especially as a basis for translating discoveries from bench to bedside - the importance of justifying experimental research with animals becomes paramount. The disputes have recently been featured in *The New York Times* and *Slate*, raising questions about the internal and external logics of science funding under the banner of translational research.

In this presentation, we explore the establishment of one animal model - the prairie vole - in one set of brain disorders - Autism Spectrum Disorders (ASD) - to assess the character and epistemic warrant of claims about how an experimental animal is or isn't “the right tool for the job”.

We situate our historical and philosophical analysis within the current political economy of animal experimentation, and the changing nature of Autism Spectrum Disorders as disease categories in the development of DSM-V. Drawing on literature review and data gleaned from semistructured interviews, we explain how prairie voles came to be models of ASD, and evaluate the supporting justifications provided by neuroscientists in regard to the reliability and validity of the vole ASD model.

Anthropological Ecology (submitted papers)

Cultivated plants and culture: Hypotheses of the origin of bread wheat

Iida Kaori, The Graduate University for Advanced Studies, Japan

In this talk, I explore “origin hypotheses” of bread wheat proposed in the 20th century. Bread wheat as a major staple had attracted various speculations about its history based on scientific and cultural arguments. In the first half of the 20th century, the crop was often associated with civilization and “civilized races”, and was also assumed to have a relatively short history. In the 1920s, the Japanese plant geneticist Hitoshi Kihara criticized this idea of the recent origin because it implied, as he understood, that the crop entered the East only after the Western imperial nations approached the East. About 20 years later, an American team of botanists proposed immediately after the Second World War a similar hypothesis that bread wheat had arisen recently in the “European side” of the Caucasus, the great boundary between Asia and Europe, and claimed that East Asia in ancient time did not have bread wheat. Opposing their idea, Kihara proposed an alternative hypothesis that placed the origin within the great boundary in much older time and speculated that the birthplace served as the common resource for both Eastern and Western sides. Based on these hypotheses of the origin of wheat, I would like to discuss how cultural meanings attached to crops could affect discussions of the origin/history of the plants.

Crop diversity patterns as a mirror of communities' social organization: an illustration from the Tharaka people of Mount-Kenya region

Labeyrie Vanesse, Rono Bernard, Leclerc Christian, all at CIRAD UMR1334

The efficient conservation of crop genetic resources requires understanding crop populations' evolution processesin-situ, and especially the influence of farmers' management. Indeed, farmers' practices of seed exchanges and selection are involved in crop evolution and shape their diversity in subsistence farming systems. Farmers' practices are usually studied at the individual level while in most rural societies the social organization shapes the seed and information exchanges networks. The influence of communities' social organization on crop diversity patterns has thus been overlooked. This study investigates the relation between crop diversity patterns and the social organization of Tharaka farmers in Kenya, linking quantitative ecology approaches and ethnographic information. The assemblages of crop species and sorghum landraces, as well as the specific richness of cropping systems were analyzed regarding neighborhood-groups, clans and age-sets, which are three major Tharaka social institutions. The distribution of crop species and sorghum landraces was not random as crop richness and composition differed significantly between adjacent neighborhood-groups. The results for species were consistent with those obtained for sorghum landraces, confirming the relationship between Tharaka social organization and crop diversity. These results are discussed in relation with the influence of social organization on seed networks and selection processes in order to address the implications for the conservation of crop genetic resources.

Models of plant-human interaction and the characterization of the indigenous knower in ethnobiology

Méndez Diego, UAM-C, Mexico

Thirty years ago, Janis Alcorn's bench mark work, *Huastec Mayan Ethno-botany*, provided a model of plant-human interaction that profoundly influenced the field of ethno-botany; such a framework is still relevant today. Alcorn´s proposal situates the indigenous ecological knower in a physical environment, a cognized environment, a variegated agricultural and plantexploitation practice, and a social niche within a national (Mexican) class society. It truly is of an interdisciplinary nature, since it integrates agronomical, anthropological, botanical, ecological, and historical perspectives. My presentation explores, from a dialectical standpoint, the conceptual mappings and reconfigurations that such a model entails. The social characterization of the indigenous ecological knower in other ethno-biological literature is also discussed. Focus is mainly on reports dealing with traditional farmers and agro-ecosystems in Latin America. An argument is made that, beyond the fact of being indigenous, the social identity of the agriculturalist has been either circumvented or described under such general and timeless headings as "subsistence farmer" or "peasant". Few papers, like Alcorn´s, have sought a more thorough treatment, which is unfortunate since the social placement of the farmer may influence selection pressures affecting cultivars and associated flora in the anthropogenic environment.

Optimal Foraging Models and The Impact of Culture on Behavioral Variation

Vernon Kenneth, University of Utah, USA

Physical anthropologists recognize that modern hunter-gatherers (HG) are not "living fossils". They recognize that history and culture have played a large role in shaping modern variation in behavior, but insist that one can infer variation in past behavior based on modern variation. Critics argue that culture mediates between ecological and behavioral variation making any such inference impossible. This criticism has different senses based on the nature of the mediation. I argue that in some of these senses, at least, the impact of modern culture on HG behavior can be treated as an experimental intervention. In that sense, it does not limit evidence. In fact, it provides additional evidence. Using optimal foraging models, I explore various ways that culture mediates between behavioral and ecological variation and consider what sense the general objection has in each case. I conclude that reconstructing human evolution based on modern human behavioral ecology is enormously difficult, but not impossible. And, although modern HG groups are not "living fossils", investigating systematic variation in their behavioral responses to a changing ecology provides a wealth of information that can be used to reconstruct the history of our species.

Antimetabolites, Magic Bullets & New Ways to Diagnosis (submitted papers)

Using integrated history and philosophy to inform diagnostic medicine: The case of heart failure

Binney Nicholas, University of Exeter, UK

I will present a history of the diagnostic practices associated with heart failure, and use this history to show that many philosophical assumptions made by physicians are problematic. Historical work shows that the development of diagnostic practices associated with heart failure was a complex, iterative and historically contingent process. This process has produced several logically incompatible diagnostic practices which select different groups of patients as diseased, some of which are potentially useful today in different medical contexts. Despite this, many cardiologists express their concern that physicians in general practice frequently misdiagnose the disease. Physicians appear to expect that there is a single 'correct' method of diagnosis, which will classify patients optimally for any medical purpose. Cardiologists argue that physicians in general practice rely too much on the clinical signs and symptoms associated with the disease to make a diagnosis, and that echocardiographic measurements should be made as well. Some physicians, however, argue that heart failure is diagnosed accurately using symptoms and signs alone. All parties use empirical evidence to support their arguments. However, their arguments are problematic, and often self-contradictory. I will present an analysis of some of these arguments, pointing out how they are problematic, where they are self-contradictory, and how they are revealing of philosophical assumptions made by physicians. I will argue that the contradictions identified are the result of physicians' attempts to present these different practices as part of a single 'correct' version of heart failure. Overall I will argue that integrated historical and philosophical research can be used to inform medical practice.

The right drugs for the job: the use of antimetabolites in biological research (1940-1960)

Serviant-Fine Thibaut, ENS & Université Claude Bernard Lyon I, France

With the advent of the sulfa drugs in the mid-1930s came the so-called era of the wonder drugs, which raised considerable hopes that medicine could be revolutionized through the power of chemotherapy. In 1940, a young biochemist, Donald D. Woods, presented consistent proofs that sulfa drugs acted by interfering with an essential metabolite, a substance necessary for cell growth. This was the main starting point for the expansion of the theory of antimetabolites, which was rapidly thought of as providing a general mode of drug discovery. As such, it generated a lot of disillusion, although it also produced some lasting therapeutic successes.

In the meantime, the fields of biological and medical research were being "molecularized" through the understanding, visualization and manipulation of mechanisms situated within the cell. Some of the newly synthesized antimetabolites were used as biological research tools, to unravel metabolic pathways, identify essential metabolites, understand the biochemistry of nucleic acids, and produce detailed knowledge concerning the functioning of enzymes.

This paper analyses the interplay between research in fundamental biology and drug discovery exemplified by the antimetabolites. Thus, this case study seeks to connect the history of drugs and pharmacology with the history of biochemistry and molecular biology.

Theoretical Assumptions and Instrumental Strategies in Early Detection of Cancer

Le Roux Ronan, Cetcopra, Université Paris 1 Panthéon-Sorbonne, France

So-called "hypothesis-free" research strategies, relying on powerful instruments, have led to claim the "end of theory" as a new scientific age and brought considerable hope of identifying molecules with robust link to early-stage carcinogenesis and leading to specific clinical detection procedures. Unfortunately, the overall results have remained poor hitherto: almost no new biomarkers have been discovered following this method, while the translation from bench to bedside remains exceptional.

Following a twofold argument, I deny that molecular diagnostics is merely technology-driven:

- Poor epistemic constraint allows collaboration as well as competition among diagnostic strategies, thus controversies between antagonistic approaches. I focus on the 2003-2004 controversy about nascent clinical proteomics; it revealed antagonistic convictions as to defining a specific biological level that would display the frontier between health and disease, that is, as to the importance of genetic determinism in the vision of Man.
- Instead of questioning assumptions that led to the failure of most data-driven strategies, there is an overbid that still more sophisticated instruments will eventually enable the discovery of relevant molecular biomarkers (which existence is postulated).

These underlying assumptions are not a discursive artifact due either to a division of labor, either to fund-chasing rhetoric; they are rooted in deeper cultural representations. Then, I argue that technological development is not independent from these assumptions. On the one hand, indeed, technological hype may impinge on the popularity of research strategies, while, on the other hand, such popularity may reciprocally introduce non-epistemological criteria in the evaluation of technology.

Magic Bullets
Stegenga Jacob, University of Utah, USA

The metaphor of a magic bullet is often invoked as an explanation for the effectiveness of medical interventions or justification for the expected effectiveness of novel medical interventions. Examples include insulin moderating glucose levels, antidepressants moderating serotonin levels, and proton-pump inhibitors blocking ATPase. The magic bullet paradigm represents three related ideas regarding diseases and medical interventions: the monocausal disease model (macro-level symptoms constitutive of a disease are caused by the presence or absence of a single micro-level entity); intervention specificity (a therapy intervenes on, and only on, the single micro-level entity constitutive of the disease being treated); and micro-level effectiveness (a therapy eliminates the micro-level entity constitutive of the disease being treated, or adds the entity for diseases that are constituted by the absence of that entity). The magic bullet paradigm gained currency in the mid-twentieth century with the introduction of antibiotics. However, scientists have begun to recognize the complexity of many pathophysiological mechanisms, and philosophers have noted what such complexity entails. I argue that once we appreciate the complexity of mechanisms, the expectation of effectiveness ought to be mitigated, and concomitantly, we ought to expect many “side effects”. The simplistic notion that drugs can intervene on one or few micro-level targets and thereby bring about an effect which is both clinically significant and symptomatically specific is, for many of our contemporary medical interventions, false. Nevertheless, the magic bullet paradigm is a good normative standard for medical interventions, and the low effectiveness of many contemporary medical interventions can be understood in virtue of the fact that these interventions and their target diseases do not satisfy the three principles of the magic bullet paradigm.

Asking the Hidden Questions Raised by Stem Cells: History, Philosophy, and Biology

What’s Surprising about Stem Cell Research?
Maienschein Jane, Arizona State University, USA

Even before 1998 brought human embryonic stem cell research and expanded public awareness, stem cell research has generated surprising observations and has challenged cherished assumptions. This talk will explore historical examples of such challenges and will lay out key steps in stem cell biology before 1998. At first, discoveries challenged understanding of how development and differentiation work. Then new observations undercut core assumptions about cell determination. And each new major research innovation with stem cells adds to other research on embryos that challenges social assumptions about what makes up an individual developing organism. The history illuminates our understanding today and calls for a different and more complex understanding of what an individual developing embryo really is.

Stem cells in an evolutionary perspective

Vervoort Michel, UMR7592, Université Paris Diderot, France

Most discussions about stem cells are usually fuelled by data that come from a few model systems, in particular mammals, and focus on a few stem cell types such as those found in adult tissues (multipotent tissue-specific stem cells) and embryonic stem cells (ES cells). In my talk, I will present experimental evidence of the widespread existence of pluripotent adult somatic stem cells in many non vertebrate lineages, including cnidarians, ctenophores, flatworm, and annelids. I will discuss the importance of these adult stem cells for key biological features of these organisms, such as continuous growth, asexual reproduction, high phenotypic plasticity, and extensive regenerative capabilities. These stem cells found in distantly-related species, show striking similarities in their molecular signatures, opening the possibility to define a conserved “stemness” or “pluripotency” repertoire in animals. In addition, these somatic pluripotent stem cells share many molecules with primordial germ cells, suggesting an evolutionary link between these two cell types. I will discuss these similarities in the light of recently proposed models about stem and germ cell evolution. Finally, I will point out the interest of these evolutionary data for our general understanding of the stem cell concept.

Stem cell ontology: why does it matter?

Laplane Lucie, IrePh, IHPST, URSHS (IGR), Université Paris-Ouest Nanterre, France

Stemness (ability to self-renew and potency to differentiate) is the property by which stem cells are defined. Since few years, there is a debate on the kind of property “stemness” really is, mainly between the proponents of the “entity” and “State” views. According to the formers, stem cells are entities belonging to a particular kind, or type of cells, defined by the stemness properties. According to the latters, stemness describes a cell state rather than a category. The main concern of my talk will be to evaluate the consequences of the “entity” and “state” visions of stem cells for therapeutic strategies against cancers. This concern is related to the recent emergence of the “cancer stem cell” (CSC) theory. According to this theory: (1) cancers are initiated, maintained and propagated by CSCs exclusively, (2) CSC can escape classical therapies and lead to relapses, and (3) killing the CSC would be necessary and sufficient to cure cancer. We will show that (3) is true only in the "entity" framework. The state views are suggesting other therapeutic strategies against cancers. This analysis will highlight the critical importance of determining the ontological status of stem cells.

Leaping from Waddington's landscape: premature theorizing in stem cell biology

Fagan Melinda, Rice University, USA

Several scientists have recently argued that stem cells should be understood, not as a kind of cell with stable traits, but in terms of dynamical systems models and concepts such as state, attractor, noise, and oscillation (e.g., Huang 2012, Furusawa and Kaneko 2012, Selvarajoo and Tomita 2013). This argument begins with the idea that stem cell experiments have outrun our understanding of stem cell capacities and behavior. The point is well-taken. But dynamicalsystems theorists fail to consider what kind of understanding is needed - i.e., the kind of explanation sought by stem cell biologists. Instead, they assume a mathematical theory will suffice. I argue that, according to prevailing standards in stem cell research, the dynamicalsystems account does not offer an explanation, but merely re-describes the familiar stem cell concept. This description, however, can play an explanatory role. To see this, a more measured approach is needed, which considers (i) results of stem cell experiments, (ii) their relation to explanatory models of cell development, and (iii) identifies deficiencies in those models. I conclude by discussing general implications of this result for ideas about theory and explanation in experimental sciences.

Biodiversity, Conservation, and Sustainable Development (submitted papers)

Save the planet: eliminate biodiversity

Santana Carlos, University of Pennsylvania, USA

My claim is that biodiversity should not play a central role in conservation science. In conservation biology, biodiversity is generally held to be a primary target of conservation and the chief comparative measure of conservation value and success. Nevertheless, it is notoriously difficult to operationalize biodiversity in both a theoretically satisfying and empirically practical way.

Recent work in the philosophy of biology has attempted to both clarify and defend the use of the biodiversity concept in conservation science. I argue against these views, and give reasons to think that the biodiversity concept is actually a poor fit for the role we want it to play in conservation biology on both empirical and conceptual grounds. Against pluralists such as Maclaurin and Sterelny, who hold that biodiversity consists of distinct but correlated properties of natural systems, I argue that the supposed correlations between these properties are not tight enough to warrant treating and measuring them as a bundle. I additionally argue that deflationary theories of biodiversity such as Sarkar's don't go far enough, since a large proportion of what we value in the environment falls outside the conceptual bounds of “biodiversity”. I suggest that in current scientific practice biodiversity is generally an unnecessary placeholder for biological value of all sorts, and that we are better off eliminating it from conservation biology (or at least drastically reducing its role) in favor of clarifying what exactly composes biological value and forming direct measures of those values.

From “Anthropological Natural Monuments” to “Ecosystem People”: Hunter Gatherers and the Discourse of International Nature Conservation

De Bont Raf, Maastricht University, UK

Scientists involved in cross-border nature conservation have historically shown a strong interest for hunter gatherer cultures. In the 1910s, one of the pioneers of international nature protection, the Swiss zoologist Paul Sarasin, described contemporary groups of hunter gatherers as true “anthropological natural monuments”. He believed that, like rare animals and plants, they should be “preserved” in “integral reserves”. In the following decades, such ideas would become increasingly marginalized among conservationists, but the fascination for “primitive people” remained. In the 1970s, the American Raymond Dasmann, then a leading ecologist at the International Union for the Conservation of Nature, described hunter gatherers as “ecosystem people” of whom he hailed the sustainable societies. No longer seen as objects of preservation they were presented as models for westerners, exemplifying man's “old partnership with nature”. From the time of Sarasin to that of Dasmann, the international conservation movement engaged in discussions about which parts of global nature counted as valuable, how these parts of nature should be administered, and who should be allowed access to them. My paper will explore the role that hunter gatherers were attributed in these discussions - and this from the earliest attempts to establish international conservation institutions in the 1910s to their heyday in the 1970s "environmental age". The paper will look into the intellectual origins of the prevalent discourses on hunter gatherers, how these discourses shifted through time and the ways in which they inspired concrete policies.

The Scientific and Technological Knowledge as a Common Good: Towards a "Sustainable Socially Justifiable Development"

Almeyra Carlo Marcello, UNAM, Mexico

The current environmental, social, political and economic crisis forces the scientific communities to reflect on the role they play in the maintenance of the dominant development model. From the niche construction theory, we propose a need for a shift of paradigm from reductionism and positivism towards a holistic view that takes into account the complexity of the systems being studied and its relations with society. It is no more time to see the object of study distinct from the subject: to explain society as an ecological community, with their different contexts and from a transgenerational point of view, allows a deeper understanding of the problems affecting our time and lets looking for a "sustainable socially justifiable development". In our case studies we present institutions that consent participatory government, democratization of science and technology and that facilitate open access to scientific and technological knowledge. Understanding scientific knowledge as a common good (interpreted as the common heritage of mankind), governed by the value in use, within a relational structure and qualitatively responsible consumption, allows it to be disseminated in a socially fairest way, with improvements in the citizen's standard of living (particularly in the case of third world countries) and opposing serious and multiple effects of anthropogenic activities.

Biological Theories and Theories in Medicine

Does pathophysiology contain a theory of disease?

Lemoine Maël, University of Tours & Inserm, France

Medicine stands at the intersection of many sciences, of which pathophysiology seems to be the only one to be both fully biological and specifically medical. Roughly speaking, it is the science of diseases, as biological dysfunctions. The purpose of this contribution is to explicate this notion through three questions. First, it is obvious that 'dysfunction' does not refer to every effect that is not a function (Davies 2000): accidental effects, side effects, statistical anomalies are neither functions nor dysfunctions. A typology of all non-functional effects, as they are encountered in experimental physiology, is proposed. Second, it is noteworthy that organisms are not dysfunctional in all possible ways: pathophysiology is not a conceptual, but a factual science, that of actual dysfunctions, which are natural phenomena of their own. The natural consequence seems to be the theoretical independence of pathophysiology from physiology (Nervi 2010). The third question is that of the existence of a general notion of disease. Instead of using conceptual analysis of the usage of the term in medical sciences (Boorse 1977), a more theoretical approach is investigated. Three views on what a biological dysfunction consists in are examined. They are respectively based on theoretical biology, genomics and microbiology. Together, they give a global idea of what a unified theoretical framework of pathophysiology could look like.

DSM-5 and the Removal of the Multiaxial System for Psychiatric Diagnosis: What Is at Stake?

Demazeux Steeves, Institut Faire Faces, Université de Picardie, France

Alongside the adoption of an atheoretical (i.e. purely descriptive) clinical approach, the introduction of a multiaxial format for psychiatric diagnosis was a key change in the *Diagnostic and Statistical Manual of Mental Disorders*, third edition (APA, DSM-III, 1980). It was said to represent a "paradigm shift" (Millon, 1983): by providing the clinician with a multivariable and comprehensive picture of the whole pathological state, from its biological to its psychological and social aspects, it aimed at departing from the traditional medical disease model. Unfortunately, the multiaxial system failed its mission: psychosocial stressors (Axes IV and V) were not fully recognized inside the classification, whereas the articulation between the Clinical Syndromes assessed with Axis I and the Personality Disorders assessed with Axis II was far from clear. Moreover, excessive diagnostic comorbidity has been found between Axis I and Axis II categories, as well as between categories within each Axis, and this has led to further theoretical questioning in the past decades.

In this presentation, I will discuss the reasons and motivations behind the decision to remove the multiaxial system for diagnosis from the DSM-5, which will be published in May 2013. I will argue that this decision can be seen as a desperate attempt to mask the general failure of the atheoretical perspective adopted by the DSM since the 1980s. More fundamentally, I will argue that this failure reveals a deep nosological crisis in contemporary psychiatry.

Network medicine as a genetic theory of disease

Darrason Marie, Université Paris 1 & IHPST, France

If some authors challenge the very existence (Severinsen, 2011) or the usefulness of theories in medicine (Kincaid, 2008), others (Thagard 1999, 2006) acknowledge their diversity but consider that there is a strong delineation between ancient medical theories such as the humoral theory of disease and our modern medical theory. While ancient theories would rely on a general definition of diseases as imbalances, our modern medical theory would be nothing more than a sum of heterogeneous theories, each of them being specific to a class of diseases (such as the germ theory for infectious diseases). We beg to differ and in this contribution, our aim will be to demonstrate that such a general *theory of disease* by opposition to a mere *theory of diseases* is not only possible but also desirable. We will achieve so by presenting network medicine that is recently born from the synthesis between genomic medicine, systems biology and network theory (Barabasi, 2011) as a genetic theory of diseases. Indeed network medicine (a) relies on a general and interactionist definition of disease, based on the identification of functional modules (Lesne et al., 2010) (b) explains new classes of facts such as comorbidity and syndrome families through the common genetic origin of diseases (c) explains differently the distinction between monogenic and polygenic diseases (d) questions the way we classify diseases and (e) has a heuristic dimension since it predicts the existence of new diseases genes and suggests new therapeutic targets.

Biomobilites - Travel, movement and relationality in the emergence of contemporary biological materials and knowledges

The biomobile brain – on the pragmatics and politics of travelling between the neural and social sciences

Fitzgerald Des, Interacting Minds Centre, University of Aarhus, Finland

This paper argues that the mobility of neurobiological knowledge is one of the most important features of the new brain sciences. While there has been much attention recently to the potential "neurobiologization" of the methods and approaches of the social sciences - with scholars arguing passionately both for and against such a move - this papers offers a new perspective on this debate, by focusing on *how* it is, in fact, that neurobiological knowledge may be so mobilized.

The paper is empirically rooted in an autoethnographic account of the author's participation in an interdisciplinary brain-imaging experiment that worked to entangle sociological and neurobiological perspectives. Side-stepping arguments for and against such entanglement, the paper argues that what this experiment reveals, more than anything else, is (1) the sheer mobility of neurobiological methods and concepts, and (2) the pragmatics through which that mobility is achieved But the paper uses this ground to analyze the epistemological politics threaded through such movement - as neurobiological knowledge becomes mobilized in ever-greater amounts of intellectual space.

In this panel, the term 'biomobilities' calls attention to the ways in which contemporary biologies may also be defined by their mobility. The term describes not only the physical journeys of biological material, but also the epistemic travels of biological explanation. This paper illuminates these dynamics through an analysis of the biomobility of neurobiological knowledge especially. At its heart is thus an argument that empirical attention to movement and mobility opens up an important new perspective for the social study of biology.

Cutting off the circulation: ordering and managing excessive evidence

Clinch Megan, The Open University, UK

During the last two decades a multitude of social scientific studies have demonstrated how diseases are accomplished through an emergent, and often pragmatic, system socio-technical relations. Developing this concern with the relations that constitute and sustain categories of disease, this paper will address what happens when they are excessive and cause the process of diagnosis and disease management to break down.

Based on an ethnographic account of the diagnosis and treatment of thyroid disease within the United Kingdom the paper will attempt to illustrate a situation where the are *too many* discordant relations for diagnostic categories and disease management systems to bear. Consequently, it will be described how the relations that constitute thyroid disease are, under particular conditions, cut in order to manage the excessive forms of evidence and possible accounts they produce.

The latter half of the paper will explore the sites and situations where such cuts are made and attempt to develop a framework through which visible and disappeared or “ghost” relations, can be observed. In doing so the paper seeks to trace the “biomobility” of thyroid disease, and other similar contested diseases, by tracing the logics that guide the cutting of relations and the consequent emergence of broadly intelligible and unintelligible biological assemblages.

Before and After the Return: Repatriating Indigenous DNA

Hinterberger Amy, University of Oxford, UK

Recent work in the social studies of genomics has pointed to increased sharing practices and collaboration as a way to develop more ethical approaches to the interpretation and ownership of genetic samples and data. In this paper, I explore the repatriation of 883 vials of blood and accompanying documents from the University of Oxford back to the Nuu-Chah-Nulth First Nations in Canada twenty years after they were collected. By examining the travels and relations sustaining these materials, I offer an analysis of the cultural and scientific work that repatriable materials do before and after their return. In extending an analysis of repatriation to recently collected DNA for biomedical research, my first aim is to attend to the institutional relations that create the conditions for transatlantic journey and return. While the international circulation of biological samples and data from indigenous peoples in North America is not unusual, the return of it to the source community is. Moments of return reverberate beyond the case at hand and become enfolded and reactivated in current debates over ethics, identity and ownership. The second aim of the paper is to query the current thrust in contemporary genomics which seeks to bring biological materials under the domain of property in the name of ethics.

Can Human sciences be applied to animal societies?

Introduction
Kohler Florent, CREDA UMR 7227 CNRS-Paris 3, France

Culturally Constructed Concepts in Animals
Goodrich Grant, The citadel, USA

The last couple of decades have seen an increased interest in the study of culture in animals. Most studies of culture in animals have been focused on the cultural transmission of behaviors. For the most part, they have not considered whether or how culture influences the concepts that the animals have. Researchers studying animal concepts have also (mostly) not asked whether animals' concepts are socially constructed or otherwise influenced by the animal's culture. In this talk I will argue for the heuristic attribution of socially/culturally constructed concepts to animals, and I will consider how supposing that some animals' concepts are socially constructed can inform both the study of culture in animals and also the study of animal concepts.

Japanese wisdom? Natural cultures and cultural natures
Wels Harry, VU University Amsterdam, Netherlands

Japanese society and academics from various disciplines have displayed a particular interest in the analytical and explanatory power of the concept of culture. In the eighties of the previous century Japanese scholars were the first to “apply” the concept of culture to organisational and economical performance, in order to explain the economic successes of Japanese businesses. Japanese primatologists were also among the first to recognise and describe culture in monkeys. Japanese were to become the “sushi masters” (cf. de Waal 2010) in “culture talk” (cf. Mamdani 2005).

In both instances Western anthropologists have followed suit: first by embracing the notion of organisational culture, and now by cautiously, and maybe sometimes even reluctantly, joining the stage of the debates on animal cultures. This paper is a reflection on “Japanese wisdom” and in its wake tries to answer the question what an anthropological interpretation of culture can add to studying animals.

Social networks and animal behavior
Allen Colin, Indiana University, USA

Scientists studying animal sociality have not ignored the growth of “network science”. For example, Barocas et al. (2011) argue for a link between centrality in a social network and longevity in hyraxes, and Lea et al. (2010) argue that position in agonistic networks may, counterintuitively, provide heritable fitness benefits to marmots who are the recipients of aggression rather than to those who are initiators of it. To what extent, if at all, does network science move the study of animal sociality simultaneously towards the human sciences and towards the exact sciences?

Cancer and Viruses (submitted papers)

Cancers, viruses, and the contrastive model of disease
Broadbent Alex, University of Johannesburg & University of Cambridge (HPS), UK

If there is any value in the idea that disease is something other than the mere absence of health then that value must lie in the way that diseases are defined. Elsewhere I have identified and criticised two distinct trends in thinking about disease definition: “monocausal” and “multifactorial” models of disease. Instead I have endorsed a "contrastive" model of disease, which is intended to retain the benefits of the monocausal model without the implausible commitment to classification in terms of just one cause (Broadbent 2009; Broadbent 2013, Ch 10).

An obvious difficulty for the contrastive account is that some kinds of ill health, such as instances of particular cancers, seem to be fruitfully treated as belonging together. Yet on the contrastive account they cannot be called instances of a disease unless a classificatory constellation of causes is known or at least suspected. (Of course one might prefer to mark the distinction with a word other than "disease"; but my hope is to get at an important distinction without getting tangled in semantic disputes.) This raises an objection of irrelevance: the objection would be that the contrastive account of disease lays down distinctions between disease and non-disease that are irrelevant both to clinical practice and to scientific understanding.

In this paper I get to grips with the irrelevance objection to the contrastive model, using the cancer-virus link as a focus point.

Political Viruses: RNA Tumor Viruses and the War on Cancer

Scheffler Robin, Yale University, USA

The passage of the National Cancer Act (NCA) of 1971, colloquially known as the “War on Cancer,” is often regarded as a notorious example of political enthusiasm outstripping scientific evidence. A different view emerges if we examine the enthusiasm surrounding one of the four major areas of research targeted by the NCA: cancer viruses. During the late 1960s it appeared that the field was on the verge of discovering a human cancer virus and developing a vaccine. The creation of knowledge about these viruses provided common political ground between a community of molecular biologists and lay advocates of the creation of an aggressive, “moonshot,” cancer research program.

During the discussion of the NCA, the nature of these cancer viruses was therefore the target of both scientific and public controversy. I juxtapose the public and scientific reception of two announcements in 1970 concerning RNA tumor viruses, reverse transcriptase and the ESP-1 particle. One of the discoverers of ESP-1, Leon Dmochowksi, became a vocal advocate on behalf of the NCA while the discovery of reverse transcriptase was enlisted as an example against state direction of biological research. While ESP-1 was later deemed a laboratory artifact and reverse transcriptase research earned a Nobel Prize, both illustrate how the status of basic questions of RNA tumor virology became entangled with heated debates over the organization of patronage for biological research and the appropriate relationship between molecular biology and medicine.

The virus, the prisoners, and the past: Historical ontology and the craft of history through the case of cancer virus

Stark Laura, Vanderbilt University, USA

During the 1960s, the US National Institutes of Health moved federal prisoners from penitentiaries across the country to the NIH main campus in Bethesda, Maryland to serve in clinical studies of viruses, including simian virus-40 (SV40). Federal researchers at the NIH hospital were interested in SV40 because it was known to cause cancer in animals, and yet it was unclear how the virus affected humans. Millions of Americans, however, had received polio vaccines between 1954 and 1961 that contained SV40. Thus, in the early 1960s, prisoners in the wards of Dr. Vernon Knight, clinical director of NIH's National Institute of Allergy and Infectious Diseases, were used in studies of SV40.

This paper has two aims. First, the paper provides a comprehensive history of the NIH prisoner program by reviewing the studies of SV40 on inmates moved to Bethesda. To do so, the paper draws in published primary sources and unprocessed manuscripts from the public records of the US National Institutes of Health. Second, it connects the history of cancer-virus studies to the history of clinical research, which historians have often treated separately. The prisoner program at NIH helps to flesh out what scientists came to learn, overlook, and imagine about cancer viruses through federal research programs. In so doing, the paper links themes in the philosophy of science, particularly the ontology of natural kinds, to the practice of history writing.

Challenges for Molecular Biology (submitted papers)

Prevalence-knowledge and the changing store of molecular biology

Germain Pierre-Luc, European School of Molecular Medicine, Università degli studi di Milano, Italy

One can distinguish two kinds of generalizations in biology (Shaffner 1994; Waters 1998): the first concerns causal regularities (same cause, same effect), while the second, which I will call "prevalence-knowledge", has been described as the scope of kinds over which such regularities are valid. The contemporary focus on mechanisms deals with causal regularities, but leaves prevalence-knowledge largely unanalysed: with the exception of evolutionary studies, knowledge about the prevalence of mechanisms is not perceived as relevant. I object to this, and argue that prevalence-knowledge is the object of major scientific transformations and plays an important role in scientific inference and discovery.

Prevalence-knowledge has mostly been discussed in terms of inter-species generalizations, which however constitute only a subset of it. My paper therefore focuses on intra-species/organism generalizations, or prevalence-knowledge concerning schemata, abstract entities and their mapping to activites. Such knowledge is critical in bioinformatics and "omics", where generalization of basic organizational schemes is methodologically necessary. Indeed, as I show through a discussion of the ENCODE project, this knowledge is now explicitly sought in and for itself. However, I argue that it has played the same role, albeit more implicitly, throughout the history of molecular biology. Elaborating on Darden's (2006) notion of the "store" of a scientific field, I propose a way of integrating prevalence knowledge in a mechanism-based understanding of molecular biology.

The central dogma and its implications for gene-centrism revisited: from DNA-centrism to NA-centrism

De Tiège Alexis, Ghent University, Belgium

Both the "Weismann barrier" and Francis Crick's "central dogma" of molecular biology nourished the gene-centric paradigm of life, i.e. the conception of the gene/genome as a "central source" from which hereditary information unidirectionally "flows" or "radiates" into cellular biochemistry and development and not the other way around. Today, due to advances in molecular genetics and epigenetics such as the discovery of complex post-genomic and epigenetic processes in which genes are causally integrated, many theorists argue that gene-centrism is getting falsified. Here, we explore the causal implications of the following four, to the central dogma related issues: (i) widespread reverse transcription (arguing for a shift from DNA-genome to "Nagenome"); (ii) the absence of a mechanism of reverse translation (arguing in favour of the "structural primacy" of NA over protein in cellular biochemistry); (iii) pervasive transcription (arguing in favour of the "behavioural-functional primacy" of NA over protein in cellular biochemistry); and (iv) the fact that functional (post-genomic and epigenetic) biochemistry can only edit and not integrally recode structural genetic sequence (arguing for a "sequence-centric" perspective on cellular biochemistry). We conclude – in spite of the embeddedness of genes/genomes into the complex biochemical (post-genomic and epigenetic) dynamics of the cell – in favour of a gene-centric conception of cellular biochemistry, i.e. biochemistry at the sub-cellular level, although a shift from traditional narrow “DNA-centrism” to the broader “NA-centrism” seems mandatory. We will also ask whether this conclusion can be extended to the cell as a whole, and further to the organismal and ecological level.

The gene after encode: a Wittgensteinian approach

Ratti Emanuele & Boem Federico, European School of Molecular Medicine, Italy

The notion of “gene” has become a classical topic in philosophy of biology. Most of the philosophical attempts to deal with the notion of gene have been devoted to provide a unitary (or binary) account of what a gene is. We propose a different approach, by using the wittgensteinian notion of “family resemblance concept” to address the issues coming from the ENCODE project. First, we deconstruct any attempt to provide a definition, or a group of definitions that intersect the most recent outcomes of ENCODE. Thus we re-focus our question considering not what a gene is (the ontological question) but rather how the term “gene” is used and, as a consequence, what kind of term is “gene”. By taking into account also some features of “gene” (e.g “gene has blurred edges” or “the distinction between Gene-P and Gene-D”) discussed in the literature we consider the gene as a cluster of characteristics at the epistemic level. Moreover, due to its semantic flexibility, it is possible to easily draw a line, as Wittgenstein claims, for practical purposes. As argued for species by Pigliucci, we suggest that “gene” lies in the semantic intersection of all “practical” definition used in biology. We finally propose to change the focus of philosophical analysis regarding this field privileging the notion of function rather than that of structure.

Can Ecology Inform Molecular Biology?

Nathan Marco, University of Denver, USA

Molecular biologists often borrow ecological concepts to describe the complexities of molecular interactions within cells and embryos. For example, individual molecules are sometimes said to be part of ecosystems that integrate them in a complex network of relations with many other entities (Gilbert, 2006). Similarly, cytological gears are frequently described as occupying – and sometimes engineering - their own niches (Gilbert and Epel, 2009). The aim of this article is to scrutinize the application of these ecological metaphors in the molecular sciences, a practice that, despite its longstanding history, has seldom been discussed in detail. The first part of the essay argues that the cellular milieu is analogous to the biosphere in important and surprising respects. I begin by drawing methodological parallels in the individuation of molecular and ecological units. Next, I argue that the cytological machinery instantiates characteristic ecological relations, such as predation, competition, mutualism, and density-dependent effects. Finally, I spell out some structural parallels between ecological environments and cellular modules metaphorically called ‘ecosystems.’ In the second part, I explore some ways in which ecological concepts can inform theoretical and experimental developments in the actual practice of molecular biologists. My first conclusion is negative. If the purpose of these metaphors is simply to debunk the obsolete view that molecular mechanisms and processes are rigid, self-regulated, deterministic gears, then there is no real reason to appeal to ecosystems; the simpler notion of a system will do just as well. At the same time, I argue that ecological notions play an important role in conceptualizing external (environmental) influences on the ontogeny of the phenotype: ecological models capture the ‘openness’ of the cellular environment.

Charles Darwin and the Scientific Revolution

Charles Darwin’s Particular Theory of Evolution

Delisle Richard, University of Lethbridge, Canada

For obvious reasons, Darwinian scholars have often focused on the dynamics at the heart of Charles Darwin's theory of biological evolution or change. Yet, Darwin's theory, view, and approach also appeal to numerous explanatory components more properly congenial to a static worldview: (1) living matter is inert (not active); (2) life as a whole is seen more as a mechanism than as an organism; (3) because life is passive an external force (natural selection) is required to put it in motion; (4) nature is structured around definite and limited adaptives places in the economy of nature, hence the numerous instances of extinctions; (5) truly directional or lineal evolution is denied and replaced by "horizontal" (side-way) evolution as seen in evolutionary divergences; (6) evolution occurs only when the milieu (biotic/abiotic) is changing, the natural state of living matter being rest, etc, etc. From this list, one wonders if Darwin's Darwinism is as universal as it is often depicted to be. Clearly, Darwin's route to his theory of biological change was anything but straightforward. After all, why not simply postulate (like Lamarck did) the existence of a vital force pushing life forward? This paper is devoted to exploring some of the explanatory components of Darwin's particular theory. More than just being the heir of the British tradition of natural theology, Darwin's worldview was apparently also strongly influenced by a static Newtonianism, both as an epistemological model and a scientific ideology.

Darwin and the Mechanical Philosophy: Likening Nature to Artifice

Inkpen Andrew, University of British Columbia (UBC), Canada

Many scholars of the early modern period explain the rise of modern science, and in particular the rise of experimentalism, during the scientific revolution as intimately tied to the collapse of an ancient distinction between nature and artifice. Pre-modern natural philosophy, it is claimed, was the study of nature on its own terms or in its due course. The innovation of modern science was to study nature, as Francis Bacon put it, “constrained, moulded, translated, and made as it were new by art and the hand of man.” This innovation, however, presupposed a new understanding of nature itself: nature as artifice, as like a highly wrought machine. For instance, in order for his experimental apparatus, the air-pump, to say anything about nature, Robert Boyle had to argue that what happened in the air-pump's chamber could stand for what happened in nature. This may seem like a fairly uncontroversial inference to us now but it was the product of years of debate about how we learn about the natural world and what it?nature?is like. The question was, can artifice stand for nature? Boyle's answer was yes. Interestingly, as with the scientific revolution, the Darwinian revolution has involved a significant amount of discussion pertinent to the relation between artifice and nature; especially, for example, with regards to the relation between domestication?or artificial selection?and natural selection. In this paper I explore the ways in which nature and artifice are likened in these two revolutions.

Darwin's Experimentalism

Richards Richard, University of Alabama, USA

It is well known that Darwin conducted experiments at his home in Down on earthworms and plants, and then published his results in “On the Movements and Habits of Climbing Plants” (1865), “The Power of Movement in Plants” (1880), and “The Formation of Vegetable Mould “ (1881). But few seem to regard these experiments as significant to the development of Darwin's thinking, and for obvious reasons. The experiments occurred long after the first statements of his theory in 1842 and 1844, and its publication in *the Origin*. In reading his major works, *the Origin* in particular, there seem to be little significance placed on experiments like those he would later conduct. In many ways Darwin's experiments seem to be mere afterthoughts – trivial albeit informative exercises.

Darwin's experimentalism, however, extends beyond the experiments that he conducted. In the preface to his *Origin*, Darwin tells us that he cannot give the facts on which his conclusions are based. A decade later he gives these facts in his (1868), facts based on that "grand experiment," domestic breeding. Here Darwin gives experimental evidence for first for the existence and force of natural selection, and second the laws of organic nature. That Darwin did not perform these experiments himself does not diminish their significance to the experimental nature of his approach.

Classification and Taxonomy (submitted papers)

Type-specimens and the (historical) metaphysics of taxonomic practice

Witteveen Joeri, University of Cambridge, UK

Type-specimens have recently come under close scrutiny by historians and philosophers of science. Historians have highlighted the remarkable shift in meaning and function type-specimens underwent in the nineteenth century, which has culminated in their rather "puzzling, even paradoxical" metaphysical status in today's taxonomic practice (Daston, 2004). Philosophers who have -independently- also zoomed in on the metaphysical status of contemporary typespecimens have been reaching similar conclusions (Haber, 2012; Levine, 2001). From both sides it is argued that type-specimens fulfill a role in current taxonomic practice that cannot be captured by standard philosophical accounts of reference and designation, for various reasons.

I argue that this conclusion is false. There is nothing puzzling, let alone mysterious, about the current metaphysical status of type-specimens or about how they acquired this status. On the historical side, I show that the apparent paradox arises by viewing the history of type-specimens through the lens of a too restrictive historical-epistemological framework (Daston & Galison, 2007). Revising the history of type-specimens, shows reciprocally how that framework can be improved. On the philosophical side, I argue that the latest contribution to the debate about whether or not types necessarily belong to their species, by (Haber, 2012), is specious. Typespecimens do not present a complication for the theory of causal reference and rigid designation, as Haber argues. To the contrary, I will show that type-specimens actually satisfy this theory better than the reputed exemplars from the literature: H2O and the standard meter bar. In short, type-specimens can illuminate both historical and philosophical schemes.

Complex Objects and Integrative Pluralism

Havstad Joyce, University of California, USA

In *Unsimple Truths* (2009), Sandra D. Mitchell argues that studying complex systems in the biological and other sciences requires a new approach, called "integrative pluralism", to scientific explanation, generalization, models, and laws. In this paper I characterize proteins as complex objects (rather than systems), and diagnose the multiplicity of protein classification systems as arising from their complexity. In doing so, I extend Mitchell's view of complex systems to include complex objects, and adapt her approach of integrative pluralism to apply to classification in addition to her other targets.

Mitchell's complex systems are characterized by multilevel organization, multicomponent causal interaction, contextual plasticity, and evolved contingency. I argue that certain objects display these (or closely related) features as well, and that these objects can therefore also be designated as complex. Using proteins as a paradigmatic case, I show how what I call entity complexity arises from their multilevel organization, multipart causal interaction, and contextual plasticity.

As a result of their complexity, there are many different ways of classifying proteins. Looking carefully at the proteins within one particular superfamily, I show how their evolved contingency both generates a plurality of classifications even within this one superfamily and inhibits the total integration of these classification systems with one another. But some integration of the systems does occur during scientific investigation of the proteins within the superfamily. So, I develop an account of this partial integration and show that it is a species of Mitchell's integrative pluralism.

Clustering Humans

The Israeli population-geneticists' conceptualisation of "Jewish Difference" – 1945-2012

Gissis Snait, Tel Aviv University, Israel

The ways biological boundaries are delineated to create and maintain dichotomous individual and collective identities apart, such as "Jew" and "non Jew", are intertwined with the work of culture and its practices. To understand the endeavor of the three generations of Israeli population geneticists who have worked on the genetics of Jews since the establishment of the state of Israel, and in order to conceptualise the mutual constituting and entanglement between science (genetics, genomics and medicine), culture and state policies and practices, I have surveyed and analysed all the relevant genetics papers written by Israelis in the issues of the major periodicals (both in Hebrew and in English, local and international) in the period from 1946 until 2012 . This corpus of scientific work has been deeply affected by the changing tools and technologies of genetics during that period, by advances in genomics and the changing notions of clustering humans. In particular, I looked at the evolutionary questions and explanatory mechanisms that the Israeli population geneticists and medical geneticists used in constructing their work: questions on genetic diversity, differences and genetic similarities, which particular genetic diseases were investigated among which sub-populations, controversies on the use of genetic evolutionary mechanisms, the role of non-genetic narrative components and their entanglement into a population evolutionary narrative.I shall argue that while maintaining biological boundaries, these investigations by Israeli population geneticists, and their transformations, are part and parcel of the work of culture and state.

Genetic Clustering and the Definition of 'Race'

Hochman Adam, The University of Sydney, Australia

Genetic clustering studies have shown that despite the small proportion of genetic variation separating continental populations, it is possible to assign some (geographically separated and not recently admixed) individuals to their (or their ancestors') continents of origin, based on genetic data alone. Is 'race' vindicated? In this talk I argue against such a conclusion. I begin by discussing three problems for a racial reading of clustering studies: (1) the grain of resolution problem, (2) the non-concordance between clustering studies, and (3) the clinal (gradual) distribution of genetic structure and diversity. Then I consider some arguments for racial naturalism, and I find a surprising amount of agreement between myself and my 'opponents'. It turns out that much of the disagreement in the race debate turns on the definition of race adopted by its participants. As a consequence the best way to settle the race debate may be to settle the semantics. I suggest that this should be done in a way that is both historically sensitive and consonant with how race is understood outside of biology. The difficulty of such an endeavour has caused many to argue that race has no definition. I propose that we can indeed define race, but only if we separate that definition from the question of how race is constructed. On my proposed – and, I hope, well-grounded – definition of race, genetic clustering studies do not support racial naturalism. I propose that our racial categories are best understood through an approach I call 'interactive constructionism'.

Human Genetic Clustering and Ontological Inference
Spencer Quayshawn, University of San Francisco, USA

Many scholars have expressed enthusiasm about various ontological inferences that can be made from recent human genetic clustering analyses done by population geneticists. Scholars have claimed that we can legitimately infer human genetic diversity, genetic structure, genetic distance, phylogenetic structure, migration history, population structure, and even subspecies and racial groups. Although there is a lot to say about each of the different sorts of ontological inferences scholars make from human genetic clustering analyses, for the sake of time, my talk will be limited to one, especially controversial, ontological inference: the inference to the existence of racial groups.

The purpose of my talk is twofold. First, I will disambiguate two different senses of what it could mean to "infer the existence of racial groups" from human genetic clustering results. Particularly, I will emphasize that one could be attempting to infer biological races or the biological existence of folk races. Second, I will clarify the sorts of auxiliary assumptions – semantic, metaphysical, mathematical, methodological, and biological – that one would need to adopt in order to legitimately infer the existence of racial groups from human genetic clustering results. I will use the current U.S. racial scheme as an example. The hope is that by making these clarifications, we will be in a better position to understand what one can and cannot legitimately infer about race from human genetic clustering results.

Human Genetic Diversity: Fact and Fallacy
Gannett Lisa, Saint Mary's University, Canada

R. C. Lewontin's 1972 paper "The Apportionment of Human Diversity" sought to undermine racial classification by showing that only 6.3% of total human genetic diversity is found among races (with 85.4% found within populations and 8.3% found among populations within races). These data have been widely used to contest the biological significance of race. In 2003, A. W. F. Edwards published a paper titled "Human Genetic Diversity: Lewontin's Fallacy," which argues that Lewontin had succumbed to an "old statistical fallacy" of analyzing genes without allowing for the correlation of loci. I am sceptical, however, that Lewontin was ignorant of the importance of such correlations. In the early 1990s, Lewontin criticized DNA forensic scientists for establishing match probabilities by using the relevant reference database ("Caucasian," "black," or "Hispanic") and multiplying frequencies of alleles at typed loci (as if independent). Lewontin argued that this wrongly ignores allelic correlations due to ethnic subdivision.

In this paper, I address several questions raised. Was Lewontin's 1972 reasoning indeed fallacious, or does the widespread acceptance of Edward's critique of Lewontin evidenced in the literature indicate a lack of appreciation for context, one in which Lewontin aimed to counter racism by showing that stereotyping individuals on the basis of group membership ignores that within-group differences dwarf between-group differences? Do facts about population genetic structure and the distribution of human genetic diversity tell us anything interesting – whether scientifically or socially – irrespective of particular contexts and aims? Did Lewontin's leftist politics get in the way of sound science when he paid attention to correlated loci in order to protect civil liberties in the early 1990s but ignored such correlations when it came to fighting racism in the 1970s?

Comparative Psychology (submitted papers)

Basic Emotions, Flexible Aggression, and Angry Motivation
Wiegman Isaac, Washington University in St Louis, USA

There is a widespread view that the evolved mechanisms responsible for basic emotions like anger can only explain certain dimensions of an emotional response. The mechanisms for coordinating basic emotional responses, affect programs, are thought to explain only reflexlike behavior sequences, such as involuntary facial expressions of emotions like anger, and not goal-directed motivations like Frijda's action-tendencies. This hypothesized limitation on the mechanisms for basic emotions cannot accommodate the empirical evidence. I introduce a set of innate behavioral adaptations for conspecific aggression in rats that nonetheless include flexible, goal-directed forms of behavior adjustment. I argue that this undermines the claim that affect programs cannot include goal-directed behavior sequences. I point out further experimental data on human anger, which shows that anger includes a corresponding form of aggressive motivation. In conclusion, I consider how basic emotion theory fares if basic emotions are to include goal-directed motivations. Such a possibility comports well with its commitment to universal emotion antecedents and its focus on fundamental life tasks such as those involving conspecific aggression and modelled by game theoretic analyses of resource competition.

Anthropomorphism and anti-anthropomorphism: A plea for synthesis

Nakao Hisashi, Nagoya University, Japan

The validity of anthropomorphism (i.e., attributing human properties to non-human animals) has been a famous and long-lasting problem in comparative cognition research especially since the Morgan's cannon (Morgan 1894). Although many papers have pointed out that the cannon is vague and not so useful (e.g., Fitzpatrick 2008; Sober 1998, 2005), the development of cognitive ethology (e.g., Griffin 1984) and the growth of comparative cognition research (e.g., Shettleworth 2009) have still stimulated the debate on whether anthropomorphism is a decent strategy or not (e.g., Allen and Beckoff 1997; Fujita 1998; Wynne 2004, 2007). This paper offers a solution to the debate. First, I argue that anthropomorphism is a good heuristic strategy (e.g., de Waal 1999; Fitzpatrick 2008; Fujita 1998) while anti-anthropomorphism is also a useful heuristics as well (e.g., Penn et al. 2008). Moreover, both strategies are not contradictory in principle. Finally I conclude that anthropomorphism and anti-anthropomorphism as methodological heuristics should be synthesized to find similarities and differences between humans and non-human animals more efficiently.

Complex Diseases: Evolutionary Models, Systems, and Explanations

The impact of biological uncertainty on our understanding of complex biological systems. Cancer as a paradigmatic case

Bertolaso Marta, University Campus Bio-Medico of Rome, Italy

Understanding life implies explaining the mode of organization of living beings. Cancer compromises the normal structure and function of tissues, cells and genes so that it appears as a multilevel phenomenon. The biology of cancer is thus giving us interesting insights on the organization of a biological system and its hierarchical phenomenology.

My thesis is that understanding the dynamics of this physio-pathologic process implies making explicit the characteristics of biological uncertainty from an epistemological and conceptual point of view, and that acknowledging the explanatory relevance of systemic perspectives allows us to overcome tensions between mechanistic and evolutionary models of complex multi-causal diseases. The argument follows the analysis of some features of the biology of cancer and some experimental problems that biological uncertainty arises in experimental practice.

I thus first analyze how the notion of uncertainty characteristic of biological complexity contributes to the emergence of the systemic perspectives in cancer research and in contemporary biology in general. Secondly, I spell out some characteristics of this systemic perspective, looking at the convergence of interpretative models of cancer and diabetes towards concepts that focus on the dynamic control of levels of biological organization. Finally, some implications for the relationship between different explanatory models of complex diseases are discussed, and reasons for an integrative approach in biomedicine exploreded.

Recent reemergence of an evolutionary model of cancer growth
Morange Michel, Ecole Normale Supérieure & IHPST, Paris, France

In an evolutionary model of cancer growth, development of a tumour is compared to evolution of organisms. Cancer growth is the consequence of mutations that lead to the formation of different cell clones competing one with the other.

An evolutionary vision of cancer growth is not new. The idea that cancer cells are in competition with other cells, and in particular normal cells, was present in models of oncogenesis as diverse as those proposed by Otto Warburg and John Cairns. It was not foreign to the well accepted idea that tumours "progress" through successive steps.

Nevertheless, the recent reemergence of the evolutionary model of cancer growth is the consequence of technological developments permitting the fast sequencing of full genomes. These technologies were intially introduced to discover new oncogenes and tumour suppressor genes. The reemergence of an evolutionary vision of cancer growth was a collateral effect of these research programs, and a consequence of the development of deep sequencing methods.

Evolutionary models used to account for tumour development are different from those of the past. Evolution of tumour cells is seen as an open process. The importance of neutral mutations and exaptations, as well as of catastrophic events, is highlighted. The role of cancer cells in modifying their own environment (their niche) is also pinpointed.

Whether this renewed evolutionary vision of cancer growth will open new therapeutic perspectives remains an open issue.

The Ecology and Evolution of Cancer
Plutynski Anya, University of Utah, USA

There are a variety of ways in which cancer and can be understood from an evolutionary perspective: as a kind of "regression" to "cellular autonomy", as a by-product of evolution, or cooption of traits otherwise advantageous to the organism as a whole, or, neoplastic progression may have an "evolutionary dynamics." In other words, cancer can be conceived of both a dysfunctional state, and an adaptive process, on a multi-level approach. As a corollary, the debate over whether medical explanations of dysfunctional states may be mechanistic in character is seen to lose its apparently problematic character. This paper will explore the character of evolutionary explanations of cancer; what purpose do such explanations serve, or how should an evolutionary perspective be interpreted. While an evolutionary perspective may add to our understanding of cancer, cancer may also serve as a case study for addressing a variety of questions of interest in evolutionary theory: about the possibility and character of multilevel selection, the evolution of intercellular signaling, the nature and evolution of evolvability, the role of ecology and niche construction in evolutionary processes, and the explanatory power of selection versus drift. In sum, cancer serves as a test case for exploring the character of evolutionary explanation: and in particular, the problem of explanatory integration of distinct accounts of the same phenomena, at different temporal and spatial scales.

Explaining Obesity: Implications for Treatment and Prevention
Skipper Robert, University of Cincinnati, USA

Once upon a time, the explanation for obesity was the Energy Balance Equation (EBE), a simple equation rooted in thermodynamic principles: delta$E = Ein - Eout$ where E is energy measured in kilocalories/day. Obesity is explained as a positive energy imbalance to be treated and prevented via recommendations of a combination of increases in *Eout* and decreases in *Ein*. But treatment and prevention of obesity guided by the EBE has failed.

Presently, obesity is understood as a complex system: Explaining obesity requires articulating multiple, heterogeneous causes at multiple levels, nonlinear causal interactions, interdependence between causal factors, feedback within causal mechanisms, and so on. While understanding obesity as a complex system is an improvement over the EBE, I argue that it unnecessarily complicates treatment and prevention: Precisely where to intervene in the system is problematic and controversial.

I suggest understanding obesity as an evolutionary mismatch between humans and their environment: Briefly and very roughly, the contemporary environment, rich in sugar and fat, is maladaptive for a species adapted to an environment scarce in sugar and fat and the consequence is obesity and the diseases associated with it. Now, the idea that there is an evolutionary explanation for our current corpulence is not new. However, not only has evolutionary mismatch not been sufficiently explicated for obesity, its implications for treatment and prevention are not well understood. The purpose of this talk is to improve that situation.

Conceptual Challenges for Human Microbiome Research

Methodology and Ontology in the Human Microbiome Project

Huss John, The University of Akron, USA

The term “human microbiome” has been interpreted in the biomedical literature in both ecological and molecular terms. The ecological view suggests that we think of the microbiome as a microbial biome. The molecular view suggests that we think of the microbiome as the genome of our microbes, easily assimilated to the list of other “omes” and in some sense continuous with our nuclear genome, mitochondrial genome, and virome as yet another component in an apparently incomplete and emerging concept of “the” human genome. Moreover, one can view metagenomics as a set of tools either for identifying genetically the ecological actors in the human microbial ecosystem, or for arriving at a “metagenome" that black-boxes the identities of phylotypes for the sake of capturing the overall functional capacities of the microbial "community." Restricting myself to the molecular perspective, I shall examine the ontological categories that emerge from the Human Microbiome Project, for example metagenome, "core" microbiome, and enterotype. I shall argue that these categories are artifacts of the biotechnological, conceptual, and statistical tools of investigation. The result is that the tools are supplying – not uncovering – the biological ontology, and that these methodological artifacts are on a path toward reification as units of nature.

Ecological Metaphors in Microbiome Research

Sagoff Mark, George Mason University, USA

Microbiome researchers often employ ecological metaphors to describe the objects they study as “communities” or “ecosystems” and to characterize the human subject as a “metacommunity” or “super” or “supra” organism. This paper will analyze and assess the application of ecological metaphors in the context of conceptualizing and understanding the relation to each other and to the human body of the microbes that are found in or on it. The paper will argue that ecological concepts and metaphors are so thoroughly contested and so variously understood in ecological science they are more likely to confuse that to clarify the study of the ways these microbes behave together and affect us. It will explore the extent to which microbiomes should be seen as coevolved, integrated complexes, or should be conceptualized as fluxes of organisms that happen to be found together at a place and time. Are the most significant interactions reducible to the work of a few key microbial players or should they be understood in more holistic or emergent terms? Since only a small percentage of the microbiota are culturable with present methods, extraction or detection of nucleic acid, either DNA or RNA sequences, represents the first step to identifying many others. The paper will explore conceptually the relation between the study of microbial ecology at the phenotypic vs. genotypic level, e.g., with microscopes vs. sequencers.

Changing views on individuality and organismality: A role for the human microbiome
Borrello Mark, University of Minnesota, USA

The investigation of the nature of biological individuality has a long and interesting history. Biologists have been fascinated by the wide range of biological entities that might count as individuals. Perhaps not surprisingly, humans have generally been perceived to be among the most coherent kinds of individuals. In this paper, I will examine the ways in which concepts of individuality have developed in biology since the mid-19th century with a particular focus on humans. I will then use this history to illuminate the role of the microbiome in changing concepts of human organismality and individuality. I will suggest some ways that the discussion of the human microbiome might contribute to the long standing, and ongoing discussion on the levels of biological organization and the processes of selection.

Conceptual Difficulties Associated with Evo-Devo A (submitted papers)

The inception of modularity in biology
Caianiello Silvia, ISPF, C.N.R., Italy

The modern history of modularity starts with Modernism, as Le Corbusier merged in the “modulor” the ancient architectural measure with the new taylorist standardized mode of production. The term inspired in the 1960s early computer scientist for renaming the “subroutine”, anticipated by Zuse's Plankalkül. This transposition involved a shift from “modularity in construction” to “modularity in design”, as a strategy for dealing with increasingly complex software systems.

Since the late 1970s, the two different acceptations both appear in biology: 1. along the line of the “constructional” meaning, as iteration of genets in clonal, renamed “modular organisms” by J.L. Harper. 2. with a prevailing "design" meaning, in protein architecture and metabolic control theory. But in either case the term broke through, neither conveyed a more general epistemic shift. A stemmatic analysis of early occurrences of the term in biology indicated that it didn't get established before the “second phase” of Evo-Devo, about 1995, with a significant delay with respect even to other kindred disciplinary fields, such as cognitive sciences. I will argue that further shifts were necessary for making the term palatable for life sciences, which made it possible as well to dispel the rigidity of the constructional meaning as to move from a “hierarchybased” to a “network-based” notion of modularity.

Developmental explanation
Parkkinen Veli-Pekka, University of Oslo, Norway

Individual development can be described as a series of changes in a system's causal capacities over time. Explaining development involves showing how characteristics of later developmental stages are caused by the manifestation of the system’s developmental capacities in the past. This presupposes an account of how these capacities depend on the properties of the system's components at each stage – an explanation by appeal to constitution.

I outline similarities and differences between causal and constitutive explanation, and investigate how the two-aspect structure of developmental explanation can give rise to problems in interpreting evidence. Since causal and constitutive explanations have slightly different evidence conditions, careful specification of what aspect of the developmental process one intends to explain is needed to assess what kind of evidence is called for.

I then discuss the reductionism debate concerning explaining development. Explicating the structure of developmental explanation removes ambiguity about what kind of information is requested for when explaining aspects of developmental phenomena. When explaining a specific developmental capacity, the explanation naturally flows bottom-up, following the constitutive dependence of system's capacity from its components. To answer how the system came to have a certain constitution at a certain stage, one must account for how the system's earlier developmental capacities acted to produce the structures of interest. This requires citing factors beyond the constitution of the system, such as interactions between the system and its environment. Whether a "reductionistic", bottom-up explanation suffices to explain a developing system therefore depends on the specification of the explanation-seeking question.

Conceptual Difficulties Associated with Evo-Devo B (submitted papers)

The integration between functional and evolutionary biology and the promise of EvoDevo

Folguera Guillermo & Lavagnino Nicolás, CONICET-Universidad de Buenos Aires, Argentina

Since its proposal by Mayr, the distinction between functional and evolutionary biology occupies an important place in Biology. However, different researchers have noted several problems associated with the use of this distinction. EvoDevo (evolutionary developmental biology) emerged as one of the areas of knowledge that finds this distinction problematic and is proposed as being able to accomplish an integration between functional and evolutionary biology. However, it is not obvious that EvoDevo as an area of knowledge really achieves this integration and it is even less clear how it would do so. To deal with these questions our research analyses whether EvoDevo's mechanisms accomplish functional and/or evolutionary roles by means of elucidating if they are involved in proximate and/or ultimate causes of biological phenomena. Our proposal is that one of the possible strategies to tackle this problem is to consider mechanisms that generate biological variability as examples of proximate causation and mechanisms that only modify variability as examples of ultimate causation. Then, the main question in our analysis is: do EvoDevo's mechanisms have a function of generators and/or modifiers of biological variability? In particular, we focus on three of the main EvoDevo mechanisms: environmental induction, hypervariability/somatic selection and developmental bias. Our analysis shows a different characterization in terms of the causalities in which each one of the mechanisms analyzed are involved. Then, since there are not uniform results in terms of causation of EvoDevo mechanisms it's not trivial how EvoDevo would build a bridge between functional and evolutionary biology.

Rethinking innateness as a primitive term within developmental scenarios

Reynaud Valentine, IrPhiL, Université Jean Moulin – Lyon III, France

The concept of innateness remains extremely unclear although it is widely used by biologists and cognitive scientists. However, when researchers talk about “innate traits”, they obviously mean “genetically specified traits”. But is it not the case for every trait to be “genetically specified” in one sense? Furthermore, in crossing distinct disciplinary boundaries or in following the folk's misconceptions like uninformative dichotomies (innate/acquired, innate/learnt), innateness seems to produce a confusing and unhelpful notion. Relying on the complexity of ontogenetic development, some researchers thus hold that this concept should be rejected (Lehrman, 1953; Oyama, 2000; Griffiths, 2002).

In this paper, I will argue that the complexity of ontogenetic development, instead of being a reason to abandon the notion of innateness, reveals its usefulness. With this in mind, I propose to show that Ariew's account of innateness (2006) as empirical developmental canalisation is perfectly relevant for some traits. Yet, I will argue that this account is not sufficient for other more complex traits. In other terms, Ariew's identification of three developmental patterns (innate/ acquired/triggered) from isolation experiments with songbirds is not always feasible. I will then state that, as innateness seems to be a theoretical term depending on specified theoretical contexts, it has to be viewed as a primitive term intervening within explicit and empirically robust developmental scenarios. It means that every innateness ascription today is relied upon a specific developmental theory. Therefore, it is likely to change with regard to progress in understanding development.

Typological thinking and essentializing from a practical point of view
Diteresi Christopher, George Mason University, USA

Typological thinking, long-rejected by biologists and philosophers as perniciously essentialist, is receiving renewed attention. Ernst Mayr's seminal dichotomy of typological thinking and population thinking has, by different authors, been variously reconsidered, challenged, updated, interrogated, reconfigured, and even reasserted and extended. One persistent thread running through this recent work has been the concern to disentangle typological thinking from the essentialism that motivated its rejection. All, or nearly all, agree that some typological practices are unproblematic. The difficulty is how to understand such cases without losing track of a legitimate general worry about mistreating variation. In this paper, I resolve this difficulty by developing a practical notion of *essentializing* as asserting the warranted ignorability of ignored variation. By contrast, the absence of such an assertion, i.e., the opposite of essentializing, I call *variational*. I contend that the traditional typological-populational dichotomy conflates two distinct dichotomies, typological-populational and essentializing-variational. Separating the two dichotomies permits drawing a distinction between *essentializing typological thinking* and *variational typological thinking*. This distinction, *within* typological thinking, closes the gap between specific typologies and the generic worry by suggesting *practical* criteria for determining whether particular typological practices mistreat variation. I conclude by considering two examples from evolutionary developmental biology – staging embryos and generalizing from model organisms – that illustrate the significance of *variational* typological thinking.

Conceptual Issues in Ecology A (submitted papers)

Dynamical kinds and ecological theory
Jantzen Benjamin, Virginia Tech, USA

Ecology has a theory problem. On the one hand, fine-scale models that attempt to capture detailed causal interactions tend to be analytically intractable and sui generis. On the other, tractable theories with broad scope are viewed with suspicion. This is a consequence both of the assumption that a model should be tested by checking whether time-series data can be fit to one of its solutions and the fact that a typical experimental trajectory is statistically indistinguishable from the solutions of multiple candidate models which assert very different things about ecological dynamics. I argue for an ontological view with methodological consequences that circumvents this intolerable underdetermination. When we assert that behavior of a biological system is governed by a particular set of equations, we are asserting the existence of a dynamical kind – a class of causal systems bearing a characteristic set of features. In this paper, I sketch an account in which dynamical kinds are defined via sets of dynamical symmetries – transformations of the variables that leave intact the way in which states unfold through time – and the algebraic structure connecting them. I then demonstrate the immediate methodological gains that arise from adopting this view of model identification. In particular, I show how models of population growth which are statistically indistinguishable under the old approach can be readily discerned by their behavior under applied dynamical symmetries. In the case of growth models, this can be done with strictly observational data of the sort we already possess for a number of organisms.

But isn't the neutral theory of ecology a null model?

Bausman William, University of Minnesota – Twin Cities, USA

Why has the neutral theory of ecology been so controversial? It is tempting to locate the source of controversy in a conflict of worldviews between (a) a view where natural selection via interspecific competition is the dominant mechanism structuring ecological communities and (b) a view where ecological drift, immigration, and speciation are the dominant mechanisms. This fits both the philosophers' predilection for theoretical claims about the world and the narrative of the biological sciences in the 20th century in which natural selection first reigns supreme and then suffers a backlash. Against this received view, I argue that the controversy is better conceived as a conflict of scientific methodologies and that the tension between the selectionist and neutralist worldviews in ecology stems from this root. I frame the controversy as being about the epistemological status and appropriate use of null models. Null models in biology are often used to deny the necessity of invoking selection by establishing the sufficiency of an account lacking selection. Debate over the appropriate use of null models has moved through genetics, ecology, and paleontology over the last fifty years and forms the historical context of this controversy. Current actors' views towards the neutral theory of ecology and toward null models are shaped by these past debates. Framing the controversy as a clash of scientific methodologies emphasizes the underappreciated roles that scientists' goals and methodologies play in shaping their worldview that their enquiry produces and aids in interpreting the virtues and vices of neutral theory.

An organizational account of ecosystem functions

Lefèvre Victor, Université Paris 1 Panthéon-Sorbonne, France

Ecologists talk about ecosystem health that we should preserve and restore (for example, see Costanza et al., 1992). How to account for this medical vocabulary and for the moral obligation which seems follow from it? Literature on the problem is plentiful but the first step to its resolution had been quite forsaken: giving an account of ecological functional vocabulary in a way which allows for constructing an objective concept of ecosystem health (Callicott 1995). Indeed, the expression "ecosystem health" assumes that each ecosystem has a normal operating condition and is able to leave it for pathological conditions. Our presentation will is divided into three parts: firstly, we will describe the explanandum - the functional structure of ecosystems constituted by ecological niches and communities. Secondly, we will argue that the two mainstream accounts of biological functions – the systemic capacity account (Cummins, 1975) and the etiological-selective account (Neander, 1991) – are unsatisfactory with respect to ecosystem functions. The systemic account adopted by (Odenbaugh, 2010) denies the normativity of ecosystem functions and the etiological account faced the difficulties to figure ecosystems as units of selection (Bouchard, 2012). Thirdly, we will extend the organizational account recently proposed by (Mossio et al., 2009) inspired from (Varela et al, 1974, Schlosser 1998). This organizational account explains the normativity of biological functions by the organizational closure and differenciation of biological systems. We claim that ecosystems are organizationally closed and differentiated systems both regarding of their structuring in communities and in niches and that allow us to speak about ecosystem health objectively.

Is the neutral theory of community ecology really neutral?

Munoz François, AMAP, Université Montpellier II, France

The Unified Neutral Theory of Biodiversity and Biogeography (Hubbell 2001) has been very influential but controversial among ecologists during the last 12 years. It relies on the assumption that biological variation among organisms does not reflect any variation in their ability to survive, reproduce and disperse (fitness equivalence), but that stochasticity in life and death events alone maintain diversity. The neutral assumption is traditionally opposed to an exclusive explanatory role of niche differences in ecology, and to the idea of natural selection in evolution. The neutral theory showed a remarkably good heuristic value to predict diversity patterns in ecosystems, despite numerous evidence of functional variation across organisms. We discuss this apparent paradox by exploring the limits of the fundamental fitness equivalence assumption.

We delineate fitness equivalence so as to better assess the causality in the neutral theory. We question the extent to which apparent neutral patterns of biodiversity are possible even in presence of nonequivalence across species, insofar as stabilizing mechanisms are playing. We thereby explore two important aspects of fitness equivalence in terms of equalizing and stabilizing processes. We will then discuss the philosophical nature of the dualism in neutral and non-neutral views, and argue that spatial and temporal scales are critical aspects of the link between neutral emerging patterns and possibly non-neutral underlying processes. Therefore, the neutral theory is not as neutral as expected, and an important perspective is to assess to what extent it can be a null model in a unified framework of community dynamics.

Conceptual Issues in Ecology B (submitted papers)

What may be General Ecology?

Godron Michel, Université Paris VII - Paris Diderot, France

Ecology is the science of the relations between living beings and their environment. It is divided in animal ecology, vegetal ecology, microbial ecology, human ecology, etc. Is it possible today to find commonalities in these particular ecologies and to see what may be general ecology? To find an answer, we must remind the essential difference between living beings and inanimate objects: according to the classical definition, living beings differ from inanimate objects because they are able to move by themselves, to grow and to reproduce. More precisely, the physical reaction of an inanimate object to a stimulus coming from its environment is unique and strictly determined by the laws of mechanics. On the contrary, several reactions of a living being to a physical change in its environment are possible and they are controlled by a cybernetic system where a memory gives the information which is necessary for the control.

Any living system stays alive as long as it reacts to the perturbations, so as to evolve around a "metastable" equilibrium state. To understand this, the simplest comparison is that of a ball wobbling in a hollow dug in the bottom of a box. The ball stays in the hollow as long as the perturbations are feable. If a perturbation is too strong, the ball escapes from the hollow, and this may be the death of the living system. The ball may also fall in an another hollow where it will again wobble if the system may find a new model of control. In the language pf cybernetics, the hollows are named "attractors". The transition phase of the system between two hollows is short, because the system is then instable, and it is named "crisis" which meant in greek language "decision". The crisis is a gate opened to innovation.

The simplest example of this way of functioning is the equilibrium found by a vegetal or animal population pertaining to one species in its environment. As long as the memory included in he DNA of its genetic pool is able to counter-react easily to the usual perturbations of the environment, the population remains inside the species. But if the environment changes too strongly, the population disappears, unless its genetic pool is rich enough to create a new species adapted to the new environment. In this case, the after crisis innovation is the new species. The result of this process is the diversity of the biosphere.

This model of functioning operates at all scales of the living world, with a type of memory different for each scale.

1 At the level of the cells and tissues of an individual, where the information is "epigenetic", the stable phase is the addition of new cells to a growing organ; the crisis is the birth of a new type of organ, for example the birth of the neurons in the exodermis.

2 For the evolution of vegetation from bare soil to a grassland, and after to a forest, the memory

which contains the possibilities of change is the sets of genomes and life traits of the species present and of the species able to build the new type of vegetation. The crisis is the arrival of seeds of new species, and the transition is smoother than in the previous examples. The result is the diversity of landscapes.

3 The human societies are collections of persons who have a collective memory in the books, computers, data banks on the economy of companies and governments. Each tribe, society or nation has its own memory which gives an original functioning. The crisis is a civil or international war, which gives a new equilibrium.

At all these scales, the process is the same: the memory of each subsystem contains information which holds the possibility to regulate its functioning till the moment of a crisis which destroy it or leads to a new innovating system. In all these cases, it is the reaction of the system to the more or less important change of its environment which drives the evolution of the system. This process is therefore the heart of a rally general ecology.

Function in ecology: description of the scientific uses and an epistemological framework

Nunes-Neto Nei, Institute of Biology, Federal University of Bahia, Brazil

Functional explanations and ascriptions are ubiquitous and central in contemporary ecology, more specifically, in the Biodiversity and Ecosystem Functioning research program (BEF). This research program, which emerged in the early 1990s, has proposed a series of important changes in ecological thought. Although the functional explanations play a critical role in it, there is no epistemological foundation mentioned in the scientific literature for the uses of function, which is simply assumed as a self-evident notion. In this work we have two goals. First, we present an analysis of the uses of function in ecology. This descriptive analysis allows to map the more salient uses of function in the BEF, as well as their respective epistemological assumptions. The result is a typology with four uses of function in the BEF, which are associated, respectively, to a particular object of functional ascription (biodiversity, items of biodiversity, the ecosystem seen as a whole and, finally, the ecosystem seen as a part). Second, with a more normative goal and also taking as a starting point the descriptive analysis, we advance an epistemological framework to ground the ascriptions of function to the items of biodiversity. In this framework function in the BEF is defined as a precise effect of a given constraining action on the flow of matter and energy performed by a given item of biodiversity, in an ecosystem closure of constraints. After the presentation and explanation of this epistemological model, we apply it to a case study, evaluating the implications for ecology.

Functionality in Open Dynamical Systems: The Case of Ecology

Collier John, University of KwaZulu-Natal, South Africa

Dynamical systems theory applies to anything that changes with time. In mathematics this is interpreted rather broadly, but in physics, and often in other sciences, it applies to systems with forces and flows, often in a network, that are typically open to exchanges with the outside. This makes it well suited to the study of ecosystems. Ecosystems are not only open to outside influences, but are often nested by scale in space and time. One of the first problems in discussing ecosystem function, then, is to give a definition of ecosystem individuation and its consequences. One of the consequences is that it is reasonable to define functionality within an ecosystem in terms of contributions to the maintenance of this individuation, as I have done elsewhere for organisms, using a dynamical notion of autonomy. I will briefly argue that common etiological accounts of function are not suitable for discussing ecosystem function. We don't typically think of ecosystems as autonomous, but autonomy comes in degrees, so even if the word is not apt, the idea is. I will distinguish between ecosystem role in general and functionality in particular. Ecosystem role, which is sometimes identified with function, can actually undermine ecosystem functionality. I will also distinguish between ecosystem functions and ecosystem services. The latter serve some larger or separate systems (whence again the importance of individuation). They are important for understanding how nested ecosystems are related to each other through functional dependence.

Conceptual Tools for Neurobiology A (submitted papers)

Early nervous systems and the origins of the animal sensorimotor organization
Keijzer Fred, University of Groningen, Netherlands

The notion of an animal "sensorimotor organization", central in discussions on embodied cognition, can be clarified by turning to the evolution of the very first nervous systems. Nervous systems are usually interpreted as input-output control devices, similar to artificial ones. Nervous systems receive information from sensors; process it and use the result to control effectors. However, it can be argued that this input-output view is best fitted to relatively complex centralized nervous systems and less suitable to deal with more basic forms, most notably diffusely connected nerve nets, and their evolutionary origins. Taking diffuse nerve nets as a basic condition, an alternative view can be developed that stresses the fundamental coordination problems faced by multicellular animals that first developed muscle-based motility. This form of motility involves the patterned contraction of extended muscle sheets dispersed over the body. The key problem here was not so much to act intelligently - a problem often solved without any nervous system – but to act as a *single multicellular bodily unit*. In this alternative view, early nervous systems were central in enabling a new, extremely powerful multicellular effector by providing ongoing patterned activations across the available contractile tissue of the organisms involved. Connecting sensors to such an effector then becomes a secondary development. While this evolutionary possibility is important in itself, it also offers a way to interpret the animal sensorimotor organization as a specific form of embodiment rather than an essentially arbitrary collection of sensors and effectors.

The Explanatory Role of Mechanisms in Neuroscience
Huber Tobias, Unaffiliated

Explanations in the biological sciences and neuroscience often make reference to mechanisms. Recent mechanism-based philosophical approaches to explanation and experimentation have thus successfully captured important features of neuroscientific research. In this paper, I explore the explanatory role of mechanisms across different fields in neuroscience. Based on current debates concerning the compatibility of dynamicalmathematical and causal-mechanistic accounts of neuroscientific practice (see Kaplan and Craver 2011; Bechtel 2011, Silberstein and Chemero 2012), I argue that an adequate philosophical theory of the nature of neuroscientific explanation must integrate both mechanistic and computational explanatory strategies.

As I show, research in cognitive and systems neuroscience combines experimental methods, which provide lower-level mechanistic information about brain structure and function, with mathematical models, which target the higher-level complex dynamical behavior of multiscale cognitive systems. Whereas abstract and idealized computational models explain complex neurobiological phenomena in quantitative terms, mechanistic explanations make explicit how a mechanism's organization of structural components and qualitatively specified operations generates the cognitive or behavioral phenomena under investigation. By complementing qualitative with quantitative explanations, neuroscientists are able to develop more realistic models of the brain. I argue that an analysis of the explanatory strategies being practiced in cognitive and systems neuroscience suggests that qualitative mechanistic explanations and quantitative computational models jointly contribute to the explanatory knowledge of neuroscience.

I further argue that this integration of causal-mechanism and dynamical-mathematical models demonstrates the need for a philosophical account of neuroscientific explanation, which can accommodate the explanatory and methodological plurality of neuroscientific research.

Conceptual Tools for Neurobiology B (submitted papers)

Re-Thinking Neuroconstructivism through Dynamic (neuro)-Enskilment: a critique of Neo-Nativism

Farina Mirko, Macquarie University, Australia

In this paper I discuss three views - 1) Gary Marcus' neo-nativism, 2) standard neuroconstructivism, and 3) dynamic neuro-enskilment - that explain human cognitive and cortical development from different standpoints. I then compare these views and critically analyse the links between them. I do so with two goals in mind. First, I wish to demonstrate that neonativism is not that distinct from standard neuroconstructivism: and second, I want to show that standard neuroconstructivism, in order to fully account for recent empirical findings, needs to be updated and radicalized along the lines envisaged by the dynamic neuro-enskilment view.

In section 1, I offer the reader a short description for each of the three accounts at stake, provide some general philosophical background for each of the three understandings discussed, and thus briefly contextualize them within the current philosophical literature. In section 2, I assess Marcus' attempt to reconcile nativism with developmental flexibility. In section 3, I argue that in structurally reconfiguring nativism, Marcus ends up transforming it out of a recognizable form, and claim that his view can be accommodated within the more general framework provided by standard neuroconstructivism. In section 4, I focus on recent empirical findings in neuropsychology and cultural/social neuroscience, and propose a significant revision to standard neuroconstructivism, thus developing the dynamic neuro-enskilment view. I conclude the paper (section 5) by analyzing the implications of the results discussed in section 4 for both neo-nativism and standard neuroconstructivism.

Embodied Cognition: The Very Idea

Adams Fred, University of Delaware, USA

For twenty years now embodied cognition has been sweeping the planet. The empirical findings in support of the thesis are stunning. For example, Barsalou and colleagues have given impressive data to incline one to think cognition is taking place in perceptual regions. Glenberg and colleagues have given impressive data to incline one to think cognition takes place in motor regions. Many other researchers offer supporting data of many kinds supporting similar conclusions. Nonetheless, there has been some resistance among cognitive scientists to the some of the stronger conclusions drawn from these impressive findings. I myself have asked the question whether the empirical findings can differentiate between mere causal support of cognition taking place in these regions versus cognition being constituted by processing in these regions. The empirical data alone cannot detect this difference. Yet, until now, little has been done to push back directly on the very idea of what is required for cognition truly to be embodied. In this paper, I shall first present some strong reasons for thinking that the whole research program has gotten out of hand by extending its arguments to plant cognition and plant neurobiology. What is more, I shall present considerations from neuroscience, and from naturalized semantics that would block attribution of cognition to plants. I shall then claim that these same considerations, if they work against plant cognition, cast strong doubt on the entire research program of embodied cognition.

Embodied Cognition and Neuroethology: A Defense of Information Processing Models

Martin Jonathan, University of Cincinnati, USA

Certain strains of the research programs known as "embodied cognition" have advocated the elimination of representational or information-processing models in explanations of cognition. Radical embodied cognition theorists stress the role in which the environment and the organism's bodily form structure and govern behavior, especially perception and action with minimal reference to “internal” information-processing mechanisms. However, as I will argue, the experimental methodology known as "neuroethology" provides an example of how close attention to just these sorts of bodily and environmental factors provides reasons to postulate information-processing mechanisms, as well as an experimental apparatus for discovering their functional organization. This suggests that cognitive neuroscience can take on the insights of embodied cognition's theoretical emphases while not jettisoning what is likely an important concept for explaining complex environmental navigation - neural information-processing. After some analysis of the particular aspects of the experimental and explanatory methodology of neuroethology, I will present some recent work by Paul Williams and Randall Beer in information theory which I think suggests a method for thinking about the kind of information-processing that occurs in embodied nervous systems. By combining these two pictures, I will show that rather than give us pause about representational theorizing - when combined with this fresh information-theoretic perspective - neuroethology's attention to the crucial role played by body and environment provides empirical resources for better understanding the nature of neural information processing, the explanatory utility of representational models, and sheds light on the kind cognitive systems which warrant this kind of explanation.

Cooperation (submitted papers)

The evolution of empathy through parental care

Audisio Irene, Universidad Nacional de Córdoba, Argentina

The evolutionary approach to pro-social behavior and cooperation is widening its focus to include questions about proximate mechanisms. Empathy seems a good option in this context. A promising hypothesis presents it as a multiple-layered process, ultimately grounded in a perception-action mechanism (Preston & de Waal, 2002; Preston, 2006). This mechanism was transformed in evolution until it was capable of naturally producing helping behaviors with something like pro-social motivation. In this paper I shall attempt a hypothesis about how part of this transformation took place.

The PA mechanism probably evolved to control a very basic form of imitation, known in animal learning theory as “contagion” (Thorpe 1963): when A (the subject) sees B (the object) perform a given behavior, A performs that behavior as well. Contagion occurs usually in relation to behaviors that are species typical or instinctive. Through contagion, animals that live in groups “respond with” others, similarly and quickly, to a given affordance.

But those behaviors are still far from pro-social behaviors. How did a mechanism that explains contagion evolve into something capable of producing pro-social behavior? The most probable context for the evolution of pro-social behavior with a mechanism involving pro-social motivation is parental care. Is there any evidence of a perception action mechanism in parental care? I review empirical evidence regarding facial expressions and their role in primate communication in general, and between mother and infant in particular. There is also some initial evidence that mirror neurons control mother-infant exchanges through facial expressions.

Randomization and the alignment of biological interests: why fairness doesn't matter

Martens Johannes, University of Bristol, UK

Randomizing away the information that biological individuals could get about their own reproductive success has long been recognized as an efficient way of aligning their interests and of promoting the evolution of new adaptations at the level of social collectives? The most paradigmatic example being fair segregation in meiosis, where each allele “doesn't know” whether (and in which proportion) her type will be represented in the gamete pool, and may only gain in enhancing the total number of gametes produced by their host organism. In order to shed further light on this fact, some recent studies (e.g. Okasha 2012) have moreover noticed a close affinity between such randomization process and the veil-of-ignorance thought experiment in social and political philosophy, suggesting that the fairness or "impartiality" stemming from the randomization was the key in the process of alignment in the interests of the individuals.

Building on the kind of axiomatization approach that constitutes the core of social choice theory, I will show, however, that fairness of the randomization process per se, though central in the original version of the veil-of-ignorance argument, is not essential for getting such an alignment in biological settings. Rather, what matters is only whether the randomization succeeds or not in removing any control of the parts of the group members over the "desired" outcomes. Hence, even if there is a significant bias in favor of one type over another, a stable alignment of interests can nevertheless be reached under the right conditions.

Spatial Reciprocity and the Evolution of Cooperation

Barnett Marie, University of Pennsylvania, USA

Martin Nowak has proposed spatial reciprocity as a potential explanation for the evolution of cooperation. Spatial reciprocity occurs in spatially structured games when the strategies of successful players are copied by their neighbours; this reduces the effectiveness of defection, since a highly successful defector will soon find itself surrounded by copycat defectors whom it cannot exploit.

It seems plausible that spatial reciprocity could contribute to the evolution of cooperation. However, in his exploration of this phenomenon, Nowak uses a payoff structure which is not consistent with a true Prisoner's Dilemma. Nowak reduces the number of variables involved in his simulations by assuming the punishment for mutual defection is a "very small positive payoff" approaching zero; he considers this payoff to be equal to zero for the purposes of the model. The sucker's payoff is also set at zero. Thus, a player who faces a defector receives a payoff of zero, no matter what it does; defection is not a strictly dominant strategy.

There are non-zero punishment payoffs which maintain the effectiveness of spatial reciprocity as a cooperation-generating mechanism in Nowak's game; however, there is a limit beyond which this effect is lost. Some ways of setting three payoffs in the Prisoner's Dilemma preclude the generation of cooperation through spatial reciprocity, no matter which (allowable) value is chosen for the fourth. An understanding of the limiting conditions for spatial reciprocity is essential to a complete account of its effectiveness as a cooperation-generating mechanism. In this paper, I explore these conditions.

Revisiting Petr Kropotkin: Is competition necessary for natural selection?

Gagné Julien Anne Marie, Université de Montréal, Canada

Petr Kropotkin (Mutual Aid: A Factor of Evolution, 1902) has been read with enthusiasm mostly by political thinkers and critical theorists. However, except for S.J. Gould (1997), L. Margulis (1991) and K.A. Peacock (2011), few philosophers of biology and biologists have paid attention to his biological writings. Recently, the work of some historians like D.P. Todes (1989) and J. Sapp (1994) indicates a growing interest in his biological thoughts (and more broadly in Russian evolutionary theories). Thus far, this interest has almost strictly been historical. In my presentation, I first want to argue that Kropotkin's work has been underestimated in biology and in philosophy of biology, and that it deserves to be reconsidered. Secondly, I would like to illustrate how such reconsideration can shed new light on contemporary evolutionary issues. I reframe these ideas in the broader context of the current debates on the relative importance of competition and cooperation in selective and evolutionary processes (See for example Carrapiço 2012). I focus on Chapters I and II of Mutual Aid (on mutual aid among animals), and show how an emphasis on the role of abiotic pressures/checks (such as the direct action of climate) can make evolutionary phenomena clearer. Following Kropotkin, I argue that when such forces are at play, strict competition is not always necessary for natural selection to occur, even when the selective challenge is a lack of resources.

Criticisms Addressed to Evolutionary Psychology (submitted papers)

The Difference Between Ice Cream and Nazis: Evolution and the 'Hard Problem' of Human Moral Psychology

Stanford P. Kyle, UC Irvine, USA

I first argue that the most puzzling aspect of our moral psychology from an evolutionary point of view (the "Hard Problem") is our inclination to treat moral demands and considerations as anything more than mere subjective preferences regarding our own and others' behavior. I discuss recent empirical evidence more precisely delineating the character of such moral objectification or externalization and then argue that existing evolutionary approaches abjectly fail to account for this crucial, salient, and robust feature of our moral psychology. I then propose a novel evolutionary hypothesis on which the adaptive advantages of such objectification arose from the opportunity it offered to increase the reliability (rather than strength) of moral motivation, and thus to increase our attractiveness to others as potential partners in exploitable forms of social interaction as humans evolved to become (unlike other primate species) default, domain-general cooperators. I draw on a wide range of both classic and recent empirical work to support this hypothesis, as well as explaining why the need to effectively advertise the objectification of our moral commitments in order to make ourselves more attractive cooperative partners renders it unlikely that any non-human organisms also externalize or objectify moral or prosocial motivation in this way. I conclude by revisiting the question of moral objectivity, illustrating how this evolutionary hypothesis enables us to understand why the status we ascribe to moral demands and considerations involves the distinctive (and otherwise puzzling) combination of objective and subjective elements that it does.

Why psychiatrists shouldn't care about evolutionary psychiatry

De Block Andreas, University of Leuven, Belgium

Most philosophical critiques of evolutionary psychiatry focus on the explanations that evolutionary psychiatrists have produced to account for the spread and/or persistence of particular mental disorders (Adriaens 2007; Faucher & Blanchette 2011). My critique is more fundamental. I argue that even if the proposed evolutionary explanations for depression, autism, and schizophrenia would be supported by all the available evidence, the value of evolutionary psychiatry for the rest of psychiatry would still be very limited. If true, my argument subverts the claims made by both evolutionary psychiatrists (Nesse 2008, Nesse & Jackson 2006) and philosophical proponents of evolutionary accounts of mental disorders (Murphy & Stich 2000). In their view, evolutionary psychiatry should be the foundation for psychiatric theory and practice. By scrutinizing and rebutting four arguments of Nesse and three arguments of Murphy and Stich in favour of their view, I will show that the assumed added value for psychiatry is either not an added value at all, or that the added value cannot be brought about by evolutionary psychiatry.

Deep homology in mirror neurons? Epistemic problems with the extrapolation of evo-devo schemes in cognitive science

Yañez Bernardo, Vergare-Silva Francisco & Argüelles Juan Manuel, all at CEFPSVLT, Mexico

Evolutionary developmental biology (evo-devo) and cognitive science have been lately brought together by philosophers of biology, but the methodological/theoretical complementarities between these two disciplines have not yet been analyzed in detail. This paper addresses epistemic issues related to the extrapolation of (i) well-established inference strategies employed in developmental genetic and morphological evo-devo studies of homology into (ii) the cognitive science/primatology realm, where comparative description of behavioral traits is characteristically included at upper hierarchical levels. We analyze a specific example of such interdisciplinary extrapolation - namely, de Waal and Ferrari's postulation of mirror neuron-based homologous neural substrates for imitation behaviors in primates - and detect a problematic use of the notion ofdeep homology. In this particular cognitive primatology case - which involves functional, as well as structural homology considerations - information on the gene- or gene regulatory network-related substrate for the differentiation of mirror neurons in different primate species is lacking, therefore complicating inferences intrinsic to deep homology arguments, as conducted in more traditional evo-devo studies. Our analysis rests on well-known conceptual treatments (Abouheif; Bolker & Raff; Wagner; others) of the complexities associated to the definition of homology in biology when multiple levels of organization are implicated. We conclude with a brief comment on epistemological approaches to the interface between evo-devo and primatology/biological anthropology-oriented cognitive science.

Cultural Evolution

The Kinetic Theory of Culture
Lewens Tim, University of Cambridge, UK

We can usefully characterize a dominant approach to cultural evolutionary theory (Richerson and Boyd 2005) as the ‘kinetic theory of culture’, by analogy with the kinetic theory of gases. Mathematical tools are used to explain phenomena manifested by populations of humans in terms of the aggregated effects of interacting human individuals. These individuals are not each tracked in detail; rather, they are given idealized characterizations, and their behaviours are aggregated using statistical tools.

Cultural evolutionary theory has been treated to a hostile reception from thinkers with a background in the humanities and social sciences (e.g. Fracchia and Lewontin 1999, 2005, Ingold 2007). Many elements of this hostility are best understood not as reactions against the use of biological concepts of selection, mutation and so forth, but instead as reactions against the more general ‘kinetic’ approach taken by cultural evolutionary theory, and the correspondingly atomistic manner in which it conceives of cultural elements. What, exactly, is entailed by this form of atomism? The answer is surprisingly minimal, and this minimal atomism means the cultural evolutionist can fend off some, but not all, criticisms from social science.

Expertise, Extension, Evolution
Buskell Andrew, University of Cambridge, UK

Contemporary accounts of cultural evolution take culture to be a channel of heritable information, complementing analogous channels of genetic and individually-based information (Richerson and Boyd 2005; Mesoudi 2011). What demarcates cultural information is its propagation through mechanisms of social transmission, which can take cultural conspecifics or external artefacts as bearers of useful information. But it is an open question whether or not such a system can propagate the information of extended cognitive systems, where external artefacts form a constituent part of the supervenience base of an ephemeral cognitive system (Clark 1998, 2008, 2010). Sterelny (2010) argues that such temporary systems should, in fact, be seen instead as persisting capacities of an agent to self-assemble systems, particularly systems where the external artefacts are seen as highly trustworthy, entrenched and complementary to a single-user in a specific context. This characterisation of the underlying information of extended systems – finegrained and unique to individuals – seems to equate extended cognitive systems with artefact employing expertise. Expertise as such is not directly transmittable (Sterelny 2006), but can serve as part of the explanation for propagation in terms of model-based imitation (Richerson and Boyd 2005). Yet characterising extended cognition as expertise seems to leave out some of its more convincing cases. I will argue that when we loosen some of Sterelny's (2010) criteria, we can capture the paradigmatic cases of cognitive extension, and create a more viable picture of the transmission of extended cognitive systems through pedagogical contexts scaffolding individual learning (Clark 1998; Gergely & Csibra 2009).

Methodological Individualism and Group Selection

Clarke Christopher, University of Cambridge, UK

The behaviour of human social groups can be studied by applying models from e.g. sociology and economics, but it can also be studied by applying models from evolutionary biology. One question concerning the former models is the question of methodological individualism: roughly, the extent to which causal explanation of the behaviour of social groups can/should take place "in terms of individuals" (Watkins 1957, Lukes 1968, Kincaid 1996 1997). One question concerning the latter models is the question of group selection explanations. Can the phenotypes of biological groups or biological individuals be explained by appealing to what is good for the group? (Maynard-Smith 1964, Sterelny 1996, Sober and Wilson 1998, Okasha 2006, Lehmann et al 2007). This question is arguably of great importance to the study of cultural evolution (Boyd and Richerson 1998).

As a result there has been much discussion of how the issue of methodological individualism as regards social science relates to the issue of group selection as regards evolutionary biology. (In particular the articles collected in Koppl's "Evolutionary Psychology and Economic Theory", 2004.) Are the two compatible? I take this question to amount to the following: can one explain the behaviour of human social groups (a) only "in individual terms" and (b) by appeal to what is good for the group?

There seems to be a growing consensus that the answer to this question is "yes". I agree. I argue, however, that there is much more to the relationship between GS and MI than this alone acknowledges. In particular, I say, that to fully embrace the ethos behind MI requires taking a very particular position in the philosophical debate over the status of group selection. Namely:

(a) group selection is a causal process
(b) this causal process is distinct from the process of kin selection
(c) so group selection and kin selection models are not interchangeable
(d) none of the present measures of the strength of within-group vs between-group selection are universally applicable. Nor could they be.
(e) thinking of group selection in terms of levels of nature is, at best, misleading

Cultural Learning and Cultural Evolution

Cultural inheritance of mentalizing

Heyes Cecilia, All Souls College, University of Oxford, UK

Even those who emphasize the power of cultural evolution typically assume that ‘cultural learning’, the cognitive mechanisms underwriting cultural evolution, are genetically inherited. In contrast, I'll argue that it is not just the grist but also the mills that are cultural in origin; humans learn from others not just facts about the world and skills for dealing with it (grist), but also the cognitive processes that make ‘fact inheritance’ possible (mills). Literacy is a paradigmatic example of the cultural inheritance of cultural learning. Previously I have argued that social learning, imitation, and mirror neurons provide further examples. In this paper, I focus on mentalizing (aka ‘theory of mind’, ‘folk psychology’ and ‘mindreading’). First, to clear the ground, I'll examine experimental work that has recently re-invigorated the nativist view of mentalizing. This work seems to show that infants and adults automatically represent what others see, intend and believe; that they engage in ‘implicit mentalizing’. I'll argue that these results are due to ‘sub-mentalizing’ - domain-general cognitive processes that can simulate mentalizing in social contexts. In the second part of the paper, I'll suggest that learning to mentalize is a lot like learning to read. Both acquisition processes are typically guided by expert instruction, and involve the reconfiguration of cognitive parts into a new system. In the case of reading, the crucial parts include generic object recognition processes, attentional routines, and grapheme-phoneme correspondence rules. In the case of mindreading, they include generic inference processes, attentional routines, and behaviour rules.

Morality, Evolution and Culture
Mameli Matteo, King's College, London, UK

I will sketch an account of moral judgment according to which the ability to token moral judgment consists in the ability to acquire certain kinds of dispositional emotions. I will argue that this account is supported by the empirical evidence and show how it deals with commonly discussed features of moral judgment, such as authority independence, meriting and the links with motivation. By adapting and refining some ideas put forward by Christopher Boehm, I will discuss the important role that culture played in the evolution of this ability and the role that culture plays in shaping the variation in the way such ability is expressed in different societies.

Social Learning and Human Cooperation
Sterelny Kim, Australian National University, Australia

In recent work I have defended a three-stage model of the evolution of human cooperation. The first is a transition from great ape rugged individualism to the mutualist foraging of mid-Pleistocene hominins. The second is was a transition from mutualist foraging to reciprocation-based forager economies of the latish Pleistocene. The third was the expansion of collective action in the transition to complex societies; a transition that began around the Pleistocene-Holocene boundary, and is probably tied to the establishment of farming. I have argued that managing reciprocation-based forager economies imposed new cognitive demands, and exposed foragers to increased conflict risks. I have further argued that the appearance of physical symbols in the archaeological record (beginning around 100 kya) is a symptom of these demands and risks. In this paper, I argue that social learning (in a broad sense) played a crucial role in this second transition, enabling humans to evolve to social and cognitive tools they needed to manage economies of reciprocation. The normative life of humans is a culturally evolved response to the changed foundations of forager life.

Darwinian Ethics and Its Challenges (submitted papers)

The Moral Lives of Animals
Bradie Michael, Bowling Green State University, USA

Discussions of the moral status of animals typically address the key questions from an anthropocentric point of view. That is, in deciding whether non-human animals qualify as moral agents the discussion tends to center around the question of the extent to which members if candidate species are like human moral agents. Similarly, in deciding whether non-human animals qualify as appropriate moral patients, the discussion tends to center around the question of the extent to which members of candidate species have capacities and capabilities that are like the capacities and capabilities that are deemed necessary for human beings to be considered as moral patients. Viewing these issues from the point of view of evolutionary biology, cognitive neuroscience and cognitive ethology suggest a different approach one which focuses on the lives of animals that takes their characteristic behaviors and capacities as the basis for determining the norms of moral status for them. One might call this approach a 'speciocentric' point of view. The motivation for taking this approach is the evolutionary consideration that the moral capacities and patterns of moral behavior of human beings are evolved capacities and patterns that are rooted in shared homologies that give rise to homologous capacities and patterns of behavior in other species. In this paper, I explore the theoretical and experimental results which make this approach plausible and address two key questions: [1] To what extent is it proper to speak of the *moral* behavior of non-human animals? [2] To the extent that it is proper, what are the implications for our understanding of the nature and function of human morality and of our treatment of non-human animals?

Evolution and the diversity of moral norms

Bruner Justin, University of California, Irvine, USA

The evolutionary approach to ethics has by and large focused almost exclusively on the question of altruism. Such single-mindedness is problematic for it neglects other important features of moral systems such as *codes of behavior*. These so-called moral codes or moral norms guide individual behavior in a number of ways, from hygiene to prohibiting certain activities such as the eating of pork of engaging in violent and reckless behavior. I devise a simple game-theoretic framework to explain the sustained existence of these often costly moral norms. These norms can be easily sustained through the combined mechanisms of reputation tracking and altruistic punishment. Reputations track both adherence to the norm and whether one punishes those in disrepute. Thus all are incentivized to punish both norm violators as well as well as those who fail to administer punishment, *on threat* of punishment. This maneuver allows us to avoid the infamous "second-order free-rider problem" known to plague costly punishment. I formally demonstrate the above arrangement is evolutionarily stable and, under the right parameter values, can support norms that are detrimental to both the group and individual. This theoretical result not only sheds light on an underappreciated facet of moral systems, but can also help explain the fact of *moral diversity* – i.e., that moral codes vary wildly from society to society. This formal model allows us to precisely articulate the conditions under which we'd expect there to be much moral diversity: when there are little to no selection at the level of the group.

Descriptive and Prescriptive Darwinian Ethics

Oseguera Gamba Jorge, UNAM, Mexico
Martinez Maximiliano, Universidad Autonoma Metropolitana, Mexico

Naturalistic philosophy attempts to inform itself with the most accepted scientific theories available. Evolutionary ethics, as a naturalistic philosophy of morality, must therefore inform itself with widely accepted theories available about evolution. In this paper we analyze the implications of Darwinism in both the descriptive and prescriptive domains of ethics. By giving a theory of normative justification we offer an account of how to move from descriptive ethics to prescriptive ethics. This account works as a filter that avoids committing what some call "the naturalistic fallacy" but at the same time allows making a move from 'is' to 'ought'. We first focus in the negative implications, i.e. what does not follow from Darwinism: In the descriptive level, some evolutionary approaches to ethics are dismissed, since their teleological view of evolution is incompatible with Darwinism. In the normative level, the theories derived from a teleological view, like (the wrongly called) "Social Darwinism" and Waddington's ethical-political view, are also discarded. Then we focus on the positive implications, i.e. what we can conclude from Darwinism on ethics: In the descriptive level, models of moral psychology are extracted from Darwinian explanations and supported by experimental studies. We conclude that positive implications in the prescriptive level are too risky and point out several issues that have to be further discussed, like the problems posed by Darwinism to Moral Realism and Moral Intuitionism.

Debates About the Level of Selection A (submitted papers)

Species Selection and the Individuality Thesis: A Lesson in Ontology from a Tasmanian Wolf

Finkelman Leonard, CUNY Lehman College, USA

In the ontology of selection processes, units of selection are individuals and units of evolution are classes. In their individuality thesis, Ghiselin and Hull argue that species are individuals. One would therefore expect that proponents of species selection, wherein species are units of selection, would endorse the individuality thesis; however, this is not the case. I argue that this is because the standard of individuality in species selection is in fact incompatible with the standard of individuality in the individuality thesis.

Species selection and the individuality thesis imply different ontologies under appropriate conditions. The standard of individuality for units of selection is instantiation of fitness values. I argue that entities come to bear fitness values because of the structure of their parts, and so species would be units of selection only if they had the appropriate internal population structure. The standard of individuality for Ghiselin and Hull is extension: a species is identical with its members. I cite the example of the Tasmanian Wolf (*Thylacinus cynocephalus*), a species whose last member died alone in captivity. By Ghiselin's and Hull's standards *T. cynocephalus* would be identical with the single organism. Species selection's standards imply the opposite: as a unit of selection, *T. cynocephalus* must already be extinct when reduced to a single organism since population structure has broken down. The two standards of individuality therefore identify species with different entities. I use this argument to suggest which species concepts may be appropriate for accounts of species selection.

On the Status of the Debate About Biological Individuality

Booth Austin, Harvard University Department of Philosophy, USA

Several philosophers of biology have recently argued that some biological systems composed of heterogeneous entities that hail from independent lineages, such as biofilms and symbiotic consortia, can rightly be said to be biological individuals. Many arguments in this vein suggest that a version of David Hull's replicator/interactor framework is the best way of understanding the individuality of these kinds of systems. The replicator/interactor framework is often seen as an alternative to the classical view seen in Lewontin and developed in detail by Godfrey-Smith, which excludes biofilms and most symbiotic systems as Darwinian individuals. Here I investigate the status of the debate between these two views on biological individuality. A pragmatic or pluralistic view about evolutionary individuality is clearly an option, though nobody has developed such a view in any detail. There appear to be no decisive arguments against either the defender of the replicator/interactor framework or the Darwinian populationist. Moreover, each party in the debate advocates a substantively different and somewhat revisionist biological ontology. The entities that are cohesive with respect to the process of natural selection on each view are radically distinct. Hence, the two views each envision different kinds of causal processes at work in nature. I argue that this fact makes a pluralistic view about evolutionary individuality seem implausible. Nevertheless, I suggest that the debate as it is currently articulated is at a stalemate. I cautiously investigate some reasonable paths forward.

Variation Within and Between Hierarchical Levels
McCall Lauren, American Museum of Natural History, USA

Variation may be adaptive, neutral, or non-adaptive, and may occur both within and between hierarchical levels, in other words, both within and among groups. For those who are interested in multi-level selection, all group properties are of interest, not just their fitness. Therefore we must consider variants arising from interactions that instigate cohesion as a group, if only temporarily. How does adaptive variation arise before it is maintained more permanently by natural selection? Does it arise in similar ways at different levels? Can it arise at new hierarchical levels, before these levels evolve more permanent status themselves? I address these and related questions drawing on examples across the tree of life, including human groups.

Debates About the Level of Selection B (submitted papers)

Conceptions of Multilevel Selection and their Implications for Empirical Results
Dimond Christopher, Arizona State University, USA

Biologists and philosophers continue to debate the concept of natural selection working in hierarchical biological systems. At the core of these 'multilevel selection' debates are questions about the best models and conceptual approaches to understand selection occurring across multiple levels of biological organization and how to define or identify levels or units of selection. Most of these discussions have focused on providing conceptual clarity without addressing how well these models and approaches can be used to identify levels or units in experimental studies. In this regard, it seems important to compare the varied approaches advocated by theoreticians and philosophers of biology with the approaches used by experimentally focused researchers, in order to understand if there are important consequences when interpreting empirical group and multilevel selection data.

Here I will present the experimental design for a multilevel selection experiment using the parasitoid wasp Nasonia to serve as an in-principle model to which I will apply a selection of advocated analyses drawn from the theoretical, philosophical, and experimental literature. In doing so, my goal is to explore how the differences in proposed approaches can lead researches to different conclusions, even when applied to the same empirical example. I will also highlight the ways in which the theoretical, philosophical, and experimental approaches to multilevel selection correspond and the ways they differ, and I will suggest some ways that these different approaches can be combined to contribute to future research.

Interactionist Group Selection
Kokkonen Tomi, TINT, University of Helsinki, Finland

I will defend a position on levels of selection in the evolution of social behavior that I call “interactionist group selection” and that is somewhere between “broad sense” (quasi)individualist selectionism and trait group based (quasi)multilevel selectionism. I will first make a distinction between a behavioral trait and the mechanism underlying it and argue that they cannot be equated for evolutionary purposes. This matters because the mechanism is what gets selected but the behavior it produces is what it gets selected for, and in the case of social behavior, they can get decoupled in a way that has consequences for the levels of selection. For example, in reciprocal altruism, the behavioral disposition for reciprocity gets selected because it is beneficial for an individual in a particular social context, but that is due to the interaction it creates between individuals participating in the interaction, i.e. the trait group. This does not, however, make the psychological mechanism underlying the reciprocally altruistic behavior evolutionarily altruistic (and this is not an averaging fallacy either). I will argue that the proper interpretation of trait group selection is not that it is a form of group selection in the sense that there are two different levels for fitness beneficiaries but in the sense that there are group traits (the behavioral interactions) that get selected against alternative group traits (e.g. not interacting), and these traits are still dependent on making the individuals participating the interaction fitter than those who are not.

MLS3: Expanding Multi-level Selection Theory to Capture Hierarchical Transition by Individuation

Crawford David, Department of Philosophy, University of Bristol, UK

I expand current multi-level selection (MLS) theory to cover hierarchical transition (HT) by individuation. Current theory models HT from one- to two-level selective systems as a shift from MLS1 to MLS2 (Michod 1999; Okasha 2006; Godfrey-Smith 2009). On this model, whole (or 'collective') fitness emerges alongside part fitness via integration of parts. Recent work shows that HT can also occur via the individuation of parts within a whole (e.g., in filamentous fungi). On this model, part fitness emerges alongside whole (eventually 'collective') fitness via individuation of parts within the whole.

To accommodate this new HT form, I expand MLS theory to include a new stage, MLS3. This stage parallels MLS1 by including selection at only one level, but also allows for aggregate (or 'partitioned') fitness at a second level. In MLS3, the whole is the subject of natural selection, but in virtue of their role in whole-level fitness, parts are assigned a derivative part-level fitness. Hierarchical transition via individuation is modeled in terms of a shift from MLS3 to the MLS2 stage of current theory.

After introducing an expanded MLS framework, I show the formalization of MLS3 and HT via individuation using the Price equation, following Okasha's (2006) similar treatment of HT via MLS1-to-MLS2. I end with a discussion of major differences between the two approaches to MLS2, notably that the MLS3-to-MLS2 transition, unlike the MLS1-to-MLS2 transition, does not begin with within-system selection (the cooperation/conflict trade-off) but rather with a less formidable HT barrier (the delegation/determination trade-off).

A Defense of Superorganisms

Kovaka Karen, University of Pennsylvania, USA

The idea that some highly organized (eusocial) insect colonies are mutually dependent, functional wholes visible to natural selection is widely accepted. More controversial is the claim (Wilson and Sober 1989; Hölldobler and Wilson 2008) that such colonies are ‘superorganisms,’ biological units analogous to organisms in important ways. In this talk I defend the superorganism view on the grounds that it helps us investigate the genetic basis of eusociality.

Superorganism critics (Ghiselin 2011; Haber 2013) argue that thinking of colonies as superorganisms undermines rather than supports the idea that colonies are units of selection. They also worry that the analogy between organisms and colonies is misplaced and may obscure our understanding of colony-level processes. Part of this concern is valid. For instance, appealing to superorganisms to claim that colonies are units of selection is a mistake. However, it does not follow that biologists should discard the superorganism view.

In response to these criticisms, I consider a specific example of the superorganism view in eusocial insect research (Johnson and Linksvayer 2010). I show that in practice, the superorganism view functions as a valuable research tool while avoiding critics’ concerns. First, it reveals explanatory gaps in our current understanding of the genetic basis of eusociality. Second, it generates further research questions in response to these gaps. Third, the view highlights an evolutionary problem faced by organisms and colonies alike, but suggests that they have solved the problem in divergent ways. This result allays the concern about analogies between levels of biological organization.

Degeneration: Rethinking Teleological Conceptions of Living Organisms

Early 19th century Animal and Plant Breeders' views on Variation, Degeneration and Teleology

Holmes Tarquin, University of Exeter, UK

Much of the discussion of late 18th and early 19th century views on variation and degeneration has centred on the often opposing ideas of naturalists on the subject, e.g. Linnaeus and Buffon. This was, however, also the period in which methodical breeding techniques based on mass selection came to the fore. My discussion will focus on the conceptual frameworks that both drove and developed in response to these revolutionary changes in agricultural practices. I will in particular focus on the views of the animal breeders Robert Bakewell and John Sebright, and the plant breeders Jean-Baptiste Van Mons and Thomas Andrew Knight. I will attempt to answer, based on these sources, what degeneration meant to early 19th century western European breeders. Specifically, I will cover how they believed degeneration was related to capacity for variation and how variation was itself thought related to external environmental stability and change, and the adaptable capabilities of organisms. I will discuss how breeders manipulated the heredity and environment of their stock in order to control variation and better shape organisms to human purposes, and also what limits, both real and imagined, this control and manipulation was restricted by. In this manner I hope to establish what understanding breeders had, in attempting to shape organisms to human ends, of the teleological aspects of their practices. I will conclude by asking how these breeders' conceptions of variation, degeneration and teleology influenced and were influenced by those of contemporary naturalists.

Treviranus' Biology: Degeneration and the Boundaries of Life

Steigerwald Joan, York University, USA

In the latter eighteenth century the term degeneration became common in natural history discourses. The term marked the effects of the material world on organic forms, but also the capacities of living forms to respond variously to alterations in their physical living conditions. Evidence of the extent of degeneration through experiments with the transplantation and cultivation of plants and animals also acted as evidence for variable conditions of reproduction, making epigenesis a new problematic. Degeneration thus complicated teleological conceptions of the propagation and generation of life, by involving it in the material and contingent. In the years around 1800, it also obfuscated attempts to define a new science of life by demarcating living from lifeless nature. Treviranus' *Biology* is marked by these tensions. He drew a boundary around living beings through their excitability, their receptivity and responsiveness to stimulus; yet he acknowledged that boundary as porous and distributed, with life continually under threat of dissolution into its surrounding environment. He also demarcated living beings through their capacities for assimilation, generation and propagation; yet his study focused upon the contingencies of these processes, upon degeneration, death and extinction, as necessary to regeneration. As new investigations traced the continuities between chemical, electrical and organic phenomena, experiments meant to aid in exploring the bounds of life established only the artifice of such boundaries.

Heredity and Deviation in the Life Sciences around 1800

Mueller-Wille Staffan, University of Exeter, UK

"Around 1800" is a magical date in the history of the life sciences. Everything seems to change, and fundamental biological concepts like organisation, reproduction, heredity come into being. In this paper, I will look at these conceptual innovations from a *longue durée* perspective. On the one hand, I will trace back these concepts to late medieval and early modern fascinations with hereditary diseases and racial diversity. On the other hand, I will demonstrate their implications for "modern" biology, especially Darwinian evolution. In a nutshell, I will argue that the life sciences "around 1800" became occupied with what seems to be an oxymoron: the perpetuation of deviation. This both unsettled teleological conceptions of the living world and provided an entry point for the "experimentalisation" of biology.

Developing Scaffolds in Evolution, Cognition, and Culture

Crafting Interchangeability: A Generative Structure for the Industrial Revolution and for Evolution

Wimsatt William, U. Chicago and U. Minnesota, USA

One of the most important ways of generating deep entrenchment very quickly is to fashion an array of standardized parts which then, like alphabets, words, tinkertoys or electronic components can be used in systematically articulated combinations to produce a large variety of diverse artifacts, adaptations, or adapted systems. This pattern has played important roles in biology, in cognition, in language and in culture. I will draw on the history of technology to consider the difficult process of crafting interchangeable parts for muskets, and the processes to make them in between 1812 and 1841. Out of these processes emerged—scaffolding and scaffolded by—a number of social and technological generating other industries and trained workers who spread these changes and catalyzed the industrial revolution in the United States between then and the Second World War.

Analysis of this process and what it required reveals deep similarities and differences between these and correlative processes in biology and cognition. I will explore some of these and their implications for accounts of developmental and evolutionary processes in the three areas. It also complements the contrast between reproducers and replicators in suggesting that the search for replicators misreads the character of the causal processes and the relevant boundaries of the systems involved. This approach is also consilient with extended and distributed cognition, and with the generation and utilization of naturally forming reference groups or core configurations.

Scaffolded Development – A Reproducer Perspective

Griesemer James, University of California, USA

It is a widely shared goal, post-Modern Synthesis, that philosophical and theoretical accounts of evolution integrate development— evo-devo rather than just evo. I build an account of evolutionary units in terms of “entwined” units of heredity-development that I have called “reproducers.” Peter Godfrey-Smith challenged my “reproducer perspective” in *Darwinian Populations and Natural Selection*, especially my reliance on “material overlap” to characterize reproduction. Prion, transposon, and retroviral replication, Godfrey-Smith argues, require a distinction between material and formal modes of reproduction to fully describe the “menagerie” of reproduction processes.

I argue that biological development usually involves a complex set of interactions with environments that *scaffold* development—eco-devo rather than just evo-devo. Developmental scaffolding is any interaction through which development is facilitated in such a way that new skills or capacities are produced in the developing entity that would otherwise not have occurred, or would occur more slowly, or with more difficulty, or with lower probability. I take up Godfrey-Smith's challenge and characterize the HIV-1 RNA retrovirus as a reproducer and argue that my perspective enhances understanding of ways in which HIV-1 reproduction involves *scaffolded* developmental processes. These produce material relations between parents and offspring far more complex than Godfrey-Smith's distinction can support.

At the Juncture of Generations: Materiality and Scaffolding
Caporael Linnda, Rensselaer Polytechnic Institute, USA

The mother-infant dyad is an example of an “entwined” unit of heredity-development (Griesemer) at a level of analysis that includes culture. Infants are most frequently studied as single subjects, particularly in the search to identify innate, uniquely human, properties of cognition. Attending to the embodied, situated activity of mother and infant makes evident processes that aid in the understanding of cognition and culture at the juncture of generations.

A small case study is illustrative. Observational data indicates that a species-typical pattern of infant nursing scaffolds attributions of intentions and desires and may set the stage for turn-taking. Later in development, infants scaffold adult modeling of complex gestures and speech toward the infant, particularly in play. These interactions can be re-described in terms of processes of scaffolding, material overlap, and both deep and shallow generative entrenchment.

Viewing the repeatedly assembled mother-infant dyad as a “live model” may provide “baby steps” to identify and study scaffolding, material overlap, and generative entrenchment in other situations, including the generation of novelty and infrastructure (Wimsatt). Such situations might be quite abstract, such as agent-based computational models, or extremely rich, as in the observation of inter-disciplinary design teams working to produce novel techno-social environments.

Different Facets of Evolutionary Psychology A (submitted papers)

Phylogenetic Footprints in Organizational Behavior
Witt Ulrich, Max Planck Institute of Economics, Jena, Germany

An evolutionary tool kit is applied in this paper to explain how innate social behavior traits evolved in early human groups. These traits were adapted to the particular production requirements of the group in human phylogeny. They shaped the group members' attitudes towards contributing to the group's goals and towards other group members. We argue that these attitudes are still present in modern humans and leave their "phylogenetic footprints" also in present-day organizational life. We discuss the implications of this hypothesis for problems arising in firm organizations in relation to the coordination and motivation of organization members.

Birds Trust Their Wings, Sharks Their Teeth, and Humans Their Minds: The Critical Intelligence Argument Against Naturalism
Mizzoni John, Neumann University, USA

In this paper I discuss John Haught's ‘critical intelligence’ argument against naturalism. First I outline Haught's version of theistic evolution. Then I discuss the case he makes against naturalism with his ‘critical intelligence’ argument. He uses two versions of the argument to make his case: a *trustworthiness of critical intelligence argument* and an *ineffectiveness of naturalistic theories of the mind* argument. I evaluate both versions of his ‘critical intelligence’ argument against naturalism, and find that both versions contain false premises, and thus come up short in making a strong case against naturalism.

Conflict resolution in primates from an evolutionary approach
Perez-Ruiz Alba, CEFPSVLT, Mexico

Conflict is an inevitable aspect of primate social life. Long-term relationships in primate societies implicate conflict and it occurs in different contexts, the most common are related to competition for resources. Conflict defined as any incompatibility over objectives, is not synonymous with aggression. Many systematic researches have been focus on conflict resolution in non human primates. Post conflict affiliative interactions provide different benefits such as: reduced risk of future aggression, stress reduction and restoration of relationships. The type of conflict and the mechanism of resolution are relevant for future interactions between opponents. From an evolutionary perspective, these mechanisms of conflict resolution contribute to individual reproductive success. The purpose of this work is to analyze the evolution of conflict resolution in non human primates in relation with:

- characteristics of individuals involved in the conflict
- contexts of the conflict and costs and benefits involved
- strategies of conflict resolution (according to benefits of the contest) as:

coercion, avoidance, tolerance, problem solving, third party interactions.

The different patterns of conflict resolution in primate species are a product of the influence of different factors. Moreover, cognitive abilities are related with the types of resolution strategies that different species of primates can use.

Different Facets of Evolutionary Psychology B (submitted papers)

Towards a new evolutionary psychology

Buchanan O'Neal, Western University, Canada

Standard evolutionary psychology [SEP] takes itself to be pulling aside the curtain of illusory motivations of contemporary human behavior to reveal the true biological ones. It claims that our contemporary human minds and social organizations are, in a very real sense, fixed evolutionary adaptations. I have two goals in this paper. My first is to propose a revision to the primary method of SEP–namely, *psychological reverse engineering*. This method involves generating hypotheses about our essential psychological mechanisms selected for in the distant past. The said function of these mechanisms was to solve recurrent adaptive problems (e.g. jealousy as a solution to male sexual competition). On my revision, the contemporary functional roles of any posited psychological process should be characterized alongside a characterization of their possible roles in our evolutionary past. This would allow for a comparison between contemporary psychobiological functions and possible past functions to better assess their purported historical fixity. My second goal in this paper is to extend SEP's way of "biologicizing" ethics to include phenomena that do notl fit a *kin selection* model well. Drawing from biological leverage theory (Barker 2008) and the work of feminist evolutionists, niche constructionists, and developmental systems theorists, I show by ethological example that selection often favors the evolution of minds that can help non-genetic relatives. I conclude with a brief analysis of the evolution of *empathy* in the context of a methodological revised and theoretically expanded *new evolutionary psychology*.

The Cambrian Explosion and the Origins of Embodied Cognition

Trestman Michael, Indiana University, USA

Around 540 million years ago there was a sudden, dramatic adaptive radiation known as the Cambrian Explosion. This event marked the origin of almost all of the phyla (major lineages characterized by fundamental body plans) of animals that would ever live on earth, as well the appearance of many notable features such as rigid skeletons and other hard parts, complex jointed appendages, eyes, and brains. This radical evolutionary event has been a major puzzle for evolutionary biologists since Darwin, and while our understanding of it has recently improved with new fossil finds, richer molecular phylogenies, and better grasp of ecological, evolutionary, and developmental processes generally, unanswered questions remain. In this paper I argue that a basic cognitive toolkit for embodied, object-oriented, spatial cognition (what I call Basic Cognitive Embodiment) is a practical necessity for control of a large, mobile, complexly articulated body in space. This hypothesis allows us to relate the complexification of animal bodies to the complexification of perception, cognition and behavior in a way that can help to fill in gaps in our emerging picture of the Cambrian Explosion, as well as shed light on the deep evolutionary origins of the mind.

Different Facets of Evolutionary Psychology C (submitted papers)

Biological causes and the epistemic status of moral beliefs

O'Neill Elizabeth, University of Pittsburgh, USA

What, if anything, do the biological causes of moral beliefs tell us about the epistemic status of those moral beliefs? Numerous people have argued that evolutionary influence on morality would give us reason to be skeptical about moral claims, or at least about realist interpretations of moral claims. The potential epistemic significance of more proximate biological influences on moral beliefs, however, has received less attention.

This is particularly surprising because recent empirical work on the biology and psychology of morality has provided us with a wealth of evidence about the variety of proximate factors that may influence the production of moral judgments. These factors include emotions such as disgust and contempt, the unconscious application of heuristics and rules, and various features of the environment (such as messiness and time of day), as well as conscious reasoning. Focusing on emotions and the unconscious application of rules, I analyze the relevant empirical literature and argue that these two factors do play an important causal role in the production of moral beliefs. Then I evaluate the extent to which the influence of these two factors on the production of moral beliefs undermines (or strengthens) the epistemic status of those moral beliefs. Lastly, I consider the objection that evolution, in contrast to other types of causes, has unique potential to affect the epistemic status of moral beliefs. In response, I discuss how causal proximity affects the potential of a cause to have implications for the epistemic status of a belief.

Perception-action mechanisms as precursors to empathy

Rosas Alejandro, Universidad Nacional de Colombia, Colombia

Evolutionary approaches to morality converge with those philosophical views that place empathy at the core of moral capacities, but we currently know little about empathy as a mechanism and even less about its evolutionary descent. Preston and de Waal (2002) proposed a perception-action model (PAM) that grounds empathy in perception-action mechanisms. In order to prosper, this hypothesis must cope with some self-imposed challenges.

Neurological evidence for perception-action mechanisms surfaced when a research group in Parma discovered mirror neurons in monkeys, i.e., neurons that fire both when the subject does a goal-directed action and when it observes another individual (object) doing the same action. This gives initial neurological substance to the PAM, or at least to its precursor, but at the cost of making its evolutionary function irrelevant to helping behavior: the mechanism evolves, presumably, to facilitate automatic individual responses to environmental contingencies with the same action that is perceived in others (Preston and de Waal 2002). This accounts for simple forms of imitation that lack 1) a representation of the internal state of others; and 2) a motivation to help. Though imitation is plausibly connected to empathy and the shortfalls of simple forms of imitation are congruent with the label "precursor", a precursor needs a plausible trajectory to the derived trait. In a sketchy and inevitably speculative attempt, I search for clues of such trajectory in the selective pressures behind the complexities of primate social life: the need for a self other distinction, for predicting behavior and for communication.

Beyond Positive Illusions: Free Will as an Adaptive Misbelief

Smithdeal Matthew, University of British Columbia, Canada

Taylor and Brown have identify a number of positive biases mentally healthy individuals tend to have, challenging the claim that good mental health is correlated with holding mostly true beliefs. Likewise, McKay and Dennett argue that these positive biases are adaptive misbeliefs, where the misbeliefs are fitness increasing in and of themselves, independent of the system that produces them. It has been suggested by Randolph-Seng that one's belief in free will may be correctly regarded as a further example of adaptive misbelief. While McKay and Dennett argue that one's belief in free will should be regarded as a true belief, not an adaptive misbelief, I argue that their rebuttal is not sufficient.

In their own arguments, adaptive misbeliefs are correctly regarded as ungrounded, where the benefits are accrued regardless of their veracity. As such, the veracity of one's belief in free will must be separated from one's experience of control and McKay and Dennett fail to adequately challenge the issue at hand. I propose that we should examine from where one derives one's belief in free will, while remaining agnostic towards the veracity of the belief. In accepting that one derives a belief in control from one's experience of control resulting from a subset of cognitive systems termed "controlled systems", we have evidence for a cognitive system that produces an ungrounded belief in free will; this belief in free will is fitness increasing in and of itself and should be correctly regarded as an adaptive misbelief.

Evolutionary Psychology and Multimodularity: Rebutting Samuels' Challenge

Dahlgrün Malte, Humboldt-Universität zu Berlin, Germany

Evolutionary psychologists claim that the human mind contains a far greater number of reliably developing (“innate”), domain-specific, computational adaptations than has been standardly assumed. Perhaps the most prominent philosophical criticism of this multimodularity claim (MMC) is due to Richard Samuels, who has challenged the general arguments advanced in its support.

Emphasizing that evolutionary psychologists posit innate, domain-specific (IDS) computational adaptations qua mechanisms, Samuels argues that MMC is “unwarranted and unmotivated”, since the general arguments offered in its favour fail to give us reason to prefer MMC to a supposedly neglected alternative. According to this alternative, the human mind contains many truth-valuable IDS representations operated upon by domain-general computational mechanisms.

I argue that Samuels' criticism fails on several counts.

(1) Samuels frames the debate in terms of a false dichotomy. Pitting a model of the mind involving IDS structure only qua computational mechanisms against one involving IDS structure only qua representational structures, he associates evolutionary psychology with the first option. In fact, evolutionary psychologists consciously posit IDS mechanisms with IDS representations inextricably tied into them.

(2) Evolutionary psychologists have explicitly argued for the need to posit rich IDS representational structures.

(3) Samuels misstates the MMC, describing it as an hypothesis regarding “central cognition”. In doing so, Samuels begs an important architectural question: Evolutionary psychologists reject classical cognitive science's sequestration of a realm of central cognition. However, Samuels' argument applies only to “central cognition”.

(4) Samuels' discussions of MMC lack examples to support his persistent claim of evidential parity for domain-generally processed IDS representations versus IDS mechanisms. Many counterexamples could be given in which Samuels' alternative doesn't seem close to the former in terms of efficiency or evolutionary plausibility.

Ecological explanation at different levels and scales

Distinguishing ecological from evolutionary approaches to transposable elements

Linquist Stefan, University of Guelph, Canada

Considerable variation exists not only in the kinds of transposable elements (TEs) occurring within the genomes of different species, but also in their abundance and distribution. Noting a similarity to the assortment of organisms among ecosystems, some researchers have called for an ecological approach to the study of transposon dynamics. However, there are several ways to adopt such an approach, and it is sometimes unclear what an ecological perspective adds to the existing co-evolutionary framework for explaining transposon-host interactions. At a more fundamental level, the application of ecological thinking to TEs raises the question of what is distinctive about an ecological, as opposed to an evolutionary approach, in general. To address these issues, we offer an operational distinction between ecology and evolution. This framework allows one to quantify how much of a given pattern calls for ecological and evolutionary explanations, respectively. To illustrate how this framework applies to a concrete example, we analyzed whole-genome data for one set of distantly related mammals and another more closely related group of arthropods. Ecological factors explained most of the variation in TE abundance and distribution among closely related organisms. Evolutionary factors were not significant at this level. However, the explanatory roles of evolution and ecology become inverted at the level of TE families, or, among more distantly related genomes. The fact that ecological processes impact TE lineages over relatively short time scales further raises the possibility that transposons might serve as useful model systems for testing more general hypotheses in ecology.

Generality in community ecology

Cottenie Karl, University of Guelph, Canada

In 1999, John H. Lawton wrote a hugely influential paper (with more than 700 citations) titled “Are there general laws in ecology.” In it, he argued that general laws in community ecology are probably not possible because communities are extremely context dependent. This will make it extremely difficult to find common processes or even patterns prevalent across different systems, and, he argues, ecologists should focus instead on either populations or biogeography in search for generality. However, more than 10 years later, ecology has gone through a major shift by quantitatively synthesizing individual empirical studies through the statistical framework of a meta-analysis. At the same time, this quantitative synthesis also determines whether a pattern or process is general or not, and thus actually provides a quantitative test for Lawton's intuitive and philosophical argument. We used a recent compendium of meta-analyses in ecology collected and analyzed by Cadotte and co-authors to extract from each meta-analysis what type of ecology it studied (populations, communities, ecosystems, or biogeography), and whether the meta-analysis found evidence for generality. Contrary to Lawton's predictions, our meta-analysis of meta-analyses found considerable evidence for generality in community ecology. The levels of generality at this level were no less than for population ecology or biogeography. These results illustrate that ecology as a science has matured considerably since its roots in natural history, and provide guidelines on what specific research areas show promises in generating reliable predictions for applications such as conservation biology.

The problem of pattern and scale in ecology: what have we learned in 20 years?

Chave Jérôme, Laboratoire Evolution et Diversité Biologique, France

Over the past 20 years, major advances have clarified how ecological patterns inform theory, and how in turn theory informs applied ecology. Also, there has been an increased recognition that the problem of scale at which ecological processes should be considered is critical if we are to produce general predictions. Ecological dynamics is always stochastic at small scales, but variability is conditional on the scale of description. The radical changes in the scope and aims of ecology over the past decades reflect in part the need to address pressing societal issues of environmental change. Technological advances in molecular biology, global positioning, sensing instrumentation and computational power should not be overlooked as an explanation for these radical changes. However, I argue that conceptual unification across ecology, genetics, evolution and physiology has fostered even more fertile questions. We are moving away from the view that evolution is played in a fixed ecological theatre: the theatre is being rapidly and relentlessly redesigned by the players themselves. The maintenance of ecosystem functions depends on shifts in species assemblages and on cellular metabolism, not only on flows of energy and matter. These findings have far reaching implications for our understanding of how ecosystem function and biodiversity will withstand (or not) environmental changes in the 21st century.

Ecology and Evolution: How Ecology Matters (*Interdisciplinary session*)

Chaos and Unpredictability in Evolution

Doebeli Michael, University of British Columbia, Canada

What would happen if we "replayed the tape of life", i.e., if the history of life were restarted and the biosphere would evolve anew? This is a question about evolution as a dynamical system: is evolution fundamentally chaotic, and hence unpredictable? The possibility of complicated dynamics driven by non-linear feedback mechanisms has revolutionized science in the latter part of the last century. Perhaps surprisingly, few of these insights have entered the realm of evolutionary biology. The concept of "survival of the fittest", central to much evolutionary thinking, embodies a perspective of evolution as a directional optimization process, and hence as a dynamical system that converges to an equilibrium in phenotype space, representing the optimally adapted type. This perspective may be correct for simple scenarios, but generally not when ecological interactions are taken into account for evolutionary processes. Ecological interactions generate frequency-dependent selection, as when the success of a certain food preference depends on the food preference of other individuals. In most organisms many phenotypic properties combine in complicated ways to determine ecological interactions, and hence frequency-dependent selection. Therefore, it is natural to consider models for the evolutionary dynamics generated by frequency-dependent selection acting simultaneously on many different phenotypes. We argue that complicated, chaotic dynamics of long-term evolutionary trajectories is common in a large class of such models when the dimension of phenotype space is large, and hence that the perspective of evolution as a process that eventually equilibrates in constant environments must be fundamentally revised.

Ecological Experiments that Inform Evolution: A Typology

Millstein Roberta, University of California Davis, USA

In Chapter One of Jared Diamond and Ted Case's classic Community Ecology, Diamond provides a typology of three types of experimental methods: laboratory experiments (or LEs – these are perturbations produced by the experimenter in the laboratory), field experiments (or FEs – these are perturbations produced by the experimenter in the field), and natural experiments (or NEs – these are natural perturbations occurring in the field). In identifying the strengths and weaknesses of each kind, Diamond claims that "the NEs' expanded spatial and temporal scales open up for study a whole range of problems (including evolutionary ones) that are inaccessible to FEs and LEs" (1986, 14); he also states that "FEs are blind to whole classes of phenomena" such as "genetic changes (evolutionary responses)" that are detectable by NEs

(1986, 10). But is it really the case that laboratory experiments and field experiments are uninformative for evolutionary questions? Furthermore, are there other experimental methods whereby ecology can inform evolution? For example, social scientists describe a method called causal process tracing (Brady and Collier 2010); is this a fourth method or a combination of the other three methods? Or is it not an experimental method at all? The answers to these questions will be explored though brief case studies illustrating the different types.

Life history evolution in metapopulations

Ronce Ophelie, ISEM CNRS, Université Montpellier 2, France

I will explore how ecology matters for evolution using Life History theory from a metapopulation perspective. Life history theory deals with the evolution of those traits that shape an organism's age schedules of birth and death. Life history evolution is a very productive field organized around a few central questions with a very strong unifying theoretical background, grounded in both optimization principles and quantitative genetics. The realm of most studies of life history theory is however that of a single, large, undisturbed and spatially homogenous population. Despite increasing awareness of the importance of metapopulation structure and dynamics for the demography, genetics and conservation of many species, little is still understood about how much these characteristics have shaped basic life histories. Founding events and small local population size in a metapopulation are two causes of genetic resemblance among neighbours exploiting the same local environment. I will illustrate how this genetic structure makes life history evolution in a metapopulation deviate from that expected in a single large panmictic population. Changes in population age structure and density following disturbance and recolonization are major features of life in a metapopulation. Species whose biology is most adequately described using the metapopulation framework also often occur in habitats subject to successional changes. Such variation in selection pressures associated with colonization and succession have deep implications for life history evolution.

When Does Ecology Matter? The Stories of Fisher and Wright

Rosales Alirio, University of British Columbia, Canada

There has always been discussion on whether ecology was or not part of the "modern synthesis." And the question of the significance of ecology for evolution recurs in the literature. In this paper I explore how ecology matters for evolution by revisiting two influential and widely discussed theories of evolution formulated by R.A. Fisher and Sewall Wright respectively, namely, mass selection and the shifting balance theories.

I argue that they both have a narrative structure, as they provide generalized stories of the evolutionary process. The question then is: what do Fisher's and Wright 's stories of evolution tell us about ecology? The answer is: not much but a whole lot! Their stories reveal where ecology intervenes in the evolutionary plot. This leads to two crucial ways in which ecology matters for evolution, or so I argue.

For Fisher, ecology determines whether new mutations will be wiped out by drift or will be the subject of natural selection. And it sets limits on how fitness increases by natural selection. For Wright, the situation is more complicated. Part of his story is consistent with Fisher's, but peak shifts require drift, and further evolution requires selection between groups, in the third phase of his shifting balance story. Further theoretical work has shown that, for this to be a plausible mechanism for the spread of adaptive configurations, explicit models of population regulation have to be considered.

Ecology and Society A (submitted papers)

Where Science Meets Society: A Sociological Case for Ecology
Richard Amanda, Florida State University, USA

My paper investigates the applications and explanatory power of ecology in the social realm, specifically public policy decisions and the study of social behavior. As a sub-discipline of biology, ecology is relatively new and lacks the discernible set of objective laws possessed by the more classical sciences, such a physics or chemistry. My thesis is that, in the absence of an identifiable universal system, ecology may be able to supplement its limited objective truths through the aptness of its concepts to engage non-scientific pursuits and public appeal.

Using a population-community approach to ecology, I focus on the history and uses of biodiversity. I make the case that biodiversity, as the study of populations, communities, and ecosystems, has been appropriately politicized to contribute to solutions for resource management and species protection issues. And that not only is the public consideration of nature consistent with the intent of early conservation biologists such as Aldo Leopold and Rachel Carson, but that, contrary to dissenting claims, the current political agenda does not preclude a later re-orientation toward more rigorous science proper, nor is it damaging to ecology's scientific credibility. I argue that, while on a trajectory of becoming a more law-like science, ecology has been well suited to bridge values and scientific reasoning to a productive political end.

Between place and cosmos: biodiversity knowledge, expertise and the IPBES
Borie Maud, University of East Anglia, UK

The first official plenary session of the Intergovernmental Platform on Biodiversity and Ecosystem Services (IPBES) took place in January 2013, in Bonn. The ambition of this emerging advisory body is to encourage governments and decision-makers to take action to prevent biodiversity loss and ecosystem services degradation. Several initiatives had been preparing the ground for IPBES, especially the Millennium Ecosystem Assessment (MA) and the consultative process for an International Mechanism on Scientific Expertise for Biodiversity (IMoSEB). In this paper, using STS concepts and methods, we draw our attention to (1) the origins and the early stages of the life of IPBES and (2) the tensions and challenges facing ecology as it goes global. While ecology has traditionally been described as a “science of place” (Kohler, 2002), the inscription of the “biodiversity crisis” on the international agenda and the empowerment of ecology in global institutions of scientific advice such as IPBES raises some questions regarding the production of ecological knowledge. The “biodiversity crisis” that IPBES is meant to address has a strong local component and while for climate change it has been possible to construct “global kinds of knowledge” (Hulme, 2010), such an aspiration does not seem possible (nor desirable) for IPBES. While the Intergovernmental Panel on Climate Change (IPCC) has often been referred to as a model of success in the field of global environmental governance, weaknesses regarding, inter alia, its model of expertise have also been highlighted.

Environmental Crises and the Evolved Mind
Zinser Jason, University of Wisconsin Colleges, USA

The causes of environmental degradation are as varied and dynamic as the problems themselves. However, one cause, which is often neglected, is how our evolved (innate) psychological dispositions contribute to ecological crises. Behavioral economics and moral psychology have demonstrated that our reasoning is often irrational and our moral judgments are, at times, capricious. Global climate change, perhaps the preeminent ecological and human crisis in our history, is a paradigmatic example of how our psychological dispositions can frustrate a coordinated response to the crises.

I will highlight the challenge that climate change poses with respect to our evolved mind by contrasting it to a different environmental challenge, chemical pollution. I will argue that the threats of toxins in the environment are much easier, in some respects, to perceive and responds to than the threats posed by climate change. For example, the success of Rachel Carson in sparking the American environmental movement and advancing environmental policy is, in part, due to our ability to recognize the associated risks of pollution. Unfortunately, the threat that climate change poses does not “present itself” to our evolved mind in the same way that pollution does. I will conclude by offering some strategies to respond to these problems in light of our innate psychology.

People save the day: the influence of public activism on the history of conservation biology and why it remains important today

Koslowsky Hannah, Florida State University, USA

While conservation biology has continued to become more scientific and focused on the economics of nature, I propose that public advocacy is equally important. Origins of conservation biology in North America date to the 19th century with the publication of George P. Marsh's *Man and Nature* in 1864. Organizations initiated by concerned citizens, such as the American Forestry Association established in 1875 by Dr. John A. Warder, allowed the public to voice their concerns to government about the nation's forests and other natural resources. Government was not the motivating force; ‘conservation through wise use' wasn't politically acknowledged until 1909 when Theodore Roosevelt established conservation as a public responsibility.

Today, conservation biology continues to need public advocacy. Political decision-making uses economic models and conservation biology is predominantly considered through monetary value. Although this may be the most comprehendible way for political decisions to be made, reducing conservation to a loss/gain economic system has many shortfalls, including not considering sustainable yield. Moving away from conservation biology's game management history of consumptive value, public organizations can influence the field by demonstrating the many ways humans value nature. Environmental activist groups have varying motivations (e.g. Audubon Society, Ducks Unlimited), and yet can have better support and success by operating outside politics and bureaucracy. The goal of conservation biology is to prevent, mitigate and possibly reverse human influences on ecosystems. Conservation biology is not only an ecological and scientific problem; it is also a social problem, where public interest and activism are crucial.

Ecology and Society B (submitted papers)

Ecosystem Function and Environmental Values

Cooper Gregory, Washington and Lee University, USA

Work in environmental ethics, and on environmental values more generally, is rife with references to the concept of ecosystem function. In much of this work, the concept of ecosystem function is being asked to shoulder a heavy normative burden. Ecosystem holists of various stripes, from Aldo Leopold to Holmes Rolston, use ecosystem function support the moral standing of ecosystems. Here functional integrity plays the role that interests play in a more individualistic ethics – it allows us to determine the specific nature of our duties to ecosystems. Less radically, conservation biologists seek to underwrite the value of biodiversity by tying it to ecosystem function, thereby capturing, at last, ecology's Holy Grail of connecting diversity and stability. Ecological economists see ecosystem function as key to maintaining the sustainable delivery of valued ecosystem goods and services. The centrality of ecosystem function to ecological inquiry generally already points up the need for an explication of the concept; these normative demands render that need even more urgent. Yet problems with the individuation of ecosystems and the absence of ecosystem-level selection raise questions about whether a successful explication will be forthcoming. The goals of this paper are twofold: first, to clarify the various ways in which the concept of ecosystem function is being asked to do this normative heavy lifting and, second, to raise questions about the extent to which the conceptual foundations of the notion are secure enough to justify confidence that it will be up to the task.

From local newspaper notes to DNA profiles - The science and politics of wolf population estimates in Norway from the 1960s until today

Stokland Håkon B., Norwegian University of Science and Technology, Norway

The first population estimates of wolves in Norway were made by wildlife biologists in the 1960s, by browsing through local newspapers in search of notes about people who had observed wolves. Besides from a bounty paid for killed individuals, wolves were not managed by state authorities in Norway at the time. When the wolves got protected by law in 1971, they were simultaneously made formal objects of management for the Norwegian directorate of nature management. As a consequence of this and a rise in both wolf numbers and political controversy during the following decades, great efforts have been made at developing more accurate methods for population estimates. Today, the wolves in Norway are among the most intensively monitored in the world, and wildlife biologists and geneticists employed by the directorate have established DNA profiles, territories, kinship relations, and inbreeding coefficients for almost all wolves in Norway.

This paper will trace the efforts of wildlife biologists to record and monitor wolves in Norway from the 1960s until today. It will examine the development of increasingly accurate and extensive methods, by employing research reports and archival material from the directorate as sources. Further, the paper will investigate how the wolves in Norway have come to be so closely monitored, and explore the relations between the intensified production of knowledge and the increasingly detailed regulation of the wolves.

A Conflict between Biology and Geology: The “Thirty Years’ War” in Coral Reef Studies, 1910-1939

Sponsel Alistair, Vanderbilt University, USA

The history of coral reef science is often told in two parts, with a nineteenth-century story of the development of Charles Darwin's theory of reef formation followed by an epilogue about the widely-acclaimed confirmation of that theory shortly after World War II by geologists working at the US nuclear proving ground in the Pacific, where at Enewetak Atoll they used a drill rig to collect core samples of the reef all the way to its volcanic foundation nearly a mile below sea level. Scarcely any historical attention has been paid to reef studies in the intervening period or, indeed, to the question of how Darwin's theory remained sufficiently controversial that the postwar core drilling was major scientific news. I argue that the core drillings at Bikini and Enewetak atolls were, notwithstanding their outsize place in conventional histories, a continuation of pre-war “normal science,” and I show that the scientists brought by the US Navy to conduct pre- and post-bomb surveys brought with them the very research questions that had animated the remarkably combative field of reef studies in the inter-war years. This combat was truly inter-disciplinary, both in the sense that it formed an independent scientific discourse that overlapped the domains of multiple disciplines and in the sense that the main controversies were polarized in a way that made it seem that the disciplines themselves were combatants. At the poles of the dispute were biology and geology; clustered around them were (on one side) reef ecology and “coral bionomics” and (on the other side) physical geography or physiography. The figures in these disputes considered Darwin's coral theory to be just one among many possible explanations for the origin and shape of reefs. Throughout what the authors of a 1949 review essay called the “Thirty-Years' War” over reef formation, the questions of research location and method were primary. Alternatives ranged from the "home study" of hydrographic charts and photographs of reefs' physical features to highly localized and labor intensive experimental studies of coral reproduction and growth in the field. However, as I demonstrate, nearly all participants acknowledged that deep core drilling all the way to bedrock through a living reef would be a way to resolve many of the disputes. I close by contrasting my interpretation of the reef studies at the nuclear proving ground with other historians' descriptions of military patronage of other scientific research during and after World War II, arguing against framing the issue in terms of "exploitation."

Emergence and Downward Determination in Biological Systems?

Emergence and Downward Determination from a Philosophical Point of View

Matsumoto Shunkichi, Tokai University, Japan

As a philosopher I will critically examine the arguments of two biological scientists, Naoki Sato and Toshiyuki Nakajima, on emergence and downward determination respectively, in biological systems.

As for the notion of emergence, there has been rich tradition of philosophical arguments about diachronic and synchronic emergences, its relationship with reduction, epistemological emergence as unpredictability and ontological emergence as supervenience, and so on. In my talk, I will try to contextualize Sato's proposed notion of 'dynamic' emergence in this tradition and examine whether his notion really adds to the inventory of emergence. In addition, I will consider the legitimacy of his idea that it is genetic information which differentiates biologically emergent phenomena from non-biologically emergent ones, thereby making life really deserve to be so called.

The notion of downward determination, too, is what has been much debated in philosophical literature. I will explore whether Nakajima's radical proposal that Darwinian theory will remain incomplete until it fully recognizes the importance of, and incorporates into its framework, the downward determination from upper-level entities (like ecosystems) to the lower-level ones (populations, organisms, and so on) is really news for us traditional neo-Darwinists. For, we have already been much discussing such problems as the multi-level selections where the fitnesses of the lower, embedded entities depend on the structure or organization of the upper, embedding entities (Okasha 2006).

Dynamic notions of emergence: interplay of entropic driving principle and environmental/genetic constraints over the hierarchy of life

Sato Naoki, University of Tokyo, Japan

Life and mind are considered as good examples of emergence. As Malaterre (2010) discussed in his book, there are different notions of emergence, synchronic/diachronic or epistemic/ontological. Recent developments in biophysics revealed a new type of synchronic ontological emergence in complex systems. Synchronic emergence, in general, involves phenomena at two different levels. A structural organization at a higher level appears to result spontaneously from complex dynamics at a lower level. Bénard convection is a classical example, in which a simple mechanical causality between heat flow and convective structure is not apparent. The convection is instead a result of a conflict between thermal non-equilibrium and gravitational constraint. This, in turn, may suggest that the notion of levels is relative to conflicting forces, and that emergence should be considered in a dynamic context.

This physical model can be extended to biological models, in which internal entropic force and environmental constraints conflict with each other. I suppose a universal entropic driving force ("inhomogeneity" or Brillouin's "order") in the forms of free energy, spatial disequilibrium, or genetic information, which ultimately originates from the sunlight and drives all biological phenomena throughout various levels (*Entropy* 14, 233-251, 2012). We can discriminate biological systems from non-biological ones by genetic information, a form of inhomogeneity, which provides an additional constraint over the metabolic free energy to produce reproducible "self-organized" structures. Such dynamic interplay between internal motive force and the environmental/genetic constraints is a general feature of biological systems, which will overcome classical controversy on emergence.

Ecosystem downwardly affects adaptive evolution
Nakajima Toshiyuki, Ehime University, Japan

Darwin's theory of evolution asserts that the population of organisms evolves automatically, if the population contains heritable phenotypic variation of organisms and if their capabilities of survival and/or reproduction are different in a given environment. The theory presupposes (i) the existence of variation of organisms' heritable phenotypes, (ii) the probabilistic process that types of less fit organisms are replaced by the fittest, and (iii) an selective environment in which natural selection operates on variants. However, these assumptions are black boxes in the theory, suggesting that the theory is incomplete as a scientific theory. Accordingly, it is needed to develop a comprehensive theory that can give a predictive explanation for (i) creativity of new heritable phenotypes, (ii) mechanistic processes of replacement and coexistence of variants, and (iii) the creation and maintenance of selective environments, respectively, to clarify the black boxes. In this talk, I argue that these three processes can be understood and explained by referring to the processes at higher levels of the organization of hierarchical biological systems, such as meta-population/community and ecosystem. I conclude that community/ecosystem downwardly affects adaptive evolution by restricting the creation of new heritable variants via gene flow and inter-demic mixing, by working as a mechanistic device (machine) for replacement and coexistence of variants, and by creating selective environments for component populations.

Epigenetics and Its Challenges A

Epigenetics: a view from social theory
Meloni Maurizio, University of Nottingham, UK

Acclaimed as "one of the hottest areas of behavioural science" (Buchen, 2010) epigenetics is in "meteoric rise" (Haig, 2012) in biological publications, and in recent years also social-political scientists have started to appreciate its relevance for the social world. In my paper, I offer a preliminary cartography of the reception and growing expectations around epigenetics in social science/social theory, focusing in particular around four axes of investigation: 1) how is epigenetics increasingly operationalised in social science as "the agent of resolution" (Fox Keller, 2010) of the nature/nurture debate (Singh, 2012)?; 2) how are epigenetic discourses resonant with the increasing emphasis on developmental plasticity in biological sciences, and how is epigenetics expected to contribute to the collapse of gene-centric versions of the Modern Synthesis, rather than becoming "mired in another form of material reductionism" (Lock, 2005)?; 3) how will the rise of epigenetics impact the social sciences with notions like the "molecularization of the environment" (Landecker 2010), "molecularization of biographies", "milieu" and "social position" (Niewohner, 2011), and by making "more effective arguments" about the biological impact of social forces (Miller, 2010)?; 4) finally, how epigenetics, understood as a form "heredity that is possible to influence" (Hedlund, 2011), is expected to change notions of biological responsibility, parenting, and in particular mothering? In conclusion, I will use these four axes of investigation around epigenetics as a case-study where the tensions, complexities, and hypes of the new post-genomic biology become particularly visible, almost an anticipation of a possible future for the bio-social link.

Heredity without parents and offspring
Charbonneau Mathieu, Konrad Lorez Institute for Evolution and Cognition Research, Austria

Heredity, understood as a parent-offspring similarity relationship of some sort, is assumed to be a necessary condition for a population to undergo evolution by natural selection. Indeed, if parents with favourable traits did not transmit them to their offspring, natural selection would not cumulate adaptive changes. From this perspective, an inheritance system can be understood as a local mechanism insuring that offspring resemble their parents. This very general understanding of heredity is oft-claimed to be broad enough so that no specific form of inheritance mechanism be required for Darwinian evolution to obtain. Indeed, it seems to be opened to genetic, epigenetic, behavioral, cultural, symbiotic and cytoplasmic transmission. In this paper, I challenge the wide-spread assumption that for a process to serve as an inheritance system, it must establish a definite parent-offspring relationship. The assumption is not broad enough to include admissible cases of heredity such as some cases of ecological inheritance with diffused transmission. Rather, heredity should be understood at the level of the population system, that is, as a transgenerational process of retention of variation distribution amongst the parts of the population. An inheritance system would then be any mechanism insuring this population-level retention process. This construal of heredity allows a more inclusive notion of inheritance systems, with parent-offspring similarity being but a special case, and can unify the different inheritance systems through their common evolutionary role. It also has the potential to open new avenues of investigation in order to discover counter-intuitive forms of inheritance systems, both biological and extra-biological.

Epigenetics and Its Challenges B (submitted papers)

Dissecting the explanatory power of epigenetics
Baedke Jan, Ruhr University Bochum, Germany

The field of epigenetics is booming. This recent development has been accompanied by a philosophical debate on whether epigenetics could spur a paradigm shift in modern biology. Such a potential shift includes the expansion of our understanding of inheritance by processes of ‘Lamarckian' information transfer as well as the consideration of developmental responsiveness as an evolutionary significant factor. This paper argues that although epigenetics (re)introduces interesting historical issues into modern biology, investigations of its explanatory practices has yet been completely neglected by philosophers of science interested in explanation. In order to close this gap, the paper develops a framework of contrastive explanation to evaluate the explanatory power of epigenetic explanation in contrast to prevailing mechanistic molecular explanations and orthodox evolutionary explanations.

These two issues will be addressed: Do molecular epigeneticists’ explanations with less mechanistic detail (i.e. higher-level explanations omitting genetic explanatory information) have more explanatory power than standard mechanistic molecular explanations? Do proximate/efficient cause explanations (answering how a character evolved) have more explanatory power in evolutionary biology than standard ultimate/final cause explanations (answering what a character evolved for)? I will argue that answering these questions is crucial for establishing an explanatory framework of a new ‘Extended Synthesis' which gives precise guidance by means of which criteria (*why*) and in which explanatory context (*when*) epigenetic explanations are legitimately chosen over prevailing molecular and evolutionary explanations.

Conductor´s baton: The meaning of the cell cycle for development, inheritance and evolution
Gaub Sebastian, Technical University Kaiserslautern, Germany

The cell cycle represents the fundamental rhythm of the cell. On the one side the cell cycle oscillates by means of rhythmic activity of various cyclins and dependent kinases. On the other side the cell cycle has a strong impact on a lot of cell cycle controlled genes (CCGs). Checkpoints divide the cell cycle in different phases: growth, synthesis, mitosis and rest phase. Recent findings give evidence that cell cycle regulators play a dual role in proliferation and metabolic control. Also epigenetic oscillations of DNA methylation, chromatin state and microRNA levels show coupling to the cell cycle.

The importance of the cell cycle for the molecular dynamics deserves closer attention by theoretical biology. I made first steps of conceptualising the system features of the cell cycle as (i) a circular flow of information, (ii) the division and control of different cellular phases and (iii) the continuing orchestration of genomic expression, molecular networks and biochemistry of the cell. These systemic features are not determined genetically (ab ovo), but continuously (in medias res). So, biological polymers as DNA, RNA or AA can only "make a difference" with regard to the temporal context. Additionally, the epigenetic reprogramming of oscillating genes opens windows of opportunity for transgenerational inheritance at early stages of development.

In summary, the cell cycle reflects the temporal order of the cell and is a molecular prerequisite of inheritance systems and multicellular evolution. Therefore, I argue that we should pay more attention to the rhythmical nature of molecular ("self"-)organization.

Towards an extended epigenetics perspective

Arteaga-Villamil Xochitl, UNAM, Mexico

Nowadays epigenetics studies are based on the research of regulation of developmental and genetic networks, chromatin systems markers, DNA-binding proteins, transcription factors, chromosomal proteins as histones and Polycomb complexes. This refers to the complexities of the genome that standard genomics was not able to incorporate; however, this implies that epigenetic approach is subject only to molecular research, since much of the work in this area continues taking for granted the dimensions of development and environment.

This paper aims to show, first, the reduction and limitation of epigenetic framework. These limitations stem from historical trace: when C. H. Waddington coined the concept epigenetics in 1942, taking into account the contributions of experimental embryology and genetics of his time to find out how the phenotype of organisms came. In second place, I am looking for an alternative proposal to achieve an extended perspective that allows the interpretation of epigenetic processes in the context of developmental systems theory. In our terms expand the perspective means conceiving biological and environmental agents in a context of networks, interactions, relationships and reactions to a specific organizational level. This proposal, based on Waddingtonian thesis, supports the causal role of the genome and other cellular and environmental agents, allowing a more inclusive and integral analysis of organisms.

Ethical Issues Behind Human Practices (submitted papers)

Natural in the context of reproductive technologies

Fisher Maya, Tel Aviv University, Israel

I will examine the meaning of ‘natural’ as perceived by Clinical Embryologists (CEs) within their daily work at In Vitro Fertilization (IVF) clinics. I will describe two main protocols for egg fertilization, a tension between the bio-medical literature and the CE’s preference, and I will argue that certain moral and epistemological values can – at least partly – explain the CEs preference.

CEs use mainly two protocols to achieve fertilization: insemination and intracytoplasmic sperm injection (ICSI). In insemination one egg and about fifty thousand sperms are incubated together in a petri-dish. In ICSI one sperm is selected and is injected into an egg. Since ICSI gives, according to bio-medical literature, a higher rate of fertilization we would expect CEs to prefer ICSI. But my interviews with CEs show that in cases not involving male infertility they would rather use insemination.

One explanation of their preference rests on the tension between choice, coercion and social responsibility. Seemingly, the insemination protocol follows a process of natural selection where the "egg chooses" the "best sperm," as one CE noted. But with ICSI a CE chooses a sperm, based on its morphological appearance alone "forcing it on the egg where the egg has no possibility to resist." Hence, the responsibility for fertilization passes from the egg to the CE and this may explain why they would like to avoid ICSI. Additionally, CEs are concerned whether they are passing-on infertility to the next generation, something that would not occur if the protocol used was insemination so that regeneration is left in the hands of "nature."

Un/Cut: The Ethics of Routine Infant Male Circumcision
Kober Gal, Bridgewater State University, USA

Routine circumcision is performed in a medical setting on a majority of newborn males in the US. This paper assesses the history of the procedure and the rationales given for this practice, and evaluates its potential benefits and drawbacks. Despite the common belief that the procedure is medically beneficial, routine infant circumcision is not endorsed by a single medical association worldwide, and its health benefits are considered marginal. While findings regarding the prophylactic effect of circumcision in the reduction of HIV transmission have been widely circulated, they remain controversial, especially in regard to their validity in countries with low HIV prevalence, and when performed on infants rather than on adults. I argue that in the absence of sufficient clinical motivation to justify infant circumcision as a public health measure, and given the risks and harms involved, the parental choice to circumcise an infant cannot be regarded as a choice between two ethically equivalent options, as it is commonly presented. Further, I argue that in the absence of clinical justification, infant male circumcision violates the infant's autonomy, and medical personnel should thus be barred from performing it.

Body and Ren: Historical and Ethical Perspective on Organ Donation in China
Li Zhuran, Nanjing Normal University, China

According to statics provided by Ministry of Health, there are only 1, 0000 out of 150, 0000 patients who can get organ transplantation and national organ donation rate is as extremely low as 0.03 per 100,000 persons. Based on stating the current situation of organ donation in China, the paper points out that the cultural-dimension cause of weak donation awareness roots in traditional Confucianism views on body, which attach symbolic importance to the completeness of human body. From historical and ethical perspective, the paper critically analyzes the relationship between body and Ren, the ultimate traditional principle in interpersonal communication in modern society. By reevaluating and reinterpreting the view of body and the meaning of Ren in new age, the paper proposes an ethical approach to raise awareness of organ donation, in way of encouraging intrinsic value purists for united goodness in community.

Ethical foundations of biodiversity communication
Eser Uta, Nuertingen-Geislingen University, Germany

Communication, participation and education (CEPA) are considered key to the implementation of the UN Convention on Biological Diversity (CBD). To improve official biodiversity communication, the German Federal Agency for Nature Conservation commissioned an ethical expertise on good arguments in favour of biodiversity. This paper presents major findings from our analysis of the German, Austrian, Swiss and EU biodiversity strategies with regard to their concepts of communications and ethics.

First, we found a predominantly strategic use of the term "communication": It is used with a direct object rather than with an indirect object. Hence, communication is understood as a unidirectional rather than as a reciprocal process. This has consequences for what is considered to be a good argument. From a strategic point of view, an argument is good if it is effective. From a philosophical point of view, however, an argument is good if it is plausible and coherent.

Second, we found an equalisation of "ethical arguments" with "intrinsic value of nature". To broaden this restricted understanding of environmental ethics, we distinguished between prudential, moral and eudemonic arguments. In order to make this distinction accessible to practitioners, we framed it in lay-terms as 'Prudence', 'Justice' and 'The Good Life'.

Third, we found a predominance of prudential arguments that present conservation and sustainable use of biodiversity as a mere matter of enlightened self-interest. I will argue that such a communication wrongly neglects issues of justice (within generations and between generations) and issues of a Good Life.

Ethics and Its Difficulties (submitted papers)

Backtracking and the Ethics of Framing: Lessons from Voles and Vasopressin

Mckaughan Daniel, Boston College, USA
Elliott Kevin, University of South Carolina, USA

When communicating scientific information, experts often face difficult choices about how to promote public understanding while also maintaining an appropriate level of objectivity. Research ethicists have argued that scientists have at least two different kinds of obligations in communicating scientific work, which often stand in tension. On one hand, experts are expected to "stick to the facts" so that they can preserve the self-determination of those who receive information from them. On the other hand, scientists are sometimes said to have a competing responsibility to interpret or frame their work in ways that serve the public good. Using recent research on vasopressin and oxytocin in voles and humans as a case study, we argue that one way for scientists and others involved in communicating scientific information to alleviate these tensions is to pay closer attention to the majorframes employed in the contexts in which they work. By doing so, they can ideally employ useful frames while also enabling the recipients of information to "backtrack" to relatively uncontroversial facts and recognize how these frames relate to their own values and perspectives. Important strategies for promoting this sort of backtracking include identifying the weaknesses of particular frames, preventing misunderstanding of them, differentiating well-supported findings from more speculative claims, and acknowledging major alternative frames.

Aristotle on the Material and Efficient Causes of Character

Ponesse Julie, SUNY Brockport, USA

One of the foundational claims of Aristotle's *Ethics* is that virtue is "up to us and voluntary." Provided that we have the appropriate moral education, we can mould our own characters by acting in the right ways. But the story is not as simple as it initially appears. In *Politics* VII.7, we are told that only *some* humans are "most easily led to virtue," since they have natures that are 'well-mixed.' Having a 'well-mixed' nature turns out to be a matter of having blood that is hot, thin and pure since these material properties are most conducive to the development of spirit (which is required for courage) and intelligence (which is required for practical wisdom). Aristotle's emphasis on the importance of having the right kind of material nature, therefore, has significant implications for moral development. But some have worried that Aristotle's emphasis on material nature entails that the efficient cause of character is one's material nature (which is not up to us) and not, as he insists in the *Ethics*, decision (which *is* up to us). My aim in this paper is to show that we can resolve this tension by describing a person's potential to become virtuous in two different ways: in terms of passive potentiality (which is determined by the material in which the process of moral development takes place), and in terms of active potentiality (which is determined by decision which, acting as an efficient cause, works on the material properties of his blood).

The Menace of Magisteria
Creath Richard, Arizona State University Tempe, USA

The central idea of Stephen Jay Gould's “Nonoverlapping Magisteria” (1997) is that there are at least two nonoverlapping domains of human concern and inquiry. One comprises the empirical sciences, and the other includes religion and as part of that moral meaning and value. Their subject matters are just different, and so results from one domain cannot encroach on those from the other. The idea has a certain natural attractiveness for both sides for it seems to guarantee that “we” can proceed as usual without meddling from “those other guys”. Gould himself spent little time articulating the central idea, but it is more nuanced than might be thought. Unfortunately, those nuances blunt somewhat the initial attractiveness of the idea. But the situation is worse than this. Now I have no desire to encourage or warrant imperialism from either direction, and certainly that still goes on. Even today some religious leaders make pronouncements on scientific subjects where they have no training and less understanding. And even today some scientists make claims about religion or morals far beyond their professional competencies. Silliness is as perennial as the spring. Erecting a wall between domains, that is, between magisteria, is not the answer, for the sharp separation of science from religion and morals is, as it turns out, indefensible, dangerous, and ultimately destructive of both sides.

Eugenics Part I, Eugenic Traits

Eugenic Lists
Wilson Rob, University of Alberta, Canada

To a modern eye, the language used in eugenic sterilization legislation can seem both puzzling and offensive. Here I would like to attend to the puzzle side of things and explore what explanation there is for the various traits and conditions that find their way into such legislation. These include mental deficiency, feeble-mindedness, Huntington's chorea, neurosyphylis, epilepsy, and tuberculosis. Some of the consistency and variation here surely, one might think, has a genealogical explanation. Yet there is more to a full explanation here than finding some putative ur-list of traits and conditions and tracing their descent.

Why did the Nazis sterilize the Blind?
Teicher Amir, Tel-Aviv University, Israel

In the list of diseases justifying forced sterilization according to the 1933 Nazi sterilization law, after the schizophrenics and epileptics but before the severely deformed and alcoholics, hereditary blindness and hereditary deafness were mentioned. The inclusion of both of these categories was not trivial, even in the context of the racial-hygienic worldview. In fact, prior to the Nazi law, no other sterilization law in the world defined specifically these two categories. How did the blind and deaf end up in that list? On the basis of a close examination of the developments in the research of hereditary disorders in German psychiatry from 1900 to 1933, I will argue that the answer lies not so much in the cultural and social background of eugenic anxieties but in the practices of knowledge creation and legitimization applied by German psychiatrists during the 1920s. After the attempts to fit mental disorders into the Mendelian box failed, psychiatrists changed course and found alternative statistical techniques to nail down the hereditary nature of certain illnesses. During this process, Mendelian thought changed its role in psychiatric literature, turning primarily into a rhetoric device used to legitimize non-

Mendelian research results. Then, when compiling the sterilization law it were the same psychiatrists who used the category of Mendelian blindness and deafness as part of their attempts to lend the law itself scientific respectability. Examination of internal scientific developments thus sheds a new light on a crucial moment in the history of Nazi eugenic policies.

Combining permissible abortion with prenatal testing: Risking Eugenics?

Caroline Lyster, McGill University, Canada

While abortion laws vary across the world, 56 countries currently permit the practice without restriction as to reason (Singh 2009). This permission, combined with the increasing availability and use of prenatal testing, creates the potential for the selective abortion in cases of disability. To allow this practice, I will argue, is to allow eugenics. Can we permit abortion in some cases and restrict it in others? I believe that we can, but the question will have to be addressed from several perspectives. First, I will examine the moral arguments to determine whether or not there is a morally relevant difference between abortions in general and the abortion of disabled foetuses in particular. Second, I will consider an important question related to policy: should selective abortion be prohibited in all cases, or are there certain diagnoses of disability where we think that termination may be permissible? I will also consider whether or not the consequences of a more restrictive policy place an undue burden on women who would seek abortion for reasons other than the results of a prenatal test. Finally, I will examine whether or not such a policy could be put into practice in Canada or the United States given the legal decisions that led to the unrestricted permissibility of abortion.

Eugenics Part II, politics and eugenics

Differentiating Eugenics and Social Darwinism

Roige Mas Aida, University of British Columbia, Canada

In the late XIXth and early XXth centuries, social Darwinism and eugenics were two different sociopolitical trends. One might think that their chief difference was this: eugenicists defended government intervention for the improvement of human breeding, while social Darwinists opted for *laissez-faire*, individualistic capitalism. While their positions on state interventionism are certainly different, I will argue that there's a more central point defining and distinguishing those trends. This is how they thought about fitness. For eugenicists, traits (especially those deemed “intellectual”) were subject to judgments of value. Their fitness was assessed by what was conventionally thought to provide for success in a society: cleverness, moral appropriateness, etc. Eugenicists thought those traits underlying social inequalities were highly heritable. To improve fitness was to augment the ratio of “good” traits over “bad” ones across generations. Conversely, social Darwinists weren't so much concerned with defining the traits or in their heritability. They also related fitness to socioeconomic status in a conventional sense (i.e. Sumner's famous “millionaires are a product of natural selection”, 1902). But they thought it was competitive struggle that improves fitness during the lifetime of an individual, and collectively over generations. In explaining their differences, we will see how, while conceptually different, historically both trends were easily taken for one another. This is because the core ideas of social Darwinism are compatible with assuming that the basis of what makes one “fit” is heritable (e.g., Sumner on geniality), just as eugenics is compatible with non-interventionism (e.g., contemporary “market eugenics”).

Revisiting Eugenics and the Left: JBS Haldane, Diversity, and an Independent India.

Mcouat Gordon, University of King's College, Halifax, Canada

Diane Paul's pioneering “Eugenics and the Left” (1984) exploded received myths that eugenics was a movement of the political "Right". For Paul, eugenics was just as much a platform of the *Left*: progressivists, socialists, and liberals, envisioning a state supported, planned, biological intervention into social engineering. For Paul, exemplary of the movement was J.B.S. Haldane (1892-1964), geneticist, co-founder of modern neo-Darwinism, recognized leader of the scientific left, member of both the Communist Part and the Eugenics Society, and author of the strikingly bio-political *Inequality of Man* (1937). Paul's story, however, glossed over important developments in Haldane and his associates on the far Left. For, as Haldane traveled leftward his lifelong interest in biological difference and innateness intertwined, and was radically modified, by his "Communist" view that a good society would be built on irreducible diversity (the "inequality of man") not on engineering. This embryonic critique mustered strength as Haldane abandoned his prestigious chair at University College, London (1956), and his British citizenry (1961) and threw his lot with the newly Independent India and its programme to build a new modernist anti-imperial state with an associated new science (of biology and statistics) based on diversity. Haldane's last project to create a hybrid "Indian Perspective on Darwin provided the final ground for a thorough critique of the eugenic project and the political assumptions upon which it was built. Using new archival sources, this paper explores Haldane's late Indian period, his reworking of Darwinism in favour of radical diversity, and his crucial contribution to the "progressivist" critique of eugenics.

Confronting the 'Eugenic Agitation': Herbert Spencer Jennings, the Biology of Democracy, and the American Social Welfare Community in the 1920s

Johns Schloegel Judy, Independent Scholar, USA

In 1918, in the wake of the Great War and Russian Revolution, the American biologist and geneticist Herbert Spencer Jennings (1865-1947) began to contemplate the viability of a "biology of democracy" in the face of rapidly growing evidence that genetics, in association with eugenics, was an "aristocratic system." Jennings' philosophical reflections highlighted not only his recognition of the interlinking of politics and science, but more practically, his growing preoccupation with the competing demands for public engagement while simultaneously maintaining a dynamic research program. Jennings' contemplation of the dual obligations of social action and scientific research was itself framed by the philosophy of pragmatism. In extensive philosophical writings published over the preceding ten years, Jennings had worked out a pragmatist framework for the conduct of the biological sciences that had earned him the mantle of "biological philosopher." Up until this point, these writings had been primarily academic. Now, however, in the face of the rapidly growing eugenics movement, Jennings took his pragmatism to its next logical step when he began to speak and write for non-scientific audiences, including educators, social workers, community activists, and the broader lay public. This paper explores the American social work and social welfare community as a primary vehicle through which Jennings advanced his critiques of eugenics. I consider Jennings' relationship with the social welfare community as an ideal window for an expansive view of his critiques of eugenics and their foundation in a rigorous genetics research program conceptualized on democratic principles.

Evolutionary Theory and Causation (submitted papers)

Selection and drift: why "caused by" rather than "constitutes"?

Brunnander Björn, Stockholm University, Sweden

There are many strands to the debate about the causal status of evolutionary theory. To the extent the debate emanates from different views on causation in general it will clearly be as dialectically unsettled as the general discussion is; it may be overly optimistic to hope for conclusive arguments on the topic of the metaphysics of causation in the near future. However, there is a kind of argument for a non-causal view that does not involve commitment to controversial views about causation. These arguments focus on the distinction between saying that frequency changes are caused by selection/drift and saying that changes constitute selection/drift, and conclude that we should prefer the latter on pain of arbitrariness. The arguments proceed by comparing cases where causal theorists invoke selection/drift as causes with cases where they don't and argue that there is no relevant difference to justify the difference in treatment. I intend to make clear the structure of these arguments and show their independence from controversial assumptions about causation. These arguments are somewhat limited in scope, however. They target selection and drift specifically and so will not serve to establish the general statistical view.

A major motivation behind the paper is that of clarification. Given that there are several strands in the debate there may be different opinions about what being a causal/non-causal theorist amounts to.

Are there a priori causal relations in evolutionary theory?

Schlaepfer Guillaume, University of Geneva, Switzerland

Popper famously supported the (later recanted) idea that the principle of natural selection is analytical and therefore cannot be regarded as a scientific theory since analytical claims are empirically unfalsifiable. Remarkably, Sober (2010) affirms the first of these claims. Considering examples of simple population models involving fitness, he argues for the claim that there exist causal statements that can be known a priori. This obviously calls into question Hume's widely accepted claim that causal relations can only be known empirically.

Sober's paper addresses an interesting problem pertaining to the interpretation of the concept of fitness and shows that it represents a challenge for contemporary theories of causation. In particular, he shows that the manipulationist account put forward by Woodward and Hitchcock (2003) provides no reasons for rejecting a priori causal knowledge, contrary to what the manipulationists argue.

The aim of my presentation is to refute the conclusions that Sober draws on the basis of these population models. I argue that the fact that some causal assertions can be interpreted as analytical is due to the peculiar dispositional nature of fitness, which leads to an ambiguous use of the term, conflating the causes of fitness with its consequences. Furthermore, I claim that even if a model may be postulated a priori, it doesn't provide knowledge about the world unless it is empirically tested. Finally, I urge Sober to consider that obvious propositions should not count as a priori knowledge unless their truth value does not rely in any way on experience.

An Example of “Citizen Science” (submitted papers)

Citizen Science in a Democracy

Henson Pamela, Smithsonian Institution, USA

When English scientist James Smithson left his fortune in 1829 to found an establishment named the Smithsonian Institution devoted to “the increase and diffusion of knowledge,” his endowment was specifically directed to a new democracy, the United States. After the Institution was founded in 1846, the scientists who directed its programs made a conscious effort to involve a broad array of citizens across the United States and abroad in its scientific programs. Known today as “Citizen Science,” programs such as the Meteorology Project and an international specimen exchange network were established in the 1850s. Farmers, medical doctors, soldiers, teachers and telegraph operators, for example, recorded daily weather observations and sent them to the Smithsonian to be compiled and analyzed for patterns. For their efforts, these volunteers were listed in the Institution's annual report and sent copies of scientific publications. Isolated trappers and rural doctors could maintain some ties with cultural and educational centers.

This paper will discuss how Citizen Science arose and was cultivated at the Smithsonian in the 19th and 20th centuries, from weather observations to satellite tracking, from specimen collecting to panda pregnancy watches at the National Zoo. The role of amateurs has ebbed and flowed as attitudes towards professionalization changed. This paper will trace the various ways citizens in a democracy have participated in Smithsonian scientific work and how their relationship to the Institution has varied over the decades.

Technology and Access: Naturalists in the Backyard

Graham Gabrielle, Florida State University, USA

Available technology has continually enabled the democratization of observational field biology and natural history. This paper seeks to highlight the influence of citizen participants in the naturalist history tradition, beginning with the establishment of a standardized scientific nomenclature in the 18th century, through the present-day naturalist activity resurgence made possible by new and developing smartphone apps. Topics covered will include artisan participation in collection and identification of specimens in the age of gentlemen naturalists, the increase of popular interest in natural history in the 19th century due to naturalist essays and museum dioramas, present-day uses of mobile technology for recognizing and recording data, and a problematic position of the naturalist tradition as both a leisure pastime and a pursuit of scientific understanding. I intend to show that natural history science obtains real data benefits from work done by amateurs, but that we should be sensitive to the double-edged sword of popular interest. Although the enthusiasm of amateurs collecting data is beneficial, it does not cater to the research interests of professional scientists but to the passions of the amateur.

The explanatory role of mathematical and dynamical models in molecular and cell biology

The Mathematics of Molecular Mechanisms

Baetu Tudor, Konrad Lorenz, Austria

According to current accounts, a satisfactory mechanistic explanation should include all the relevant components of the mechanism (entities, activities and organizational features) and exhibit productive continuity from input to output conditions. It is not specified, however, how this kind of ‘mechanistic completeness’ can be demonstrated. Experimental interventions can demonstrate that a mechanism is necessary to produce a phenomenon. Nevertheless, interventions do not demonstrate that a mechanism is sufficient for producing a phenomenon. This creates a cluster of related problems: it is not clear to what extent the explanation is complete, whether the mechanism postulated by the explanation can be detached from the system in which it is embedded and treated as an independent module, and where a mechanistic explanation can safely bottom out.

I argue that mathematical modeling of mechanisms can provide a solution to these sufficiency related issues. More and more studies in leading journals complement traditional descriptions of mechanisms supported by the experimental practices of molecular biology with quantitative models aiming to demonstrate that the proposed mechanism can generate the quantitative-dynamic aspects of a phenomena in the right amount/intensity, and thus support the claim that the mechanism is sufficient to produce the phenomenon. While this kind of extrapolative inferences from surrogate mathematical models need to be carefully regimented, they provide a workable solution to the ‘explanatory leakage' problem whereby it is not clear how systemic a mechanism needs to be and how deep it needs to bottom out in order to explain a phenomenon.

Mechanisms, models and explanatory force
Issad Tarik, INSERM, France
Malaterre Christophe, Université du Québec à Montréal, Canada

A major type of explanation in biology consists in mechanistic explanation. Mechanisms are generally defined as particular types of models that include entities performing certain sets of activities (e.g. Machamer et al. 2000, Kaplan and Craver 2011). The explanatory force of mechanisms is apparent in such typical cases as neuron firing or molecular receptor functioning. It is however much less clear how mechanisms explain in the case of the complex biomolecular networks that are increasingly being uncovered in biology, be they metabolic networks such as the regulation of glucose by insulin, or genetic regulatory networks. In this contribution, we argue that the very concept of mechanism faces a dilemma. Either it is defined in fairly broad terms so as to apply not just to elementary biological systems but also to more complex biological networks, and in this case it loses its specificity as a particular type of model. Or it is defined more strictly, and in that case it does not apply to an increasingly larger domain of complex biological models. The first option makes the concept of mechanism redundant with that of model, hence useless. The second preserves the relevance of the concept of mechanism in biological explanation, but can only do so at the cost of reducing its scope of application. In both cases, we argue that the explanatory force of models in biology does not come from their being mechanisms but simply from their empirical adequacy.

Explaining with mathematical models: the contribution of systems engineering to biology
Braillard Pierre-Alain, Université Lille 1, France

Systems biology is known for its heavy reliance on dynamical modelling of molecular mechanisms and networks. Various mathematical and computational tools have been developed and different empirical data (partly coming from high-throughput methods) are used to build these models. They play different heuristic, explanatory and theoretical roles and one task of philosophical scrutiny of systems biology is to analyze and clarify these roles. In this paper, I will focus on dynamical analyses inspired by engineering methods. Traditionally, engineering's contribution to biology has been mainly technical (e.g. ultracentrifugation, the electroencephalograph), but engineering has also developed along more fundamental lines, with general analytical methods, theoretical results and peculiar explanatory concepts that might be relevant to explain biological systems. Many systems biologists have strongly argued for the transfer of methods and explanatory models from engineering to biology. My goal is to show the originality of these approaches in terms of explanatory strategies (decomposition methods) and models, stressing the differences with the classical mechanistic framework of molecular and cell biology, as it has been characterized in recent philosophical literature. There is more in these mathematical models than a way of representing the dynamics of biological mechanisms. Engineering offers new ways to look at biological systems, to decompose them, and to explain them. But of course, these transfers of methods and knowledge (partly based on analogies between natural and artificial systems) are not without limitations and dangers, as I will also discuss.

The Relevance of Irrelevance: Explanation in Systems Biology
Gross Fridolin, University of Milan, Firc Institute of Molecular Oncology, Italy

Explanations in systems biology often rely on the tools of dynamic modeling. Here I argue that accounts of mechanistic explanation that are based on 'change-relating relationships' between the components of a mechanism and its overall behavior do not easily make sense of certain features of dynamical patterns, even though these can be accounted for in mathematical models. I suggest that when investigating the use of such models, one should distinguish between the ideas of 'causal relevance' and 'explanatory relevance.' I show that the explanatory function of mathematical models often consists in elucidating relationships of non-dependence, that is, relationships that are not change-relating. Notably, the robustness of biological systems, a property that has been of great interest to many systems biologists, is often best accounted for in this way, and not by invoking separate 'robustness mechanisms.' Drawing on examples from the scientific literature, I show that an important aspect of explaining the behavior of a biological mechanism consists in elucidating how in the systemic context components are not, or only weakly, dependent on each other.

Exploring the evolution of culture and social behavior A

Explanatory Appeals to Hormones in Evolutionary Anthropology
Downes Stephen, University of Utah, USA

Debates between evolutionary psychologists and evolutionary anthropologists have centered on a contrast between explanatory approaches (or explanatory styles). In these debates, evolutionary anthropologists have emphasized their debt to behavioral ecology. Evolutionary anthropologists apply optimality models derived from behavioral ecology to human behavior and use these models to generate adaptationist hypotheses about many aspects of human behavior. This explanatory approach stands in stark contrast to that of evolutionary psychologists, who appeal to evolved psychological modules in their accounts of human behavior. Many human behavioral ecologists reject evolutionary psychologists' explanations due to this appeal to internal mechanisms. Many in evolutionary anthropology also appeal to hormones in their explanations of many areas of human behavior, for example, aggression, dominance hierarchies and parenting. One way of viewing such appeals to hormones is that they are also appeals to internal mechanisms and if so, this constitutes the adoption of an explanatory style that is rejected by many human behavioral ecologists. I look at the work of a few evolutionary anthropologists for whom hormones play a key role and assess their explanatory options. Here I also assess the extent to which explanations invoking hormones can or should be considered evolutionary explanations. The cases I focus on come from work by Elizabeth Cashdan, Mark Flinn and Sarah Hrdy.

Fitness measures and the evolution of social behavior
Forber Patrick, Tufts University, USA

Evolutionary models of social behavior, both biological and cultural, depend on measuring the fitness costs and benefits of behavioral interactions. The classification of such social behavior as altruistic, selfish, or spiteful also depends on such a fitness measurement. For instance, acts count as altruistic if they involve paying a fitness cost to confer a fitness benefit on another. Yet many common measures of fitness that are quantified over the entire life history of an organism, such as number of offspring, make classification difficult. Immediate costs or benefits of a single behavioral interaction can be offset by downstream indirect costs or benefits of the interaction. An act of punishment might appear to be altruistic (paying a cost to punish non-cooperative behavior creates a public good for the rest of the population) but actually may be selfish by increasing long-term average payoff from future interactions.

This project is motivated by evolutionary game theoretic models of spite, and will explore possible fitness measures proposed in the literature using these models as examples. The challenge is to find a fitness measure that is both theoretically coherent and empirically measurable, allowing clear quantification of costs and benefits from behavioral interactions.

Learning to Spite and the Evolution of Envy
Smead Rory, Northeastern University, USA

The occurrence of spite in nature presents an evolutionary puzzle similar to that of the evolution of altruism: if spite is costly how could it ever evolve? Hamilton identified that spite

could evolve if the behavior was directed at non-spiteful individuals. In recent years, other accounts of the evolution of spite have been developed which suggest that there are several possible explanations for the evolution of spite: anti-correlation of types in a population, out-group conditional behavior, or even reciprocity-like mechanisms. However, one possible explanation that has received relatively little attention is that spiteful behavior may be learned.
Of course, this raises other evolutionary puzzles. If learning mechanisms lead to costly behavior such as spite, why should we expect those learning mechanisms to evolve as opposed to some other learning mechanisms? Furthermore, learning to spite may require some degree of cognitive sophistication such as the ability to recognize the payoff of others. These mechanisms are, presumably, more costly because of the increased complexity, which makes the evolutionary questions even more pressing. This paper presents a model of the evolution of learning that explores this issue. Learning rules that are "envious" (i.e. negatively react to the payoffs of others) have a tendency toward spite in some games. And, this tendency toward spite can generate strategic advantages in some interactions that are not possible if individuals are simply trying to maximize their own payoffs. Consequently, such learning rules may be evolutionarily successful despite their apparently detrimental properties.

Exploring the evolution of culture and social behavior B

The Logic of Research Questions: Adaptationism, the Null Hypothesis, and the Lack of a Stopping Rule

Lloyd Elisabeth, Indiana University, USA

I introduce my framework, the "logic of research questions," and contrast a standard "methodological adaptationist" approach, to the "evolutionary factors" approach. In the former, the key research question is: "What is the function of this trait?" while in the latter, the primary research question is: "what evolutionary factors account for the form and distribution of this trait?" I use my case study on the evolution of the female orgasm to illustrate how the "methodological adaptationist" approach can lead scientists astray. Biases induced by methodological adaptationism – specifically, the belief that the non-adaptive bonus/byproduct explanation is a "null" hypothesis — have led biologists to apply no stopping rule to the search for selective accounts of female orgasm, and to fail to see the bonus/byproduct explanation as a distinct and alternative *positive causal hypothesis*, and as one that can have evidence in its favor. The biologists also fail to compare the byproduct hypothesis *directly against* an adaptive one with regard to the evidence. Perhaps, then, it is past time to reevaluate whether the "methodological adaptationism" is truly as benign as both philosophers and biologists assume it to be.

Cultural phylogenetics: bringing anthropology, linguistics and biology together to understand cultural evolution

Jordan Fiona, Archaeology & Anthropology, University of Bristol, UK

Multiple disciplines have emerging interests at the productive interface of evolutionary science and human culture. In the last 20 years, evolutionary anthropologists interested in understanding cross-cultural patterns and processes have turned to the population histories afforded by linguistic relationships to reinvigorate comparative approaches. At the same time, language researchers have revolutionised how we infer linguistic relationships by using the quantitative computational tools developed in biology for inferring the trees and networks of species. Working at the language-family level where emic categories are likely to be genuinely comparable, the vast ethnographic record is now being put to good use asking questions about the patterns and processes of cultural and linguistic change. In particular, phylogenetic comparative methods allow us to test evolutionarily-motivated hypotheses about adaptive features of human behaviour and norms in a genuinely productive framework. In this talk I show how cultural phylogenetics allows us to answer a host of questions (old and new) about migration, kinship, and the coevolution of language and culture.

Patterns of Discordance
Haber Matt, University of Utah, USA

Lineages at different levels of the biological hierarchy will interact with and be embedded within one another. This produces patterns of evolutionary history, the study of which provides insights into the process of evolution. These patterns, though, may also be confounding in a multiplicity of ways. For example, the relatively recent recognition of the prevalence of lateral gene transfer (LGT) – especially among microbes – has some questioning the Tree of Life metaphor and even the phylogenetic project itself. At first pass, the transmission of cultural traits appears to be susceptible to similar complaints; e.g., cultural traits are transmitted horizontally, and the mode of transmission may undermine standard phylogenetic models.
I remain more optimistic, instead seeing a new challenge for systematists: the elucidation of the patterns of genealogical discordance. This acknowledges the genuine challenge LGT (and other sources of genealogical discordance) presents to phylogenetic thinking, yet recognizes the value of the patterns they produce. My levels of lineage theoretical perspective frames research on these patterns, and here I consider how that applies to recent phylogenetic studies of cultural evolution. This carries implications for testing cultural evolution, the relation of biological and material cultural evolution, and, more broadly, suggests a robust response is available to concerns about reconstructing tree-like phylogenies, e.g., singular focus on one source of discordance may distort estimates of how prevalent that source is in a system being studied.

Explaining adaptation: Organism/environment interactions accross time and spatial scales

Niche construction theory and the concept of adaptation without selection
Pocheville Arnaud, UMR7625, CNRS, France

Niche Construction Theory (Odling-Smee et al 2003) aims to complement the Modern Synthesis by pointing to the fact that merely by living, organisms necessarily modify their or other's environments, which leads to modifying the selection pressures stemming from these environments. From this, Niche Construction Theory concludes that there are two independent routes towards the fit between organisms and their environments: either organisms adapt to the environment (natural selection), or they adapt their environment to their needs (niche construction).In this talk, I will show that this reconceptualization of evolution crucially depends on the criterium retained for the organism-environment delineation, and on some hidden assumptions about the time-scales of ontogeny and evolution. This will lead us to propose a new formulation for Niche Construction Theory, that will open new lines of empirical research.

Explaining the emergence of a global order out of biosphere-environment interactions: a critical appraisal of the Gaïa hypothesis theoretical foundations.
Dutreuil Sebastien, Université Paris 1 & IHPST, France

The Gaïa hypothesis (GH), proposed by Lovelock and Margulis (1974) is interested in three related points: (i) the influence that the sum of all living organisms have on their environment at a global scale, (ii) the eventual benefit that they could gain by influencing their environment, namely, a “regulation” or so called “homeostasis” of the environment, which led Lovelock (1979) to suggest, (iii), to compare the biosphere/Earth to an organism.Based on the fact that

Earth/the biosphere does not reproduce and therefore cannot undergo natural selection, Dawkins (1982) famously dismissed (ii) as theoretically problematic and (iii) as an illegitimate analogy. He was henceforward followed by all evolutionary biologists and philosophers of biology, with scarce exceptions. Nonetheless, a small community of scientists has since made important and various theoretical suggestions to account for the existence of a "regulation" of the global environment without genuine natural selection occurring at the global scale.The aim ot this presentation is threefold: first to clarify the explanda of GH, second to critically assess the theoretical elaborations that have been made since 1982, three to enlarge the scope to other later suggestions (extended phenotype, niche construction, extended organism) that seem to bear theoretical similarities to GH so as to evaluate their effective resemblance.

The extended organism. Scale, adaptation, and the nature of the individual

Turner Scott, State University of New York, USA

Evolutionary biology has long been roiled by controversy over what might the proper focus of natural selection be: gene, individual, group, ecosystem or biosphere? At the heart of this controversy lie many unresolved issues of the nature of the relationship between heredity and function, structure and function, and individual and environment. The current focus on gene selection, for example, presupposes certain tenets of the relationship between hereditary memory and functional adaptation that severely limits the scale of operation of natural selection, to the point where ideas like the evolution of an ecosystem or the biosphere become literally inconceivable. Similarly, our current models of gene selectionism have nothing meaningful to say about the origin of biological design and convergence, cognition and consciousness, the origin of life, or a host of other central issues in the science of life. I propose here that what has been missing is a frankly physiological approach to evolution and adaptation, that refocuses our attention away from the supposed supremacy of the gene in evolution and to the role and nature of the "organism-like system", the extended organism for short, as a recurrent motif in the evolutionary history of life.

The Extension of Evolutionary Theory and Its Difficulties A (submitted papers)

Reciprocal causation or hermeneutic spiral? Anthropological reflections on the theoretical integration of organismic development and niche construction with culture history

Schultz Emily, St. Cloud State University, USA

Theorists of organismic development and theorists of niche construction currently argue for enlarging the scope of the modern evolutionary synthesis, while anthropologists and others have adopted models from population biology to study the evolution of culture. While welcome, these efforts remain problematic for anthropologists whose understandings of individual development and cultural change cannot be captured by formal theoretical models that focus on individuals and ignore material culture. In this paper, I begin by reviewing attempts to theorize connections between development, niche construction, and cultural evolution that rely on some version of "reciprocal causation." I then argue that the shortcomings of these attempts can largely be overcome by adopting archaeologist Ian Hodder's notion of the "hermeneutic spiral," but only if theorists of niche construction and biological development are willing to reformulate key assumptions about "the individual," "the cultural," and "the social."

"Memetics is Dead! Long Live Memetics!" The importance of conceptual framing in replication-based approaches to evolution

Garvey Colin, Rensselaer Polytechnic Institute, USA

As a scientific concept, the meme had a short, tumultuous life. Born with a bang in the provocative final chapter of Dawkins (1976), it died with a whimper three decades later when the *Journal of Memetics* closed “due to a lack of quality submissions,” (Edmonds 2005). What happened?

The shift of conceptual frame Dawkins performed when he looked at the world “from the gene's-eye-view” has been powerfully employed to explain biological complexity, yet failed to provide a lens onto the subtleties of cultural organisms. Here I demonstrate that the difficulty of adopting the “meme's-eye-view” of culture with anything like the rigor of the genocentric view of biology eluded not only Dawkins (1976, 1982), but also Dennett (1991, 1995), whose wide influence proved disastrous for the burgeoning field of memetics. Dennett's focus on semantics over syntax leaves his theory unable to demonstrate the existence of replicators forming a lineage—exactly the kind of individual we're looking for to justify shifting our point of view in the first place (Hull 1982, 1988). After showing how Dennett used the meme to cloak a theory of cognition and culture based on non-Darwinian type/token relations in the dubious language of “information,” I draw together work in material agency and evolutionary development to reexamine what it would mean to take the hypothesis of extra-genetic replicators (memes) seriously, what lineages thus formed should look like, how we could visualize them, and why such an approach is still worth pursuing.

The role of analogy in cultural transmission and human dispersal
Abrams Marshall, University of Alabama at Birmingham, USA

Research on evolution and cultural transmission has focused on mathematical and computer models, on field work on effects of social network structure, and on laboratory experiments on cultural transmission. However, there's been little focus on how adoption of some cultural variants might affect the adoption of others (apart from occasional mention of this idea, and some experimental work in which background culture influences transmitted variants). The importance of interactions between cultural variants is suggested by anthropological views of culture as constituted by interacting thought processes, linguistic elements, behaviors, or practices; by research on reasoning and cognitive dissonance in psychology; and by research on the role of logical or explanatory coherence in justification. Research in anthropology and cognitive science also suggests that analogical relationships can mediate interactions between cultural elements. While analogy sometimes seem like mere embellishment, and sometimes helps to motivate spurious inferences, it's been argued that it plays an essential role in scientific practice and in problem solving. I argue that analogies between cultural variants can bias cultural transmission, and that analogies may have played an important role in human dispersal, facilitating adaptation to new environments. I illustrate these possibilities using agent-based models that incorporate cognitive models of analogy processing, and discuss empirical methods that may allow further investigation.

The Extension of Evolution Theory and Its Difficulties B (submitted papers)

The evolution of technology is Darwinian
Bedau Mark, Reed College, USA

Darwinian evolution happens when natural selection shapes an evolving population, even if that population is not biological. Here, natural selection is understood along the lines of the traditional account made famous by Lewontin (1970) and recently developed by Godfrey-Smith (2009). This talk investigates whether there is empirical evidence that Darwinian evolution shapes the population of patented technologies. Analysis of the past thirty years of patent records reveals the signature of Darwinian evolution, although a form with highly tangled and “incestuous” genealogies that are quite unlike those found in biology. These empirical results illustrate the promise of a Darwinian analysis of the evolution of technology, and they answer many familiar criticisms of Darwinian analyses of culture.

Beyond Generalized Darwinism: Considering Alternative Ways to Articulate Evolutionary Economics

Callebaut Werner, Konrad Lorenz Institute for Evolution and Cognition Research, Austria

In two recent papers ("Beyond Generalized Darwinism. I. Evolutionary Economics from the Perspective of Naturalistic Philosophy of Biology. II. More Things in Heaven and Earth." *Biological Theory* 6:338-350, 351-365, 2011) I reflected on "generalized Darwinism" as currently discussed in evolutionary economics. Focusing on Hodgson and Knudsen's generalization of Darwinism in terms of "generative" replication and interaction (*Darwin's Conjecture: The Search for General Principles of Social and Economic Evolution*, University of Chicago Press, 2010), and the debate it spurred, I concluded that extant evolutionary economics as a whole (1) continues to resist consistent "Darwinizing," (2) is incompletely naturalized (e.g., invoking teleological and intentional reasoning at the population level), (3) disregards the importance of analogical and metaphorical reasoning for knowledge transfer between fields, and, most importantly, (4) is based on a dated gene-centric, adaptationist, selectionist, and externalist Modern Synthesis view of evolution.
Against this background, I attempt to do three things in this talk:
(1) To schematically mine alternative biological 'source fields' for concepts and models that could be more fertile in inspiring evolutionary economics as 'target field.' These range from theories of self-organization as employed, in, e.g., biophysics and developmental biology to epigenetics and EvoDevo (evolvability, innovation, modularity...) to niche construction theory.
(2) To discuss the comforts and pleasures of a more pluralistic approach to generalizing evolutionary thinking.
(3) To suggest how evolutionary economics could escape from its current *cul-de-sac* by designing new formats for the interaction between economists, biologists, philosophers and historians of biology, and others.

The Relevance of Human Evolutionary History to Evolutionary Game Theory

Macintosh Rebecca, Rotman Institute of Philosophy, University of Western Ontario, Canada

This paper explores problems regarding the use of moral language in game theoretic models intended to illuminate the evolutionary origins of human cooperation. Interpretations of such models often include not only misrepresentations of the relationship between the phenotypic 'strategies' that they are tracking and *moral* behaviours, but also fail to recognize the role of language, cultural knowledge and expectations, as well as early human social structures in solidifying moral norms and attitudes. The highly contextual nature of early human social interactions precludes meaningful discussions of human actions as mere phenotypic expressions--this holds despite our increasing knowledge of the complex interactions between genetic and extra-genetic information. I argue that these omissions are not only problematic for existing game theoretic models, but may be so also for the field of evolutionary game theory as a whole since there is currently no apparent method of reconciling our knowledge of human evolution with economic models. In particular, I argue that evolutionary game theory has thus far provided us with models representing general trends in evolving biological populations, but no models that represent early human populations as such. Drawing from anthropology, evolutionary biology, and philosophy, I point to information that could be used to model early human interactions with greater accuracy and explanatory potential.

Figures in the History of Cell and Molecular Biology A (submitted papers)

Edmund Beecher Wilson: Amphioxus, the comparative and the exemplary

Lowe James, University of Exeter, UK

The experiments that Edmund Beecher Wilson conducted in 1892 with the marine invertebrate *Amphioxus* (now *Branchiostoma lanceolatum*) have commonly been interpreted as a move towards experimental embryology, and the causal morphology or developmental mechanics proposed and pioneered by Wilhelm His and Wilhelm Roux. The disagreement in the literature on Wilson's 'experimental turn' has largely focused on the extent to which his entry into experimental work constituted a 'revolt from morphology' (cf. Allen, 1978). While I generally agree with Maienschein and others (e.g. Maienschein, 1981; Benson, 1981) that there was continuity between Wilson's earlier morphological and his later experimental work, I would like to take this a step further. I will detail how Wilson's work on *Amphioxus* derived from, and constituted an investigation by other means, of embryological problems that had evolved over the preceding years. In particular, I will highlight how Wilson tracked the origin of later adult and embryological characters and structures to the earliest stages of the embryo, and how he tried to make sense of the phenomenon of cleavage. *Amphioxus*, in this context, lent itself to experimentation since it showed a large degree of natural variation in cleavage patterns already. In understanding the *Amphioxus* work in this way, one can see how it actually formed a bridge between Wilson's established comparative methods and his venture into experimentation.

Wilhelm Roux's "The Struggle of the Parts in the Organism": a physiological synthesis of Darwinism

Bolduc Ghyslain, Université de Montréal, Canada

Wilhelm Roux's *Der Kampf der Teile im Organismus* (1881) is commonly considered to be a Haeckelian thesis unrelated both to the birth of experimental embryology and to Roux's well-known research program (*Entwicklungsmechanik*). Although the influence of the School of Jena on Roux's early work cannot be denied, a re-examination of *Der Kampf* reveals this work to be a complex physiological synthesis of Darwinism, which combines mainly four theoretical frameworks, namely (1) Wilhelm His' biomechanist methodology, (2) Rudolph Virchow's physiology, (3) Ernst Haeckel's conception of biological individuality, and (4) Charles Darwin's theory of natural selection. Roux's rejection of Haeckel's law of recapitulation clearly establishes a distinct theoretical system based on a mechanistic view of causation whereby the relationship between ontogeny and phylogeny in terms of the internal selection of the fittest parts. The main condition of such a physiological application of Darwin's mechanism lies in the implicit conception of the organism as a *milieu intérieur* such that it is exemplified by Virchow's theory of cell autonomy and his notion of cell territory. In addition to performing Darwin's natural selection, the struggle between parts contributes to a global functional adaptive process which is responsible for the emergence and the maintenance of purposeful dispositions. In this sense it acts as an epigenetic and homeostatic phenomenon in a coherent way with the self-regulative nature of life. I will argue that this theoretical system falls within Roux's quest of providing an explanation for inherited and epigenetic developmental causes as specifically maintained by the *Entwicklungsmechanik* program.

Biometrics: the controversy on telomere length as biomarker of aging

Moreira Tiago, Durham University, UK

In the spring of 2011, a variety of media platforms reported on the commercial release of tests to measure telomere length as a proxy of biological age, and on the related controversy opposing two winners of the 2009 Nobel Prize for Medicine - won for work on the function of telomeres - Professor Elizabeth Blackburn and her former student and assistant Dr. Carol

Greider. Normally conceived as caps at the end of chromosomes that appear to regulate cell replication, telomeres have been associated, since the 1970s, with ageing processes in the cell, but their validation as a biomarker of ageing has been fraught with controversy. This paper is integrated in an on- going project concerned with the history of attempts to measure aging since the 1950s, and explores the 2011 controversy as a means to understand the dynamics of contemporary research on biological aging. Drawing on documentary data and interviews, the paper suggests the telomere controversy enacts wider tensions about knowledge making, and in particular, measurement in biology in the 'era of molecularisation'.

Figures in the History of Cell and Molecular Biology B (submitted papers)

Understanding Life: It's Not All Genes; An Examination of the Work and Thought of Daniel Mazia

Lyons Sherrie, Empire State College, USA

The cell biologist Daniel Mazia (1912-1996) was best known for his work elucidating the structure of the mitotic apparatus as he investigated the general problem of cell reproduction. Mazia was concerned with understanding life at the most fundamental level and brought a deeply philosophical approach to his life in the laboratory. For many years genetics has dominated the thinking in understanding a variety of biological problems from evolution to cancer. Embryology was essentially left out of the evolutionary synthesis. This is supposedly being rectified by evo-devo. But even this field has been dominated by looking at what gene gets turned on at what stage. Yet what is responsible for turning on those genes, what causes a cell to differentiate? Cancer at its most fundamental level is a problem of unregulated cell growth, i.e. a disturbance of the cell cycle. In exploring the "origin of twoness" in cell reproduction Mazia suggested that the cycle be thought of as a bicycle with a growth wheel and a reproductive wheel. He brought attention to the importance of the centrosome and thought that elucidating the underlying structure of the cell would provide insight to development. Although much of Mazia's work involved identifying molecules that were critical to the various stages of cell division he advocated the importance of microscopy: *think with the eyes and see with the brain*. I argue that much can be learned from his approach in furthering our understanding of life.

August Weismann's First Embryological Investigations 1861-1866

Weissman Charlotte, Tel Aviv University, Israel

August Weismann is one of the most influential evolutionary biologists of the 19th century, generally considered second only to Darwin in importance. He was an uncompromising selectionist, challenging prevalent, seemingly self-evident ideas, the most significant of which was the inheritance of acquired characters. In this lecture I show that Weismann's theories were heavily dependent on the progress made in cytology, and that he based his far-reaching conclusions on his early embryological-cytological work on dipterans. I suggest that his two major discoveries in the field of dipteran embryology, the discovery of the imaginal disks, the precursors from which body parts of the adult muscids differentiated, and that of the pole cells, which sequester the formative material of the gemline, were the crucial for the construction of his later ideas on development and evolution. In contrast to most modern scholars who have overlooked Weismann's early embryological studies, I argue that Weismann's most important ideas, such as developmental segregation, unequal nucleus division, particulate, pre-formative heredity, and the non-inheritance of acquired characters, are firmly related to his first microscopical investigations of dipteran embryogenesis.

Fitness and Fitness Wars A (submitted papers)

Process and Product Concepts of Natural Selection and Genetic Drift
Pence Charles, University of Notre Dame, USA

Are natural selection and genetic drift best thought of as processes, as products, or as some hybrid of the two? While this is a well-known issue in the interpretation of evolutionary theory, it has seemed in the last several decades to have both made relatively little progress and not often enough connected to actual biological examples. In this paper, I lay out this problem, diagnose the reasons that it might have been difficult to resolve, and indicate the direction in which I believe a solution can be found. Of course, since process and product notions of selection and drift are intended to be definitions of the same concept, their extensions – the individual biological instances that they mark out as selection and drift – will be nearly identical. But their intensions – the conceptual structures that they propose for evolutionary theory – are quite different. The fact that this stark choice between interpretive frameworks in evolutionary theory is not mirrored by equally stark consequences for our classification of biological cases, I claim, can help explain why this debate has been intractable. How, then, should we expect to move forward? While the extensions of these differing concepts are nearly identical, they are not *precisely* identical, and it is here that we can make progress. There do exist (even plausibly empirically relevant) biological cases that these definitions of selection and drift classify differently, and it is here that we can hope to determine which of these conceptual frameworks is correct. I close by laying out a few examples and offering some indications for future research.

Will Simpson's Paradox and the Sure Thing Principle Resolve the Fitness Wars?
Takacs Peter, Florida State University, USA

The ontological status of organismal or trait fitness has been a topic of heated debate in the philosophy of biology. On one side of the issue there are those who claim that fitness is a causally efficacious, probabilistic dispositional property (i.e., a propensity) of the individual organisms comprising a population. For ease of future reference, let us refer to this position as “the orthodox view” regarding natural selection explanation. In stark contrast, opponents of the propensity interpretation contend that fitness is a mere statistical, noncausal property of trait types; explanatorily but not causally efficacious. Dennis Walsh, one of the architects of the statistical interpretation, has recently (2010) argued that the causal commitments of the orthodox view *entail* a probabilistically non-benign version of Simpson's paradox and ultimately the violation of a principle in decision theory known as the “Sure Thing Principle.” If correct, this would constitute a fatal result for the orthodox view since causal claims must conform to the directive of the aforementioned principle. In this paper I argue that Walsh has overstated the case against the orthodox view. I begin by sketching out the relevant differences between the two competing positions with respect to the concept of fitness and its explanatory role in theoretical population biology. This is followed by a brief review the pivotal distinction between probabilistically “pathological” and “benign” instances of Simpson's paradox, and a careful examination of the problem case that supposedly stymies the orthodox view. I shall conclude by contending that it is only via a conflation of conditional probability and logical implication that Walsh's critique can be construed as decisive.

Measures of fitness: opening the Pandora’s box
Lenormand Thomas, Centre d'écologie fonctionnelle et évolutive, CNRS, France

“Although there is no difficulty in theory in estimating fitnesses, in practice, the difficulties are virtually insuperable” (Lewontin, 1974). Fitness is a key concept in evolutionary biology. In many models, this is a quantity that can be defined without (too much) ambiguity. When it comes to test these models of evolution and measure fitness empirically, however, many difficulties arise, in addition to these definitional problems. In this presentation, I will try to summarize and provide an overview of these issues. I will present different approaches to measure fitness in the lab or in the field, distinguishing ‘forward’ and ‘backward’ methods. To illustrate each case, I will use examples from my work that include the most precise estimates that have been obtained to date. I will finally relate the problems of fitness measures to the neutralist-selectionist debate.

Fitness and Fitness Wars B (submitted papers)

Revisiting fitness: Trait-based Fitness
Bourrat Pierrick University of Sydney, Australia

The notion of fitness, although fundamental in evolutionary theory, is not a unified concept. Several authors have even concluded that looking for a general concept of fitness is doomed to failure. I disagree with these conclusions. In the vast philosophical literature on fitness, two approaches have been put forward. One the one hand, under the *statistical* interpretation of the concept, fitness is the per capita rate of increase of a given type and does not play any causal role in evolutionary changes. On the other hand, under the ecological approach of the concept, fitness is a property of organisms (or more generally entities) forming a population in a given environment and it plays a causal role in evolutionary changes. While both approaches have some advantages over one another they also come with many drawbacks. In this paper, I propose a concept of fitness which takes the advantages of both approaches while eliminating their problems. I start by detailing different problem cases for each approach and propose “local” solutions for each of them. I then show that each solution can been integrated in a more general concept of fitness, yet consistent both with the idea that fitness is a property of entities and that it causally affects their evolutionary fate in the context of natural selection. I call this concept *trait-based fitness*. Further on, I show that trait-based fitness is perfectly equivalent to the notions of fitness used in classical evolutionary disciplines with the advantage of being more general.

Assessing Methodological Adaptationism: an Historical Approach
Allegra Alessandro, London School of Economics (CPNSS), UK

In his 2001 paper Peter Godfery-Smith distinguishes between 'Three Kinds of Adaptationism', arguing that three related but independent views have been conflated under this term. He then suggests that distinguishing between these three ideas sheds light on the debate regarding the testability of adaptationism, showing how this is relevant in the case of empirical adaptationism.

In the present work I follow Godfrey-Smith's taxonomy and focus on an often neglected aspect of it, addressing the issue of the testability of methodological adaptationism. In the attempt to respond to Gould and Lewontin's criticism that adaptationist methodologies are sterile, I propose to test the validity of adaptationism as a heuristic device through an analysis of the history of evolutionary biology.

I will argue that, under a reasonable account of what scientific success is, both the actual and potential validity of methodological adaptationism can be assessed historically.

The conceptual tools to carry out this analysis are based on Lakatos' Methodology of Scientific Research Programmes, namely on his account of scientific progress in terms of progressive problem shifts and his distinction between internal and external history. These will provide the criteria to evaluate the success of adaptationist heuristics and understand the reasons for such success.

After having outlined my proposed methodology and addressed some of the obstacles it might encounter, I suggest it to be applied to (a rational reconstruction of) the history of evolutionary biology to show its effectiveness in assessing methodological adaptationism.

The Formation of Language (submitted papers)

Language Acquisition, Rule-following, and the Individual Species Concept

Glackin Shane, University of Exeter, UK

This paper builds upon a family of positions independently developed by Yale linguist Steven Anderson, Tel Aviv evolutionary theorist Eva Jablonka, and myself, concerning the possible mode of evolution of a "Language Acquisition Device" as posited by the followers of Noam Chomsky.

These positions hold, roughly, that such a faculty is likely to have evolved *in response* to innovations by the community of speakers, allowing their use to be more easily learned. Consequently, to the Chomskyan distinction between "competence" and "performance" (more recently, "I-language" and "E-language"), we must add something like Saussure's *langue*; language as a *public object*, manifest not in the minds or utterances of individual speakers, but in the community practices to which those speakers respond.

This paper develops and links two theoretic consequences of the position. In his seminal lectures on Wittgenstein's rule-following argument, Saul Kripke suggested that Chomskyan generative linguistics fell foul of the "sceptical paradox" he presented there. The Anderson/Jablonka/Glackin approach, I argue, allows a reconciliation of the two theorists' approaches to language by emphasising the role public linguistic practices, of the sort Kripke appeals to in his solution to the paradox, play in an evolutionarily plausible theory of generative grammar.

David Hull and Michael Ghiselin have controversially proposed that we view species as individuals rather than as classes or kinds. Following this, I argue, we can use the Kripkean sceptical paradox to understand the difference between language acquisition by an individual organism, and the way a species "learns" it in evolving the LAD.

Is syntax equals to language? A debate on a trait of human uniqueness

Tapia Mercedes, Centro Lombardo, Italy

Language has been considered one of the characters that distinguish humans from other species. But syntax is the trait that might be separating our communication system from those of other species. Only syntax is not language. Language is a merging of various aspects that enables us to communicate. As we know, it has been set forth that it would be better to place the idea of syntax in the context of an evolving sociability, because its biologization does not explain what language really is. Therefore in this work I will restate some of the observations of incipient syntax in other species and reintroduce some evidences of how some processes of cultural learning can be equated to language "acquisition". Specifically I will show how the reading and writing learning process exhibits similarities to that of oral learning. The correspondences can help us explain not a gene or a prewired grammar in our species, but the importance of learning in general, the role of highly systematic cultural practices in language learning and brain specialization. Accordingly I propose that a social approach centred in learning can give us a better understanding of the origins of language and some bases to rethink what is uniquely human.

Frameworks and Representation of Cells and Genes I. Lineages

Stem trees, stem lines, stem cells – Ernst Haeckel´s and August Weismann´s legacy to stem cell research

Dröscher Ariane, Dep. of History Cultures Civilizations, Bologna, Italy

Today, the current definition of stem cell is increasingly objected. Shinya Yamanaka's works may represent the crossroads of a profound rethinking. Besides the experimental results there are also historical reasons that have formed our understandings and conceptions of stem cells. In particular, Ernst Haeckel's metaphor and August Weismann's model and diagram of development had and still have great explanatory power. My talk will focus on the role of historical diagrams, especially stem trees, cell trees and cell lineages.

Between Molecular Ecology and Cytophysics

Brauckmann Sabine, Université Aix-Marseille, France

From the 1940s onwards Paul A. Weiss and his group at the University of Chicago started a new research program on cell migration. This program relied upon Weiss' approach stating that the position of the molecules inside a cell determines the development (molecular ecology). 'Position' here means that cells coadapt to the physical and chemical conditions prevailing at that particular location. He interpreted development as the sorting and segregation of biochemically distinct entities into definite locations. Thus, two cells with similar components could develop and mature differently, depending on which molecules were situated on the inside and which on the outside. Weiss's approach to cellular development presupposes the spatial conditions of solid stare systems as, for example, all surfaces and interfaces in the cell demonstrate them. These systems are the physical basis for the selective localization and the traffic management in the chemical machinery of the cell (cytophysics). My objection here is to briefly outline the experimental program of the Chicago Group, and to map it to Weiss' cell conception by images, with some incursions into the notions of positional information (Wolpert) and topobiology (Edelman).

Justifying molecular imagery in cell biology: Goodsell vs Roberts

Serpente Norberto, University College London, UK

A common assumption held by philosophers of science and implicitly by most scientists is that claims of a scientific nature (hypothesis, theories) need to be justified. A set of criteria is proposed to specify the validity and/or productivity of such claims chiefly among them: a) their correspondence to experimental data; and b) the capacity to predict the behaviour of the system in different conditions (productive deductions and testable consequences).

On the contrary, scientific images have customarily been exempt from questions concerning justification.

This assertion however, turns problematic, when images are conceptualised as ‘self-sufficient modes of thought', that is, as having an independent or almost independent role on scientific reasoning and theorising.

A reconstruction of the process of image production in molecular cell biology since it emerged in the early 1980s could provide us with some insights for this paradox.

Key questions to be addressed in this paper are:

How much justification goes into image creation in this field of knowledge? And, when producing images of a molecular nature are elements of justification already in place?

This paper explores the justification process (if any?) of the use of molecular images in cell biology through the work of David Goodsell and Keith Roberts, two well-known molecular designers.

I will be arguing that an exploration of the production of molecular imagery places images closer to discovery rather than justification and that they are crucial for a distinction between generating and securing knowledge a distinction that is perhaps more productive than the classic dichotomy of discovery and justification, for it allows incorporating other key elements for the production of knowledge such as pedagogy and aesthetics.

Frameworks and Representation of Cell and Genes II. Networks

From Pathways to Networks: Developments in the Science of Intracellular Signaling

Reynolds Andrew, Cape Breton University, Canada

In the 1970s scientists began to uncover the details of how cells communicate by means of electrical and chemical signals. The process by which an extracellular signal is received at a membrane-bound receptor and transmitted into the inner cell environment where it can trigger changes in cell behaviour was dubbed ‘signal transduction.' The complete chain of events and molecular components describing this signal transmission was called a ‘signaling pathway.' Metaphors and analogies from electronic engineering and cybernetic theory have strongly informed understanding of these processes. The cell is regarded as consisting of circuits and programs, which scientists have been busy trying to map in their efforts to understand development, health, and disease in humans and other organisms. The 1980s and 90s saw recognition of the widespread occurrence of ‘cross-talk' between signalling pathways, and as a result the metaphor of signaling ‘networks' began to appear more frequently. Increasingly one now sees criticisms that the signal pathway concept is misleadingly simplistic and impedes further progress in scientific knowledge and biomedical intervention. Signaling networks are highly dynamic processes which belie the implication of a stable entity suggested by the pathway and circuit metaphors, and yet the importance of scaffolding and adaptor proteins suggests the highly structured nature of signaling networks. This talk will describe some of the history of this shift in language and perspectives, and the implications for the philosophy of science's account of mechanism as an explanatory scheme.

Paradoxes of “Live-Cell Imaging”

Stahl Lina Maria, Universität Potsdam, Germany

Cells are considered to be basic units of life and thus serve as an essential scientific object in the study of life. Becoming visible only with the help of microscopes, their discovery goes back to Robert Hooke, one of the first microscopists of the 17th century. Hooke not only found out that cork shows regular structures of similar “cells”, but also assumed that these have a function regarding the nutrient transport. However, since the cells he dealt with were cork cells – meaning that they were actually dead – they clearly could not have had that function. Hence, already in this early scene of microscopy there emerges, though accidentally, a connection between the study of the living and the observation of dead material.

In the practice of today's microscopy we are still confronted with couplings of "life investigation" and death – but now, for the most part, this does not happen accidentally. On the one hand, the preparation of cells typically entails their fixation, meaning by implication the cells' death. On the other hand, the technical conditions that apparatus constructions impose on biological material frequently imply its death as well.

The analysis of microscopic practices as a method of studying life reveals several paradoxes leading to the hypothesis that biology is based on a constitutive difference between the examined phenomenon and the phenomenon to be examined. Eventually, this difference enables us to learn something about life in general, while, at the same time, it always contains a number of significant restrictions.

Graphing cellular regulatory networks
Denis Thieffry, Ecole normale supérieure de Paris, France

Since the second half of the 20th Century, biologists increasingly represent interactions between molecular components (genes, proteins, etc.) in terms of graphs. As long as these graphs remain relatively modest in size or in complexity, they were directly use as device to integrate data, reason about the underlying process and convey information for didactical purpose or scientific exchanges. With the advent of genome-wide methods to identify gene/protein interactions (e.g. double-hybrid, mass spectrometry, ChIP-seq, etc.), graph-based representations are still used to represent interaction data, but our intuition is not sufficient to comprehend the content of the gigantic graphs produced (encompassing thousands of nodes and even more connections). This led to the development of novel standards and algorithms to extract biological relevant information from these graphs. In parallel, different mathematical methods applied to these graph currently enable formal, dynamical analyses of cell behavior, for normal or perturbed conditions. These graph-based representation lie at the core of the trendy fields called "systems biology". Focusing on examples related to cell differentiation and embryonic development, I will attempt to decipher different aspects of these representations to emphasize the interplays between visual, cognitive and computational dimensions.

From Neurons to Knowledge A (*Interdisciplinary session*)

Making Sense of Brain and Behavioural Lateralization
Frasnelli Elisa, Center for Mind/Brain Sciences, Italy

Traditionally, only humans were thought to have strong left-right asymmetries in the brain and at the behavioural level, but recent studies have revealed that most vertebrates and invertebrates are indeed lateralized. Further, it has become apparent that two patterns of lateralization exist across species. In "individual-level" lateralizations an equal number of left- and right-biased individuals coexist in the species, while in "population-level" lateralizations a majority of individuals is right- or left-biased. The latter is the case for humans; a good example is handedness. While individual-level lateralization may have evolved because it increases individual brain efficiency, population-level lateralization is unrelated to individual brain efficiency, and remained unexplained for many years. Recently, it has been suggested that the alignment of lateralization at the population level may have evolved as an evolutionary stable strategy when individually-asymmetrical organisms must coordinate their behaviour with that of other asymmetrical organisms. Game-theoretical models developing this idea and considering group-living individuals engaging in intraspecific and interspecific interactions suggest that population-level lateralization is more likely to evolve in social than in non-social species. I evaluate this new hypothesis, and provide supporting empirical data by comparing different insect species that show different levels of sociality.

Cognitive task and brain activity: an uncertain correlation
Hernandez Chavez Paola, Centro Lombardo, Italy

As in many other reductionist projects, neurons are though to be an ideal candidate to explain once and forever how humans think, in nowadays terms, what cognition is. Under this scheme, cognition is explained as the result of what the brain does. When we ask to a neuroscientist what the brain does, he would unavoidably offer us a descriptive scenario where brain scanning is associated to the performance of a particular cognitive task. Nevertheless, the relationship between brain activity and an associated cognitive task is elusive, to say the least.

In this work, I would like to offer a general outlook of the difficulties faced when we seek to explain cognition based on neuroscientific evidence, the technical issues involved and the theoretical assumptions implied. I will provide an analysis laid out in terms of the Cognitive

Modularity debate. A main characteristic of a modular cognitive system (already formulated in Fodor 1983) is that it is associated to brain structures. This claim can be understood in a strong, weak or minimal sense, depending on the level of commitment to brain structures. After clarifying these 3 different levels of commitment, I will propose that a main difficulty with these approaches to cognition is that there is not a clear distinction between a cognitive task failure in the general competence and a cognitive task failure due to performance factors.

A Place for Levels-Thinking in Science and Philosophy

Daniel Brooks, Universität Bielefeld, Germany

Representing the world as hierarchically organized into a number of discrete levels is so deeply embedded in biological science, it is rarely merited explicit attention by working scientists. Similarly, philosophers of science routinely make reference to this stratified picture of the world for many topics, such as scientific explanation, the nature of causation, and theory structure in science. Despite this ubiquity in science and philosophy, there remain 'levels skeptics', who claim that the concept of organizational levels is a misleading, or even vacuous, notion for understanding how scientists produce knowledge about the natural world. Arguments to this effect usually focus, quite correctly, on the lack of clarity with which levels-talk is applied in the literature: ‘Levels’ can simply mean too many things. The purpose of this talk is to offer a response to this skepticism of levels by articulating more precisely the general role that levels-thinking plays in investigating complex phenomena inherent to the biological sciences, especially neuroscience. The primary feature that levels-thinking introduces into scientific practice is an emphasis on explicating *organization*, both of natural phenomena and of the research efforts that seek to explain these phenomena. While it is doubtful that a singular concept of levels can adequately capture both kinds of organization simultaneously, a plurality of more particular, mutually complementary levels concepts is possible. In other words, what the critics charge as vacuous in the hierarchical view of the world, proponents may defend as the virtue of flexibility in the concept’s range of application.

From Neurons to Knowledge B (*Interdisciplinary session*)

The neuroplasticity-neuropathology continuum: an alternative view on learning and memory formation

Sarto-Jackson Isabella, Konrad Lorenz Institute for Evolution and Cognition Research, Austria

Neuroscientists describe learning at the neuronal level as a process of long-lasting enhancement in signal transmission between neurons causing modification of cellular responses specific to external stimulation. It is widely accepted that long-term potentiation – the synaptic strengthening resulting from a synchronous stimulation of neurons (Hebbian theory) – is the mechanism underlying these modifications. On the ontogenetic level, these induced, physical changes of intrinsic brain activity are believed to be the basis for memory formation. Extending this line of arguments, the concept of neuronal memory allocation suggests that distinct brain processes specifically determine which neurons and synapses encode certain memory traces, hinting towards a Kantian view of knowledge encoding.

In this talk, I will argue that comparable neuronal modifications that underlie long-term potentiation are also involved in processes causing long-term depression or pathological and neurodegenerative conditions. Thus, molecular mechanisms ascribed to memory formation seem to represent only a narrow section of a neuroplasticity-neuropathology continuum

(McEachern and Shaw, 1999).
I will substantiate these arguments with results from my own work as well as using data from other molecular neuroscientists and electrophysiologists. This alternative view of neuroplasticity aims to trigger a discussion about the congruity between synaptic mechanisms and knowledge encoding/storing and to fuel a debate about neurodiversity and its contribution to our “knowledge society”.

Neuro-Science vs. Folk Psychology: From Deadlock to Well-moderated Controversy
Zakravsky Katherina, Philosophical Institute, University of Vienna, Austria

The scientifically informed public is facing a possible deadlock between neuroscientific experts claiming to “naturalize” any traditional self-description of the human psyche, and the critical response of the social sciences and humanities that the “brain” of naturalist reductionism is nothing but a techno-scientific construction, e.g. a semi-artificial epistemological object (following the terminology of Bruno Latour).
Rather than trying to solve this controversy I propose – in an analogy to Immanuel Kant's similar effort in “The Conflict of Faculties (1798)” – a meta-strategy of transforming this very controversy into a “machine of knowledge production, evaluation and specification”.
With reference to Latour, Foucault and Michael Polanyi's underrated concept of “tacit knowledge” I want to show that the communal “brain” (or “brainhood” according to Fernando Vidal) as an object shared by many different professions and groups can serve as a paradigm for a new kind of knowledge production in which intense and well organized controversy is itself the process of knowledge that cannot be decided or judged by any single group of experts. As the interested public of stakeholders cannot wait until experts will decide questions that cannot be decided once and for all this idea of processional pluralistic knowledge production results in a claim for a revolution in education that enables each citizen of the knowledge society to partake in the relevant controversies of his/her time.

Functions (submitted papers)

Counterfactuals and the Generality Requirement
Häggqvist Sören, Stockholm University, Sweden

Etiological theories of function appear to imply an indeterminacy of function along specificity-generality dimension.
A standard example is Sober's: a population of *Drosophilia* subject to heat stress evolves thicker skin; later temperatures drop steeply and the thickened skin remains adaptive, now as protection against the cold. Is its function to protect against high temperatures, or to insulate generally?
Millikan urges the latter on the basis of the requirement that “biofunctions should always be described according to the most general principles available”. She employs this principle – the generality requirement – widely in order to reduce various perceived threats of indeterminacy.
Now the fact that the flies in the example were actually subject to both heat and cold seems incidental to the availability of the broader ascription. The thickened skin *would have* protected against low temperatures even if they had never suffered such temperatures. Interestingly, at times Millikan herself states the rationale for the broader ascription in terms of a counterfactual.
Allowing counterfactuals in applying the principle, however, may threaten to generate unforeseen, perhaps implausibly general, function ascriptions. On the other hand, restricting the principle's application to actual, historical environments – as Millikan appears to insist in several places – may result in indesirably parochial and specific ascriptions.
My aim in this talk is to weigh the options, and to argue that Millikan's theory is ultimately committed to counterfactuals than she admits. A corollary is that Buller's so-called “weak”

etiological theory is legitimate if any etiological theory is.

Context-based functional synthesis
Daëron Marc, Institut Pasteur, France

Technological progress has dramatically changed Biology over the last 3-4 decades. High-throughput sequencing made transcriptomics accessible, and whole genome sequencing affordable. Miniaturization made proteomics amenable to normal cells. Flow cytometry with increasing numbers of fluorescent probes, mass spectrometry and single-cell sequencing permitted and revolutionized the study of individual cells. One is now confronted with an exponential wealth of information. Ascribing a function to biological objects has been a task of Biologists since ever; it is more than ever necessary. The problem, however, has changed. Instead of dissecting organisms into systems, systems into organs, organs into cells, cells into organelles, organelles into smaller parts and, ultimately of giving molecules a function in the context of organisms, one must assemble innumerable molecules with no known function into a biologically coherent whole. Functional analysis cannot anymore be applied as proposed by Wimsatt and Cummins in the 1970s. I propose instead a functional synthesis aiming at understanding how function emerges from interactions of proteins with other proteins in a given context. I will use the example of antibodies and show how they can be protective and pathogenic, generate antagonistic signals when engaging different receptors, both induce and inhibit cellular responses and select biological responses within the potential functional repertoire of cells. Finally, I will argue that the concept of "structure-function relationship" is inaccurate because, like antibodies, molecules have no function but properties, and that the function(s) they exert depend(s) primarily on the context in which their properties operate when they interact with other molecules.

The Modal Theory of Function: Lessons from Molecular Biology
Huber Maximilian, University of Geneva, Switzerland

The modal theory of biological function (Nanay 2010) states that the token trait x of an organism has a function F iff if x were F-ing, this would contribute to the organism's fitness. Nanay claims that the modal theory has two main advantages: first, in contrast to etiological or systemic theories of function, the modal theory is trait-type independent; second, the modal theory explains malfunctioning without taking recourse to normativity. In this paper, I scrutinize the modal theory's counterfactual semantics and the applicability of the modal theory to molecular biology, neither of which has received much attention in recent criticisms. Based on a case study of the tumor-supressor gene p53's malfunctioning in human cancer (Vogelstein et al. 2000), I argue that the modal theory cannot fulfill its promise. First, I show that a function ascription to p53 requires individuating trait-types because tumor suppression crucially depends on the concentration of tokens of a certain trait-type, namely the type ‘p53 protein'. Second, I reveal that by failing to ascribe the function of suppressing tumors to p53 ('if p53 were inducing apoptosis, this would contribute to the organism's fitness' is ceteris paribus false), the modal theory contradicts an established function ascriptions in molecular biology. Finally, I propose a revised modal theory capable of explaining (mal)function in molecular biology without taking recourse to normativity.

Functions in Complex Systems

Functions and Ecological Resilience
Barker Gillian, Western University, Canada

The systems view of functions seems well-suited for understanding ecological functions: It makes sense of several of their distinctive and puzzling features, in particular their appearance of possessing some but not all of the attributes of evolved organismal functions. But applying the systems view to ecosystem functions also presents distinctive problems whose resolution may cast useful light on the notion of function more generally. The systems view understands functions as linked to stability: to the maintenance over time or reproduction over generations of a particular system structure. If ecosystems are understood as stable systems characterized by negative feedback relationships that maintain equilibrium values for key variables, the systems view seems easy to apply. But the development of a more complex view of ecosystems, that recognizes that ecosystems are not simple equilibrium systems but are subject to chaotic change at various levels of organization, presents challenges for the systems view. Replacing the notion of stability (simple maintenance and reproduction) with that of ecological resilience provides a modified version of the systems view that can be applied to ecosystem functions. The picture that results offers an interesting perspective on broader issues concerning functions, including the relationship between functions at different levels or organization; the relationship between "natural" and "artificial" functions; and the role of functions not just in maintaining stability but in driving organic change.

Functional Analogical Models in Biomedical Research

Helwig Munroe Zachary, University of Western Ontario, Canada

Recent literature in human immunology charges that research based on animal models of the human immune system has underperformed compared to initial expectations. I argue that the reason for this shortfall in clinical success is a failure to be clear about the nature of the analogy between humans and animal models upon which the research is based. In particular, as a result of an uncritical reliance on the dual background assumptions of determinism and causal reducibility, the focus has wrongly been placed on the attribution of causal similarity between humans and (other) animals. This is manifest in what has become the standard view of animal models in scientific research, according to which the analogy between model and modeled system is one of certain shared or similar causal structures, such models being termed "causal analogical models" (CAMs). I present reasons for thinking that this is a flawed picture, and argue instead that the relevant analogy between biological systems is *functional*. Viewing experimental animals as *functional* analogical models (FAMs), rather than CAMs, has two important benefits: first, it can account both for the successes and instances of poor performance of these models in biomedical research; second, it provides a metaphysical framework for understanding animal models and their use in research that a) does not make an implicit appeal to reduction, and b) accommodates the emergent and complex nature of the human immune system.

Functions in Ecology

Defending Ecosystem Health: A Normative but Naturalized Notion of Ecological Function

C. Dussault Antoine, Université de Montréal, Canada

Many ecological scientists and philosophers have expressed skepticism with regard to the scientific appropriateness of the concept of *ecosystem health*, on the grounds of its supposed failure to be value-free, and its alleged implicit commitment to an organicist view of ecosystems. Because the concept is *normative*, indicating the *good* state(s) of ecosystems, it has been thought to inescapably involve ethical values and so lie beyond the scope of science. Moreover, because *organisms* are the paradigmatic bearers of health, the concept has been criticized for its commitment to the obsolete Clementian paradigm in ecology. My contribution is aimed at exploring conceptual resources from metaethics on the notion of *goodness for*, and from the philosophy of biology on the issue of the normativity of functions, in order to clarify the kind of normativity involved by the concept of ecosystem health. After explaining why this normativity can be naturalized without committing anything like what G.E. Moore has called the naturalistic fallacy, I will argue that it is not a kind of normativity that is problematic for science. I will then turn to the issue of ecological organicism and argue that though ecosystem health assumes that ecosystems have some degree of functional organization, the notion however does not require an implausible degree of resemblance between them and paradigm organisms.

On the vague and metaphorical definitions of 'good ecosystem functioning'
Dieleman Catherine, University of Western Ontario, Canada

The maintenance of ecosystems has become a driving factor for conducting ecological studies, and with this came a multiplication of notions describing "good ecosystem functioning", such as integrity, stability, resilience and health. A critical and historical examination of these concepts and the assumptions associated with them reveal two particular concerns. First, many of them are used rather loosely as synonyms, despite the fact that their respective technical meaning often differ significantly. Although some terms, like "stability" and "resilience", have had similar interpretations for decades, they nevertheless grew apart sufficiently in ecology that merging them, as it is often the case, is hardly justified anymore. Second, it remains fairly common to make a mere metaphorical usage of these terms, despite the fact that they all have received at some point precise operational definitions. Although it is a normal process to revise concepts and try them in areas alien to their discipline of origin, such vague and metaphorical usage can be counterproductive. Ill-defined language and careless transfer of ideas by researchers and policymakers only amplifies the pervasive communication gap hurting the numerous disciplines involved in the maintenance of ecological systems.

Climate change and ecological management: from historical structural to futuristic functional goals
Desjardins Eric, University of Western Ontario, Canada

Ecologists often distinguish two forms of ecological management on the basis of the type of goals pursued, namely restoration and rehabilitation. According to this tradition, ecological restoration aims at re-establishing the lost species composition of degraded sites. Although setting such structural goals is still very common, many find this traditional approach unrealistic and/or undesirable. So it has become increasingly common to see ecologists and practitioners setting functional goals and promoting ecological rehabilitation instead of restoration. One of the arguments for doing so suggests that, in a context of climate change, species assemblages that prevailed centuries ago might not be the most viable or suitable assemblages for the future. They thus advocate abandoning historic structural goals for futuristic functional goals. Although I am sympathetic to this view, I think it is important to reflect on the assumptions and consequences of making this change in practice. The functional approach may seem more realistic and desirable in a changing world, but it is not problem free. Part of the reason why a functional approach is so attractive is the multiple realizability of functions. A certain level of nutrient cycling for example can be achieved by different species assemblages. However, this multiple realizability creates a situation where it becomes important to decide which realization is best. We would not want to say: "anything goes" as long as ecological function X is fulfilled. Concerns about biodiversity or integrity for example seem to impose some limitations on the functional approach. So, this paper is an invitation to think about the prudential arguments we need to develop while moving toward a futuristic and functional ecological management.

General Issues in Philosophy of Biology A (submitted papers)

Multilevel Causation and the Extended Synthesis

Martinez Maximiliano, Universidad Autonoma Metropolitana, Mexico
Esposito Maurizio , Universidad Nacional Autónoma de México, Mexico

In this paper we argue for the necessity of reconsidering our classical independent causal models for biology, by integrating the dichotomies proximate/ultimate and bottom-up/top-down into multilevel approaches, more suitable to cope with complexity issues inherent to biological processes. In order to overcome these dichotomies, we also propose to introduce the notion of 'multilevel causation,' a relational concept that can uncover the multiple kinds of interconnections involved at different levels of living organization. In briefly reviewing some recent work on complexity, evo-devo, carcinogenesis, autocatalysis, animal regeneration and niche-construction to make our case, we will argue that such reconsideration is a necessary step for the advance of the “Extended synthesis”.

Toward a Propensity Interpretation of Stochastic Mechanism: Lessons from Fitness and Drift

Desautels Lane, University of Maryland, College Park, USA

The life sciences are rife with probabilistic generalizations. Mendel discovered that the chance of a hybrid between green and yellow pea plants to produce yellow peas in the F2 generation is .75. In neuroscience, the release of neurotransmitters only results in the successful initiation of electrical activity in postsynaptic neurons about 80% of the time. In evolutionary biology, the evolutionary consequences of genetic mutation are conceptualized in terms of the chance (per unit of time) a gene has of changing from one state to another. A question of significant import to philosophers of science is: what makes these statements true? What in the world (if anything) grounds these probabilistic facts?

The answer pursued in this paper is that these probabilistic biological generalizations can be grounded on biological mechanisms that underlie and produce these phenomena—mechanisms which are themselves (in some sense) chancy: *stochastic mechanisms*. In what follows, I draw a few important lessons from recent propensity interpretations of fitness and drift in order to present a novel propensity interpretation of stochastic mechanism (PISM) according to which stochastic mechanisms are thought to have probabilistic propensities to produce certain outcomes over others. This understanding of stochastic mechanism, once fully fleshed-out, will provide the benefits of (1) allowing the stochasticity of a particular mechanism to be an *objective property* in the world, a property investigatable by science, (2) a way of *quantifying* the stochasticity of a particular mechanism, and (3) a way to *avoid committing to the problematic causal role of propensities*.

Idealized Models, Explanatory Roles, and Realism

Rice Collin, University of Pittsburgh, Center for Philosophy of Science, USA

Among philosophers of science, it is widely accepted that in order to provide an explanation a model must accurately represent the explanatorily relevant features of its target system(s). However, biologists frequently construct models that either omit, via abstraction, or inaccurately represent, via idealization, most of the features of real-world systems. A prominent example is the use of optimality models to investigate biological phenomena (Orzack and Sober 1994; Potochnik 2007; Rice 2012). This highlights a more general question of philosophical interest: how are highly idealized and abstract models nonetheless able to play explanatory roles in biological (and scientific) theorizing? In addition, the pervasiveness of idealized and abstract models appears to raise a serious challenge to scientific realism (Cartwright 1983; Odenbaugh 2011).

In this paper, I distinguish three explanatory roles optimality models play within biological theorizing: hypothetical modeling, pattern modeling, and population-specific modeling.

Distinguishing these explanatory roles is important for understanding the variety of ways highly idealized and abstract optimality models contribute to our understanding of biological phenomena. In addition, I argue that these explanatory roles capture a common progression within model-based theorizing that is key to characterizing some of the dynamical aspects of model-based science. Furthermore, I contend that models can be explanatory—by providing understanding that is essential to answering a why question—without providing a veridical representation of (the features of) any real-world target system. Finally, my analysis of these explanatory roles reveals several important insights for the debate over scientific realism.

Causal Selection versus Causal Parity: Relevant Counterfactuals and Biologically Normal Interventions

Weber Marcel, Department of Philosophy, UNIGE, Switzerland

Ken Waters and Jim Woodward have argued that the causal role of DNA and mRNA in gene expression can be explicated in terms of causal specificity (in Waters's case in combination with his notion of actual difference-making cause). In this paper I argue that causal specificity and actual differece-making causes are not sufficient to demarcate the causal role of genes from that of other components of the protein synthesis machinery, in particular tRNA and aminoacyl tRNA-synthase. Thus, these conceptual resources do not suffice to argue against the causal parity thesis defended by proponents of Developmental Systems Theory. But I show that there exist conceptual resources that are sufficient for this task. All we need to do is to augment the interventionist theory of causation (also used by Woodward and Waters) by the concept of a biologically normal intervention, which defines a special class of relevant counterfactual conditionals. On my account, DNA and mRNA stand out from the causal field of a cell as the causally most specific potential difference-making causes of protein sequence that are realizable by biologically normal interventions.

General Issues in Philosophy of Biology B (submitted papers)

Morgan's Munificent Canon

Curry Devin Sanchez, University of Pennsylvania, USA

I offer a novel interpretation of Morgan's Canon that emphasizes the central role played by the problem of other minds in comparative psychology. I then defend the Canon (or at least its spirit) against recent criticisms.

Behaviorists and their critics have long misinterpreted Morgan's Canon as a principle of parsimony that condemns mentalistic explanations of nonhuman animal behavior. But Morgan meant his Canon to be neither pro-simplicity nor anti-anthropomorphism. Instead, Morgan realized that animal psychology could only overcome the problem of other minds by embracing inference from the human case. From an anthropomorphic starting point, mentalistic explanations are often parsimonious. Morgan designed his Canon to ensure that comparative psychologists explore the disanalogies between human and animal minds as well as the analogies.

Nevertheless, several philosophers have argued that the Canon is not a useful methodological precaution (Andrews & Huss forthcoming, Fitzpatrick 2008, Sober 2005). These philosophers claim that mistakenly attributing psychological properties to animals (anthropomorphism) is no greater a sin than mistakenly denying psychological properties to animals (anthropectomy). They suggest that comparative psychologists ought to ignore Morgan's Canon and simply prefer whichever explanation is best supported by the evidence. Against this suggestion, I argue that the problem of other minds is as great a problem for comparative psychology as ever (cf. the 'logical problem' in the theory of mind literature.) While mistaken anthropectomy is no better than mistaken anthropomorphism, comparative psychology is inclined towards anthropomorphic explanations. The Canon rightly stresses the need to thoroughly investigate anthropectic alternatives.

Biological Kinds, Physico-chemical Kinds
Bartol Jordan, University of Leeds, UK

Biological classification is the bane of natural kind theorists. Biological function is the bane of physical reductionists. These two problems seem related. They have led to calls for pluralism, on the one hand, and anti-reductionism, on the other. I survey how various biological phenomena have led philosophers to these positions. Notable recent examples include biochemical macromolecules and cell types.

My claim in this paper is that the pluralist stance is unwarranted and the issue of reductionism is irrelevant. I suspect that calls for pluralism arise when we confuse the reductionists' programme with that of the natural kind theorist.

I sketch an account whereby selection treats physical kinds as parts out of which to construct functional (biological) kinds. There is no reason to suspect that the latter would straightforwardly reduce to the former, or that the classification of the latter should correspond with the classifications of the former. Indeed, there appear to be good metaphysical reasons for assuming the contrary. I will argue that physical kinds and biological kinds are different objects (different individuals), with different modal profiles, and should be subject to different (non-competing) classification schemes.

Astrobiology and the Evolutionary Contingency Thesis
Lewis Cory, University of Toronto, IHPST, Canada

This paper will argue that the field of astrobiology is direct, empirical exploration of the Evolutionary Contingency Thesis (ECT). There has been an ongoing debate in the philosophy of biology about the extent to which evolutionary outcomes are essentially contingent. John Beatty has argued that there are no distinctively evolutionary laws – that what regularities exist in evolution are physical, chemical or mathematical. Against this, Simon Conway Morris has argued that the prevalence of convergence in evolution shows that evolutionary outcomes are predictable like any other physical phenomenon. While it is fairly clear that any answer to this question will be relative to a given framework of similarity, I hope to show that a substantive question about the distribution of contingent and necessary outcomes remains. I will argue that the emerging field of astrobiology provides a set of research projects which have the potential to directly answer this challenge. While we are not currently in a position to evaluate the ECT, I will try to show that we are pursuing the right research questions to eventually verify or falsify it.

Biological essentialism, evolutionary theory and the roles of different sorts of essences
Talpsepp Edit, University of Bristol, UK

According to the consensus among philosophers of biology, biological essentialism is inconsistent with evolutionary biology. However, the anti-essentialist arguments are only targeted against *material essentialism*, i.e. the assumption that the essential properties that all taxon members share are physical. *Relational* and *teleological* essentialism are not inconsistent with evolutionary theory. I want to demonstrate, though, that it is too simplistic to claim that as the result of adopting evolutionary theory material essentialism could simply be replaced by other sorts of essentialism

This is because in different contexts essences have been ascribed different roles: *definitional*, *semantic*, *causally constitutive* and *causally executive*. None of the essences in question - material, relational, teleological - possesses all these roles. The first two roles are taxonomic, the latter two explanatory roles of essences. Teleological essences fail to play taxonomic roles, relational essences some explanatory roles. Hence instead of talking about relational and teleological essentialism replacing material essentialism we should analyse how adopting evolutionary theory changes our attitude towards the roles of essences and the properties that are supposed to bear these roles. Adopting evolutionary theory might make it necessary to delegate some roles to other properties than previously – and even if some taxa properties preserve their role, we might stop seeing these properties as ‘essential'. I will also demonstrate which the consequences of this analysis are for the role of different species concepts - are they capable of describing taxa essences and which are the roles of these essences that they can refer to?

General Issues in Philosophy of Biology C (submitted papers)

Narrative Why-Explanations

Fuller Gary, Central Michigan University, USA

Narratives, or stories, are found in many disciplines, including history, the social sciences, evolutionary biology and psychology, and of course the writing of literary fictions. They can even be found in parts of the physical sciences. But why tell stories? There are many reasons. Stories, of course, provide explanations of many of the events that occur within the story. They explain how we got from here to there, for example, from a state of peace to one of war. But they do more than that. They often explain why the conclusion of the story occurred, or at least the conclusion of a sequence of events in the story. I am going to argue that stories, taken as wholes, do indeed often explain why their conclusions occurred: they provide what I shall call *narrative why-explanations* (sometimes for short, narrative explanations) of their conclusions. Further, I shall argue that a narrative why-explanation often has more explanatory strength than any standard why-explanation that we can come up with. In that sense, narrative explanations are often irreplaceable. Why tell stories, then? Because they provide us with why-explanations that we cannot get in any other way. To illustrate my thesis I shall be using examples from a number of areas including evolutionary biology and evolutionary psychology.

Robustness Redux

Odenbaugh Jay, Lewis & Clark College, USA

Recently, I have offered an analysis of robustness analysis in modeling. Suppose an evolutionary or ecological model implies a prediction, but we note that our model contains a worrisome idealization. One can demonstrate the prediction is robust if one can replace the worrisome idealization with another assumption and show the result is still implied. Robustness analysis thus shows how to remove worries about idealizations. Additionally, I have also raised a concern regarding robustness analysis; namely, the replacing assumption must be either strictly speaking true or idealized itself. If the former is correct, then robustness was not needed, and if the latter is correct, then robustness analysis cannot alleviate our worry regarding the idealization. In this paper, I attempt to accomplish two things by considering examples from evolutionary biology and ecology. First, I respond to the dilemma by using strategies offered by epistemological contextualists (i.e. Keith DeRose, Fred Dretske, and Michael Williams). Model skeptics might worry about either a specific idealization, a specific set of idealizations, or idealizations per se. If one is a skeptic regarding idealization per se, then one must forgo scientific investigation into complex systems and not just modeling. Absent this model skepticism, the dilemma is epistemically manageable. Second, I urge, following William Wimsatt, pseudo-robustness – a result that follows from a set of models that are thought to be independent in the relevant sense but are not – can be as important as robust predictions.

What's in a (natural) valuation?

Suárez Pascal David, Universidad Nacional Autónoma de México, Mexico

Mark Bedau's value-centered theory of teleology becomes the theoretical ground of his incursion into the objectification of values, which he explores observing the way traits react to selection pressures, that is, its “evolutionary activity”. Intrinsic to this view is the construal of selection as a valuation device. However, Bedau's views of teleology and value have certain inconsistencies, which center around, precisely, of what a valuation consist of. While Bedau's statement that there can be no real teleology without values seems to be correct, its identification of certain recurrent etiologies as *telic mechanisms* takes valuation in the wrong direction. Etiological views of teleology tend to conflate origin and value of functional traits. In contrast, my proposal offers a view of valuation which centers around the independence between the origin and the value of a trait, and explores the consequences of this view for the issue of biological functions in the context of Artificial Life (ALife). A result of this perspective on valuation and functions is a singular view of novelty and creativity in evolution.

General issues in philosophy of Biology D (submitted papers)

Are Celibate Priests Fit? The Expanded Gene Hypothesis
Khalil Elias, Monash University, Australia

This paper investigates whether celibate priesthood is fit. According to economic theory, the choice of celibacy can be rational for agents with a unique preference, viz., the consumption/production of “spiritual goods.” This paper provides a rational choice model that shows why, under some social constraints, agents select the precommitment device, viz., celibacy, in order to send a “credible” signal about the authenticity of the provided spiritual goods. This means that parishioners, under those social constraints, flock towards parishes headed by celibate priests. But such rational model would lead, once confronted with natural selection theory, to a puzzle. Namely, given that the preference for spiritual goods is based on a particular gene, and given the choice of celibacy, this gene cannot replicate itself. Thus, this gene is unfit if it entails celibacy, i.e., people with the need for spiritual goods would vanish from the population as long as celibacy is a necessary choice. This case illustrates how, at least apparently, utility maximization does not match fitness maximization.But this need not be the case. The preference for spiritual goods, with the celibacy commitment, can be a fit trait.To show how, this paper proposes the “expanded gene” hypothesis. The hypothesis supposes that the preference for spiritual goods is based on homozygote alleles. While the allele for the preference is recessive, the allele for non-preference is dominant. For a priest to assume his vocation, and for the parishioner to consume the spiritual goods, they must be carriers of the alleles of the recessive gene. In a model where there is no parish, there is low likelihood for the production of people that demand spiritual goods. In a model with a parish, where the priest is celibate, there is a greater chance for the production of people that demand spiritual goods. While priests cannot reproduce the gene for spirituality, the parish institutions allows the gene to have an “expanded” expression. The parish provides space for members who have the gene to meet and marry. In this manner, the parish secures a stable frequency of recessive alleles in the population, even when we have a depletion in the form of celibate priesthood.The proposed expanded gene hypothesis is compared to other approaches—such the inclusive-fitness hypothesis and group selection theory—to solve similar puzzles. The proposed hypothesis can be extended to explain other puzzling social phenomena: i) monks, i.e., celibate priests without parishes; ii) heroes who sacrifice their lives for the benefit of a cause or saving life; and iii) philanthropists.

Non-reductive physicalism and its discontents
Ryan Paul, University of Southampton, UK

Many philosophers of biology (and philosophically minded biologists) are in a quandry. They want to endorse physicalism - the thesis that the physical facts fix all the facts. But they also want to deny reductionism, holding that biological properties are causally efficacious (biological properties feature as difference-makers in biological explanations) and multiply realizable (a biological property can be instantiated by very many physical configurations). As is well known, Kim's causal exclusion argument can be (and often is) used to argue that if the physical facts at time t1 determine the biological facts at t1, and if the physical facts at time t1 plus the laws of physics cause the physical facts at time t2, then there is no room for any causation at the biological level (or at the level of any other 'special science'). On this view, biological properties are epiphenomenal on physical properties and have no causal efficacy. This brings trouble for those who see themselves as opposed to reductionism and who want to embrace the so-called causal autonomy of the special sciences. The attempt to resolve this apparent incompatibility of physicalism and the causal autonomy of the special sciences has led to a good deal of philosophical horse-trading. I argue that a failure to carefully distinguish between ontological and epistemic versions of reductionism is at the heart of the disagreement. Once we clearly distinguish between ontological (e.g. causal) and epistemic (e.g. explanation) claims, I show that we can reasonably be reductionist about ontology while being pluralist about explanation.

Function from Representation

Shea Nicholas, King's College London, UK

Teleosemantics offers a naturalistic account of content determination, applicable to some representation-using systems, in which content is fixed partly in terms of the system's biological functions, which are in turn determined by the system's evolutionary history. One can accept the standard view that biological function depends on evolutionary history, and also accept the insight from teleosemantics that representational content in some systems is partly determined by the system's functions, without subscribing to the view that the functions involved in determining content need all be biological, i.e. historical, functions. Causal role functions are also candidates. Of course, any reasonably complex system has very many causal role functions. This paper will explore, by reference to example cases, some suggestions for cutting down that class. However, it may be that considerable liberality in the assignment of causal role functions is unproblematic in the special case where functions are being relied upon to ground representational content, because in such cases there is a second source of constraint: that the system must have the right kind of internal organisation, such its functions are achieved in virtue of the interaction of the right kinds of internal components. The paper explores the extent to which that constraint makes problems about the liberality of causal role functions less acute, when they are relied upon as component of a theory of content.

General Philosophical Issues Raised By the Theory of Evolution A (submitted papers)

Three Kinds of Constructionism: The Role of Analogies and Metaphor in the Debate over Niche Constructionism

Archetti Emanuele, University of Leeds, UK

Throughout the year a lively debate has flourished around Niche Construction Theory. The debate involves a persistent disagreement between the advocates of niche constructionism and its critics. The critics propose a distinction in narrow construction, limited to the production of evolutionary advantageous artefacts, and broad construction, of which they are unwilling to recognise the relevance in evolutionary processes. On the other hand, constructionists point out the universality and relevance of any construction process in evolution. I will argue that those two categories rely respectively on the figure of speech of analogy and on the figure of speech of metaphor. Afterwards I will introduce a further distinction in the figure of speech of analogy, offering a three-tier categorisation of constructionism: literal, analogical and figurative construction. Throughout this categorisation I will show that, unlike the current opinions, the real core of construction theory lies in the part of what has been so far classified as broad construction, and that the constructionist research programme has a different aim from the adaptationist programme, relying also on a different kind of causation. This approach offers an economical way to categorise construction cases, to compare them with other theories, and to throw light on constructionist theories. In the context of a broader overview of philosophy of science it also shows how metaphors have influenced the structure of the theories, and which kind of constraints arise from the way a theory is develop.

The Moral of the Story: What Does the Evolutionary Contingency Thesis Teach Us About Biological Laws?

Wright Jake, University of Missouri, USA

John Beatty's Evolutionary Contingency Thesis (ECT) is supposed to reveal an important fact about biology and the laws of nature. Responses to ECT disagree about what, precisely, that lesson is. Beatty (1995) argues that ECT shows there are no biological laws. Elliott Sober (1997) claims ECT demonstrates that biological laws are not the generalizations we normally take them to be (e.g. the Hardy-Weinberg Principle), but rather a larger conditional with the biological generalization as the consequent. Robert Brandon and Daniel McShea (Brandon 2006, McShea and Brandon 2010) argue ECT holds for generalizations contingent on the outcome of evolution, revealing a privileged position for evolutionary mechanisms. Sandra Mitchell (2003) believes ECT demonstrates the natural necessity view of lawfulness should be abandoned in favor of a pragmatic view.Each account offers important lessons about the role of biological laws. However, each response has important problems. Rather than accept one view to the exclusion of others, I argue that the proper response to ECT is a synthesis of important features found in each account. I use this synthesis to sketch a virtue based account of science: disciplines that employ sufficiently virtuous tools and practices are viewed as scientific, even if a discipline is lawless.My discussion has three components. First, I discuss ECT and a range of responses to ECT. Second, I discuss the advantages offered by each response to ECT and concerns that prevent us from accepting any particular response. Finally, I outline a synthesized account of virtue based science.

General Philosophical Issues Raised By the Theory of Evolution B (submitted papers)

Metaphors and operative definitions. The case of adaptive radiation

Arroyo-Santos Alfonso, CIG, UNAM, Mexico
Olson Mark, Instituto de Biología, UNAM, Mexico

We introduce a metaphor account in which metaphors become scientific objects by grouping in one inclusive variable many different phenomena. In this grouping capacity, metaphors serve as umbrella variables for relating different phenomena. We argue that this grouping capacity is the result of the construction of numerous operative definitions inspired by the metaphor. We develop the case of adaptive radiation and discuss how, despite its popularity in evolutionary biology, adaptive radiation is not a natural phenomenon but is instead an umbrella variable. Despite not being a natural phenomenon, adaptive radiation has driven decades of productive scientific investigation; our account of metaphors as umbrella variables helps explain how concepts can be metaphoric but nevertheless have central roles in science. Our framework is both a contribution to the study of metaphors and to the new interest on operationalism. In our account, operative definitions have been shown to drive volumes of crucial scientific research but also to create artificial concepts concretized via numerous conceptions. Our work illustrates how the operative definition framework not only accounts for the dynamic processes by which objects of research are conceptualized and investigated but can also help us evaluate the nature of problematic concepts

Evolutionary Biology and the Axiomatic Method Revisited
Esanu Andreea, University of Bucharest, Romania

In evolutionary biology there has never been reached a consensus regarding the manner of presenting a theory, be it the theory of natural selection or the genetics of populations. According to the skeptical view, biological theories of evolution cannot even be presented as proper scientific theories because of their lack of uncontroversial laws. This skepticism, however, is not shared by the logicians of science, who claim that biological explanations can be molded into proper theories by means of logical reconstruction, *i.e.* by using the methods of formal logic. The logical properties of biological language might tell the important difference between empirical observations and theoretical laws in a way that would not require anything else but an adequate understanding of the biological language itself. This approach is a traditional formal approach, and it draws from the works of Alfred Tarski's and Rudolf Carnap's on the axiomatization of natural science.

In the following, I will address three developments of the axiomatic method in evolutionary biology: the hypothetical-deductive, the semantic and, perhaps the most recent one, the natural deduction method. I will point out that the key concepts in figuring out the logical structure of a biological theory concern truth and deductive consequence. Then I will argue that a minimalistic concept of truth and a syntactic understanding of deduction might be the best option in formalizing a biological theory of evolution. Eventually, this would do half justice to the skeptical view that there are no fully uncontroversial laws in evolutionary biology.

Natural Selection as Rational Inference
Morimoto Ryota, Keio University, Japan

I will sketch the probability concept mainly in natural selection models and referentially in statistical mechanics. In the classical world view, there has been thought that the probabilities appeared in the scientific context is interpreted as frequencies or subjective degrees of beliefs. But when we faced to use the probabilistic models of natural selection, we had to answer the following question. What do the probabilities represent? In this presentation, I will answer the question. First, I analyze Fisher's and Kimura's models of natural selection and show that the probabilities reflect not merely our ignorance but some aspects of reality. Second, I show that in natural selection models we can update the probabilities rationally. And I also clarify the relation between explanation and prediction in evolutionary theory. Then I conclude that the aim of natural selection models is rational explanation or prediction of phenomena.

General Philosophy of Science A

Downward Determination as a Non-Causal Probability-Raising Relation
El-Hani Charbel, Federal University of Bahia, Brazil

No account of the influence of whole systems over their parts will do without preliminary decisions on what causes are. Based on such decisions, we show that top-down relations can be construed as non-causal determination, a probability-raising relation between general organization principles at the higher level and particular events at the lower level (as relata). We use Glennan's canonical form of causal claim, stressing the distinction between causally productive events and causally relevant properties, to elaborate on the nature of ‘determining' in top-down relations. The causal relationship between two components of a living system is expressed as follows: Event *c* involving component *A1* causes event *e* involving component *A2* [in background conditions *B* of the living system] via the operation of mechanism *M* and in virtue of properties *P* of *M*, a key property of *M* being its spatiotemporal organization, as structural determiner of the probability of interaction between *A1* and *A2*. Using Schaffer's quaternicity interpretation of causal relations, we can explain how probability changes induced by the spatiotemporal configuration of *S* can explain why *c* rather than *c** causes *e* rather than *e** within *S*. This is all it takes to put forward a consistent account of downward determination as a probability-raising non-causal relation.

Mechanisms and the puzzle of explanatory relevance

Serban Maria, School of Philosophy, Norwich Norfolk, UK

On the mechanistic account of explanation, scientific models are explanatory only insofar as they exhibit the real causal mechanisms that produce the phenomena under study. In this paper, I show that the mechanistic criterion for explanatory relevance is problematic both on grounds of internal consistency and with respect to the actual modelling and explanative practices of cognitive scientists. In response, I put forward a productive compatibilist account of explanation that extends and enriches the mechanistic conception. Moreover, in contrast to Kaplan and Craver (2011) position, I argue that abstract (mathematical) models can have bona fide explanatory functions in the context of cognitive scientific research. In particular, I maintain that mathematical modelling affords an alternative, non-decompositional strategy of explaining salient features of cognitive systems. I argue that the proposed compatibilist view of explanation respects the 'individuality of the particular problems' confronting current cognitive experimental and theorising practices. As such, it promises to offer a more robust analysis of the varieties of explanatory models used in the domain of cognitive science.

Ecosystem Research and Real-World Simulation

Schwarz Astrid, Institute for Philosophy, Technical University Darmstadt, Germany

The object in question is an artificial water catchment that is a constructed natural site. "Chicken Creek" is a small hill several hectars large and situated in a former strip-mining area in North-Eastern Germany close to Cottbus. This initial ecosystem constitutes an ecosystem in its own right: It is an experimental site that simulates its own behavior in that it monitors its own performance. Chicken Creek is a specific kind of field experiment that abolishes the carefully maintained spatial separation between an experimental system and the natural system, features of which it is supposed to represent. The knowledge acquired in such projects often takes the form of an expertise that merges scientific background knowledge with experience gathered by observing the particular case. Both, real-world experiments and real-world simulations combine features of the lab-ideal and the field-ideal, and they thus connect instances of generalization and instances of individualization and valueladenness. The Chicken Creek is a paradigmatic case of this kind of conceptual merging and of mixed practices. It is a technoscientific object in the proper sense: it gathers together theoretical knowledge, instruments, skills, and purposes (see also http://www.goto-objects.eu). The artificial water catchment system was designed artificially, but it is treated as a natural system. It exhibits its own performance parameters and is thus a real-world simulation. It is an attractive object for scientists and it is unique. It pursues the lab-ideal of total experimental control in a field experiment, and finally it is a high-tech object. While science secures objects in the representation of facts, technoscience affords things through assemblage.

General Philosophy of Science B (submitted papers)

How Multiple Realization is Possible

Aizawa Kenneth, Rutgers University, Newark, USA

In "Special Sciences," Jerry Fodor claimed that "we could, if we liked, require the taxonomies of the special sciences to correspond to the taxonomy of physics by insisting upon distinctions between the natural kinds postulated by the former wherever they turn out to correspond to distinct natural kinds in the latter" (Fodor 1974). In this paper, I document a clear case in which vision scientists have had the opportunity to adopt this taxonomic practice, but have not. Instead, I will describe three other ways in which vision scientists relate the taxonomy of biology to the taxonomy of vision science. First, vision scientists sometimes postulate properties within which they will admit individual differences in vision science properties that are explained by differences in biological properties. Second, they sometimes discover that it is possible for two sets of biological properties to differ so that the differences between them cancel each other out for the vision science property. Third, they sometimes discover that small variations in biological properties induce variations in some vision science properties but not others. Each of these three taxonomic strategies reveals how multiple realization is possible.

Divergent Philosophies in Evolutionary Science
Marcous Carmen, Florida State University, USA

At a 1982 meeting of the Philosophy of Science Association, Ernan McMullin directed his presidential address to acknowledgement of the fact that subjective value-judgments play an essential role in science. McMullin identified epistemic values that were broadly sanctioned within scientific communities (e.g. predictive accuracy, simplicity, coherence, consistency, unifying power, fertility) but whose relative priority could be determined by factors outside science. He illustrated this point with the example of a famous disagreement between Bohr and Einstein concerning the scientific status of the quantum theory of matter. According to McMullin, the scientists' disagreement on the matter was not merely the result of conflict concerning how to prioritize epistemic values. Disagreement in substantive metaphysical beliefs about the nature of the world also impacted their determination of what constituted "good" science.

Michael Ruse distinguishes epistemic values from what he terms metavalues, or values concerned with the nature and limitations of science *qua* theory of knowledge. Using this distinction, the present project explored the value-commitments endorsed by Stephen J. Gould and Edward O. Wilson, two leading scientists in the field of evolutionary biology. Taking as a case study their widely publicized disagreement over the theoretical field of sociobiology, I demonstrate how evaluation of the scientists' epistemic and metavalues can (1) equip philosophers with an instructive mechanism to track diversity in the methodological assumptions directing post-Darwinian evolutionary sciences, and (2) equip scientists and non-scientists with a means for assessing the causal force of differentiated social experience in evolutionary sciences' production of scientific knowledge.

Regulation: Integrating Concept or Epistemological Red Herring?
Amidon Kevin, Iowa State University, USA

For some time, I have been studying four areas: the history of biology; the relationship between scientific practice and government policy in the sphere of pharmaceuticals; the history of early forms of government regulation, for example of transportation; and the intellectual foundations of sustainability thought. All of these spheres share the word "regulation" to indicate significant processes of mediation and modulation, in many cases based on some set of quasi-scientific arguments. In biology, "regulation" has been deployed conceptually since at least the early twentieth century to describe systems that appear to operate as feedback mechanisms. In many branches of public policy, the concept similarly emerged in the nineteenth century to describe processes of management and oversight of economic activity based on law but carried out through executive prerogative. Since ca. 1970, environmental policy has grown rapidly into a significant and controversial sphere of government-industry mediation – and arguments about the stability and sustainability of (biologically related) 'regulatory' processes in the natural world have become a substantial part of ‘regulatory' processes in public policy. Where this terminological overlap becomes more than an analogy, I propose, is in its epistemological stakes. ‘Regulation' and ‘control' often appear as (often misplaced and misleading) synonyms in both biology and public policy. This affinity indicates that a hierarchy of causes and effects appears to operate in the systems. I suggest that the troublesome element in any making-equivalent of regulation and control is that it hides the sources of interventions in and perturbations to those systems.

General Philosophy of Science C (submitted papers)

“If you can spray them, then they are real”: Evidence Construction in Fragrance Chemistry

Barwich Ann-Sophie, University of Exeter, Egenis, UK

In this paper I describe the construction of empirical facts in evidence for (or against) two rival theories in olfaction theory, and also the structure of the theoretical development of the two underlying models of the mechanism of primary odour recognition. To do so, I will focus on the investigation of structure-odour relations (SORs) in fragrance research and the diversity of molecular structures that are more or less successfully accommodated within the rival accounts. I will attempt to explain the function that theoretical models such as the two hypothetical molecular recognition mechanisms have for evidence construction and, furthermore, the impact of auxiliary assumptions, instruments and techniques on theory evaluation. The primary aim of this paper is to describe the epistemic relations that hold between different models and to justify my claim that the referential capacity of scientific representations is determined by their relations within a network of different investigative methods, models, experiments and technologies surrounding an experimental system.

Open the doors: integrating epistemology into the lab

Camus Thomas, EPSYLON, Montpellier, France
Devictor Vincent, Institut des Sciences de l'Evolution - Montpellier, France

Is epistemology useful? This question can be asked in many different ways. Here, we propose an original experiment in which we verify, into existing research projects conducted in research laboratories, what scientific research(ers) can gain from epistemological approaches. Traditionally, epistemologists treat the philosophical questions raised by science outside research laboratories. This approach emphasizes the historical analysis of scientific concepts and theories, describe the functioning of science, its relation to epistemic values, or the succession of epistemological traditions. However, studies investigating the relevance of integrating epistemological approaches *within* laboratories are missing. In this talk, we show with concrete examples how a more “integrated epistemology”, can be useful either for natural sciences or humanities. In this respect, two examples will be discussed, respectively in cognitive psychology and scientific ecology. The first project was conducted in a laboratory of psychology, the other in a laboratory of natural science and ecology. In each case, specific scientific questions have been addressed. The research project in psychology was to shed new lights on the relation between perceptions, memory and actions. We show that reframing this problem using philosophical tools such as Dewey's naturalistic metaphysic redefine the way we understand our interactions with the world around us. The second scientific project was to test the generality of the relationship between different variables of considerable importance in ecological science, namely the relationship between species diversity and functional diversity in natural communities. In each case, we discuss further possible applications and limits of this integrated epistemology.

Some examples of possibology applied to biology and its history
Allouche Sylvie, University of Bristol, CEM Bristol, UK

Possibology is defined as the science of possibilities. In part, as is often the case with emerging disciplines, it appropriates a certain number of existing approaches that it describes as fulfilling its own program, but also proposes to apply its principles to fields in their infancy or non-existent, in order to develop an original research program. My goal here is to present some examples of application of possibology to biology which borrow from these two categories.
For the first, I take the example of exobiology, the science of extraterrestrial life: this science is particularly interesting from the possibology point of view insofar as it is an empirical science, but without the experience of its object. I am assuming that this is a unique case, but it needs to be checked.
For the second category, I will look at an important part of possibology, which I call uchronology, and whose aim is to develop, from the counterfactual analysis of historical sequences, a comparative "weighing" of the necessity of their elements. The idea will be illustrated by three examples: the history of cloning technique and its reception by society, the history of the notion of genetic program, the history of Mendel's laws of inheritance.
Owing to the experimental aspect of the approach, my purpose will mainly be to initiate a discussion with the audience according to the principles of comparative and counterfactual thinking. But if the method proves fruitful, it seems to me that eventually entire sessions could be devoted to this kind of inquiry.

Generic and Genetic Explanations of Evolvability and Evolutionary Novelty

Generic and Genetic Explanations: Comparing Experimental and Historical Biology
Love Alan, University of Minnesota, USA

A genetic explanatory paradigm is predominant in biology and for good reasons. The empirical successes of experimental biology and a unified framework for evolution were major achievements in the 20th century, and genetic explanations exhibit the virtue of causal specificity. Increasing attention has been paid to how physical processes can explain biological phenomena, which involves appeals to generic features that are not unique to biological entities (e.g., viscoelasticity in soft condensed materials or shear forces due to fluid flow). Finding ways to combine these two different explanatory strategies—generic and genetic—is difficult because many biologists privilege causal specificity, such as when accounting for the origin of evolutionary novelty: "novelty requires the evolution of a new gene regulatory network" (Wagner and Lynch 2010). Others argue that new structures originated early in evolution from generic properties of cells and tissues interacting with the abiotic environment: "epigenetic mechanisms, rather than genetic changes, are the major sources of morphological novelty in evolution" (Newman et al. 2006). This paper explores the conceptual challenges that attend combining generic and genetic explanations in both experimental and historical biology by comparing the situation of developmental biology with evolutionary studies of evolvability and novelty. In particular, I argue that the increasing rapprochement between genetic and generic approaches in developmental biology is due to a shared appreciation of identifying actual difference makers with experimental intervention techniques, which does not translate into the context of evolutionary theorizing where historical explanations usually have access only to potential difference makers.

Generic vs genetic approaches to early animal evolution
Erwin Douglas, Smithsonian Institution, USA

Of some 119 eukaryotic clades, 36 contain multicellular forms, representing at least 21 different origins. Yet only three of these clades exhibit complex cellular differentiation and morphogenesis, and all three possess various developmental tools required for development. Were a strictly structuralist approach to early animal evolution correct, complex multicellularity should be more widespread. Some advocates of structuralist approaches have claimed, for example, that the organisms preserved as fossils in the mid-Cambrian Burgess Shale shared the same genome, with their widely varying morphologies (arthropods and lobopodians to cephalochordates) the result of different physical forces. Such claims are decisively refuted by comparison of the genomes of living descendants of Cambrian clades. Such speculations greatly damage the substantive issues raised by structuralism and any effort to reconcile genetic and generic approaches. Although there is little doubt that physical forces have an impact on the developing embryo, particularly in the folding of sheets and tissues, the structualist approach to development has been far less successful than comparative and experimental genomics. The difficulty in achieving reconciliation between these two approaches stems in part from the fact that most experimental (rather than comparative) approaches necessarily make uniformitarian assumptions about our ability to project results back some 550 million years, assumptions which are likely invalid. Synthetic experimental evolutionary approaches may prove more useful.

Genetic and Generic Explanations: A Pluralistic Perspective
Niklas Karl, Cornell University, USA

How much of an organism's development is directly encoded by its genome and how much is a direct consequence of how living matter generically responds to the effects of physical laws and processes? No biologist would deny the importance of the information stored in an organism's genes. However, no biologist can deny the importance of passive diffusion, temperature, gravity, and viscoelasticity during development. Thus, it is reasonable to suppose that under some circumstances natural selection favors an organism with developmental sub-routines that are actuated and subsequently driven by universally reliable physical laws, processes, and “cues” over an organism whose genome encodes these sub-routines. It is also reasonable to suppose that these kinds of sub-routines were prevalent and perhaps more important during the early evolution of some lineages. Consequently, debates about genetic and generic explanations should not be framed around “either or” questions but rather in terms of the relative importance of each. In this respect, developmental and evolutionary biology resemble alternative model-rich conceptual frameworks, similar in some respects to engineering or information theory. This “generic and genetic” perspective is illustrated in the context of gravity- and light-sensing, mechano-perception, cell wall formation, and other biophysical phenomena contributing to plant development and growth. In each case, evidence is presented for the participation of generic biophysical processes operating in an equally important genomic background. Consequently, theories about developmental biology will advance only if development is conceptualized as a hybrid of parsimonious and stable generic processes operating in dynamically evolving genomic backdrops.

Genetics: Ethical Issues (submitted papers)

“Genetic load”, How the architects of the Synthesis got trapped in a scientific ideology
Soulier Alexandra, Université Paul Sabatier – Toulouse III, Inserm, France

The term "genetic load" emerged for the first time in a 1950 paper written by the world renowned geneticist, H. Muller – "Our load of mutation". In its first version, the genetic load is used more specifically in relation to genetic mutations and refers to an accumulation of disadvantageous mutations in populations. While the idea had already been elaborated in the 1930‘s, this wording did not only describe a phenomenon but expressed dramatically the sorrows of many scientists concerning the future of human populations. According to them, the

combined actions of medical and social progress prevented natural selection from operating and genes of inferior quality were likely to spread across populations – loading their progress.
This concept reflects the so-called "typological view" of evolution, which claims that selection should lead to a uniform population composed of identical high-fitness individuals. Such a perspective was, however, invalidated by Robert Wright and Theodosius Dobzhansky, who showed that polymorphism was the rule in natural populations ... in 1946. As the theoretical model of the genetic load had already expired, how can we explain its success among the circle of evolutionists and geneticists, who elaborated the Synthesis?
An explanation for the paradoxical success of the "genetic load" would be that the concept, at least in its early and strong usage represented in the papers ofJulian Sorell Huxley, Ernst Mayr and Theodosius Dobzhansky, would respond less to a scientific inquiry than to a social concern.

The “Devil's Heritage”: Masuo Kodani, Genetics, and Social Stratification at the Atomic Bomb Casualty Commission (1946-1954).

Smocovitis Vassiliki, University of Florida, USA

This paper centers on Masuo Kodani's early organizational role in the genetics project of the Atomic Bomb Casualty Commission (ABCC). Specifically, it concentrates on his complex relations with members of the Japanese scientific community and with Japanese civilians, at the same time it explores his peculiar status as Japanese American. The extent to which his career reflected American-Japanese post-war relations is also examined in the context of cold war developments.

Genetics. From Mendel to Benzer and Beyond A (submitted papers)

What if Mendel had died in 1840? Retrodictions in early genetics

Buttolph Mike, University College London, UK

When the work of Mendel became generally known in 1900, many researchers started experimental breeding programmes designed to test his conclusions, but it was several years before these gave results. Almost all the tests of mendelism in the first few years of the century were made by *retrodiction* – the re-analysis of pre-existing data in the light of the new theory. By this process, dozens of authors then found hitherto unrecognised mendelian patterns of inheritance in their data-sets.
It is perhaps unusual that so large a proportion of the early tests of a theory were made by retrodiction, and this raises interesting questions. The mendelian idea seems to have exceeded the grasp of literally dozens of dedicated, intelligent researchers; they were unable to perceive the mendelian patterns in their data until they knew of Mendel's work. What would have happened had Mendel's work not come to light in 1900? It seems likely that mendelian inheritance would never have been discovered by means of experimental breeding, but instead by the rapidly-advancing science of cytology. And the mass of breeding data that was found to be confirmatory of mendelian theory as soon as that theory became known suggests that perhaps the ‘rediscovery' of 1900 was ‘postmature', just as Mendel's paper of 1866 has been regarded as premature.

Against Theory-Biased Classical Genetics

Shan Yafeng, University College London, UK

Classical genetics is traditionally characterised in terms of theories. Theories constitute the "hard core" of classical genetics. According to this view, classical genetics is centred on a theory of gene transmission, and all its research is organised around the efforts to improve this theory's explanations of heredity and to expand the range of inheritance phenomena that it could explain.

This paper aim to argue against the theory-centred account of classical genetics and to show that theories are not essential disciplinary components of classical genetics. First, I introduce a naive argument against the theory-centred classical genetics under the assumption that if both the rediscovery of Mendel's work in 1900-1903 and Morgan school in 1926 are the research of classical genetics, there must be some essential disciplinary components that are invariably shared by geneticists in two periods. By comparing the fundamental concepts/theories in 1900-1903 with those in 1926, I show that concepts/theories cannot be such essential disciplinary components.

Second, I propose a possible response to the naive argument, inspired by Kitcher's account of classical genetics. That is, despite the change of concepts/theories from 1900 to 1926, these seemingly different theories are in fact different versions of one theory at different times. There are certain links between these theories. The links are "pedigree problems" (that is, identifying and explaining patterns of inheritance); the seemingly different theories of classical genetics aimed to solve these problems.

Third, I dismiss this response by arguing that Kitcher's account of classical genetics seems more problem-centred than theory-centred.

The growth of Morgan's evolutionary thought: 1903-1932
Martins Lilian, Universidade de São Paulo, Brazil

In his early publications in the beginning of the 20th century, Thomas Hunt Morgan (1866-1945) considered that the evolutionary process took place by jumps and criticized several features of Darwin's evolutionary proposal. He thought that regeneration could not have been acquired through natural selection, for instance. At this time he was also a strong opponent of both Mendelian and chromosome theories. This happened until 1910-1911. In the books *A critique of the theory of evolution* (1916) and its revised edition *Evolution and genetics* (1925) in which he intended “to review the evidence on which the old theory rested its case, in the light of the newer evidence of the recent years”, Morgan did not discuss regeneration nor mentioned the objections he had raised before against the action of natural selection in this process. He mainly presented the evidence got from the experimental breeding of *Drosophila,* claiming that the slight mutations that were inherited, according to “Mendel's law” furnished the material in which natural selection would act. Only in 1932 he finally admitted that the evolutionary process was gradual and accepted natural selection as the main mechanism of evolution. The aim of this communication is to discuss the epistemic and non epistemic factors that could have contributed to Morgan's change of view concerning the subject, during the first decades of the 20th century, trying to elucidate at to extent the studies developed by *Drosophila* group could have contributed to it.

Theorising and representational practices in genetics
Vorms Marion, Université Paris 1 & IHPST, France

This paper is meant as a contribution both to the history of biology and to the general philosophy of science. As a general philosopher of science, I wish to challenge theory-biased approaches to scientific knowledge, by arguing for a study of theorising, as a cognitive activity, rather than of theories, as abstract structures independent from the agents' understanding of them. Such a study implies taking into account the scientists' reasoning processes, and their representational practices. Here, I analyse the representational practices of geneticists in the 1910s, as a means of shedding light on the content of classical genetics. Most philosophical accounts of classical genetics fail to distinguish between the purely genetic, or Mendelian level, and the cytological one. I distinguish between them by characterising them in terms of their respective associated representational practices. I then present how the two levels were articulated within Morgan's theory of crossing-over, and I describe the representational technique of linkage mapping, which embodies the ''merging'' of the Mendelian and cytological levels. I propose an analysis of the mapping scheme, as a means of enlightening the conceptual articulation of Mendelian and cytological hypotheses within classical genetics. Finally, I present the respective views of three opponents to Morgan in the 1910s, who had a different understanding of the articulation of cytology and Mendelism, and entertained different views concerning the role and proper interpretation of maps. I propose to consider these diverging perspectives as instantiating what I call different ''versions'' of classical genetics.

Genetics. From Mendel to Benzer and Beyond B (submitted papers)

Science During Wartime: Richard Goldschmidt's Internment during the First World War

Richmond Marsha, Wayne State University, USA

At the outbreak of the First World War, the geneticist Richard Goldschmidt (1878-1958) found himself trapped in the United States, unable to return to Germany following a research trip to Japan. With the assistance of several prominent biologists, Goldschmidt was able to continue his study of sex determination in the gypsy moth, *Lymantria dispar*, working in the Osborne Zoological Laboratory as a guest of Ross G. Harrison, professor of zoology at Yale University. All semblance of a normal life in science came to an end, however, on 1 May 1918, when Goldschmidt was taken into custody by federal agents and charged with spying for the German government. Sent to an internment camp at Fort Oglethorpe, Georgia, he was released a month after the signing of the armistice with Germany and finally returned to Germany in June 1919.

During his interview by an agent of the Bureau of Investigation, Goldschmidt looked toward the end of the war, "when it will be again recognized that science is international rather than national." It is clear, however, that not all scientists shared his view; indeed several were among those who testified against him. Drawing on Goldschmidt's FBI dossier, this paper examines the facts of the case and reflects on how during times of political crisis science can indeed be transformed from "international" to "national."

A Historical and Systematic Analysis of the Hardy- Weinberg Law

Lorenzano Pablo, UNQ, CONICET, Argentina

A central law in population genetics is the Hardy-Weinberg Law. In its standard formulation, it states that, if only one gene with just two alleles, A and a, is considered, it can be mathematically proved that given that certain conditions are fulfilled, the frequencies or relative proportions of the alleles A and a in the population will not change from one generation to the next, after the second generation. Thus, equilibrium will be reached in one generation and will remain unchanged after the second generation. This equilibrium is expressed by the following equation: p2 + 2pq + q2 = **1,** where p denotes the frequency of one allele, q denotes the frequency of the other allele, p2 denotes the frequency of homozygous individuals for an allele, q2 is the frequency of homozygous individuals for the other allele, 2pq is the frequency of heterozygous, and the sum p and q should always equal l.

From a historical point of view, it is worth to note that one cannot find the standard formulation neither in Hardy's nor in Weinberg's work.

From a systematic point of view, it is usually said that the Hardy-Weinberg Law is (logically) derived from the Law of Segregation of classical genetics – the so-called 'Mendel's First Law'.

The aim of this communication is to present an analysis of the different historical formulations of the so-called 'Hardy-Weinberg Law', and to compare them, as well as of its assumed (logical) derivation from the Law of Segregation.

Economic models in the cell: division of labor in the German Empire and the transition from real- to finance economy in conception and heredity 1870-1900
Bock Von Wülfingen Bettina, Humboldt-Universität zu Berlin, Germany

Ideas of heredity and conception in biology are infused with concepts usually found in political economy. Especially around the foundation of modern biology, models of heredity, genetics, and conception were formed along local economic understandings which were entangled with the problems of the growing markets of the late nations (USA and the German Empire). Most notably the foundation of the German Empire was accompanied by a unique local coupling of needs, which during the 20th century shaped the international conceptions of biological heredity. As the analysis of published and unpublished material originating in the period 1850-1900 shows, through a tight linking of natural law and national law on inheritance and family, these two bodies of law defined how the reproductive household of the citizen worked. Thereby national and natural law coincided in the introduction of an economic (and gendered) division of labor to the household: a separation was drawn between the not to be economized area of reproduction (domestic work/cell plasma) and the economically productive area (profession/nucleus). Accordingly also the study of genetics and the study of conception, especially in developmental biology, segregated.

As a prospect into the 20th century the talk describes the rising importance of finance economy (in contrast to real economy) in an interchange with concepts that separate sign and material (counter-)value. This is consistent with early genetics and later with modeling in evolutionary biology since the 1930s, finally advancing the systematic interlacing between the fields of production and reproduction, economizing both, and the rise of epigenetics.

Genetics. From Mendel to Benzer and Beyond C (submitted papers)

The French Concept of the Gene, from Microbe to Transposon?
Loison Laurent, SPHERE, Université Paris VII Paris-Diderot, France

The aim of this talk is to present a new hypothesis able to explain most of the specific features of the history of genetics in France. This hypothesis could be summed up as follow: in France, the concept of the Mendelian gene was understood – first explicitly and afterwards implicitly – as a new working-out of the Pasteurian concept of microbe (this hypothesis will now be called MGH, for Microbe-Gene-Hypothesis). Taking into account the results of the work performed by Richard Burian and Jean Gayon since 1988, I will first provide a description of the eight main chararcteristics of the history of French genetics. I will then present direct evidence supporting MGH, by examinating into detail some research programs and theoretical thoughts developed in a Pasteurian atmosphere from the 1880s to the 1930s. I will also recount the historical narrative from the MGH point of view, especially for period 1930-1960, when French genetics started to emerge internationaly as a physiological discipline. To conclude, I will focus on the explanatory power of MGH (is it able to explain the eight main characteristics of French genetics?), and I will suggest that this hypothesis could bring into light new facts concerning the specificity of French genetics, even nowadays.

Patenting life: The life of a patent
Romero Ana, IFS-CSIC, Italy

In 1989 a group of Spanish researchers were granted a patent of “An improved method for determining the nucleotide base sequence of a DNA molecule”. The improvement was provided by the activity of a DNA.polymerase of virus F29, a phage of bacteria *Bacillus subtilis*. Their research on that enzyme dated 1984, and from then until the patent granting, a set of routines and strategic alliances played to construct the meaning of an enzyme as an industrial innovation. From then until the commercialization of the kit for DNA amplification the history of the patent is traced back so as to show this type of documents as an insightful tool in the history of science and as a process of knowledge production. The patent consisted of a biological process that finally was packed in a kit, after being produced in a research project based on the molecular biology of a microorganism.

The tool and the process combined and allow offering a story of standarization, normalization and knowledge control in which travel played a central part, as it was by the circulation of practices and cultures between the research laboratory and the firm that promoted the patenting that the life of this patent developed.

Seymour Benzer, Genetic Maps, and the Junkman's Problem

Ishida Yoichi, University of Pittsburgh, USA

On December 4, 1956, in his biophysics seminar, Seymour Benzer gave a lecture entitled "Mutations and the Junkman's Problem," describing the processes of mutation and recombination and their relevance to his research on genetic fine structure. Benzer said that his research was about "the junkman's problem," whose "objective" was "to determine something about the structure [of DNA] by these operations [mutations and recombinations]" (Papers of Seymour Benzer, Box 82, Folder 1, Caltech Archives).

Using materials from the Benzer archive, I discuss how Benzer's uses of genetic maps structured his research on the junkman's problem. In the 1950s and 60s, the day-to-day operation of the Benzer lab consisted almost entirely in making detailed genetic maps. Although Benzer was interested in the physical interpretation of these maps, in his everyday research he frequently used genetic maps in ways that did not depend on his taking the maps to be representations of the structure of DNA. Benzer's failure to solve the junkman's problem at any given stage of his research did not undermine the lab work: he used genetic maps in ways that helped him successfully collect and organize "junk" despite the fact that he was not sure what (epistemic) "value" he could get out of it. I explain how particular features of genetic maps enabled him to separate two sorts of success---the success in mapmaking and the success in determining something about the structure of DNA---and explore how the former success supported the latter.

Historical and Philosophical Perspectives on Disease Biology

Confronting the Complex Causality of Cancer

Liu Katherine, University of Minnesota, USA

Translational research has become a buzzword for biomedicine. In efforts to more quickly export knowledge gained from the laboratory to clinical applications, the United States National Institutes of Health and other organizations emphasize the implementation of structural changes. What has been overlooked is whether the core research strategies of biomedicine are adequate for the generation of clinical applications. Here I show that standard molecular and evolutionary approaches to cancer research are successful in some ways but fall short of making the expected clinical impact because they rely on faulty assumptions of biological causation or can only give predictive expectations for populations. Gene-based cancer explanations have the potential to identify specific difference-making causes but are lacking when facing the complexity of causal relationships in human biology. Evolutionary medicine explanations are useful for developing population level screening practices but are limited in their therapeutic potential for the individual. I argue that an evolutionary developmental (evo devo) approach to cancer bridges the proximate/ultimate divide between molecular biomedicine and evolutionary medicine by facilitating robust causal explanations of biological phenomena. This is because evo devo addresses problems of complex causality in the context of developing organisms (i.e., the realm of molecular biomedicine), while attending to the intergenerational dynamics of evolving populations (i.e., the realm of evolutionary medicine). I demonstrate that cancer is an example of pathological modularity, which encourages a particular framework of tradeoffs, interactivity, and individuation. Thus, novel opportunities to comprehend the complex causality of cancer emerge and suggest new approaches to treatment and intervention.

“Natural” and “Artificial” Infection: Host-Specificity in Mid-20th-Century Parasitology and its Implications for Evolutionary and Disease Biology

Mason Dentinger Rachel, Imperial College, UK

In the mid-20th century, experimental cross-infection was a standard method for investigating the parasites of animals. Within the laboratory, barriers to infection could be overcome, leading some researchers to suggest that virtually any animal might be susceptible to any parasite. But outside the laboratory, highly specific host-parasite relationships were common, leading researchers to distinguish between “natural” and “primary” infections on the one hand, and “artificial” and “accidental” infections on the other. At the heart of these distinctions were attempts to use parasites' host-specificity to solve problems both in evolutionary biology and in disease biology. Resolving host-specificity allowed evolutionary biologists to infer evolutionary histories, addressing gaps in the fossil record and correcting overreliance on morphological characters in phylogenetics. At the same time, host-specificity also helped parasitologists better predict the conditions under which particular diseases might emerge or switch hosts, suggesting potential methods for disease prevention. Parasitologists T.W.M. Cameron (McGill University), P.C.C. Garnham (London School of Tropical Hygiene and Medicine), and J.G. Baer (University of Neuchâtel) led the effort to use evolutionary insights to inform disease prevention—and vice versa. This paper examines their work from the 1930s to the 1960s, arguing that the study of parasites' host-specificity affected both evolutionary and disease biology, and contributing to studies of the interplay between lab and field biology and basic and applied biology.

History and Philosophy of Life Sciences, 17th-18th century A (submitted papers)

Joseph Lelarge de Lignac (1697-1762), a friend of Réaumur against the thought of Buffon

Perru Olivier, University of Lyon 1, France

Father Joseph-Adrien Lelarge de Lignac was born in Poitiers (France) in the year 1697. He died in Paris in 1762. In 1731, he was ordained priest and he became an oratorian the following year. His *Letters to an American* are an attempt to refute Buffon and Condillac, this book was prepared in collaboration with Réaumur (J. Roger, P. Charbonnat). Here, we present some elements of the correspondence between Lignac and Réaumur which show a scientific dialogue about 1736-1748 and we try to bring some foundations of the thought of Lignac to light. Between empiricism and metaphysics, Lignac stands up for scientific questions being subject to literal reading of the Bible. But Lignac is also the first one to perceive a way of thinking in Buffon Natural history (T. Hoquet). According to him, the thought of Buffon is a deviation in an order of knowledge, because Natural history would especially be based on observation and experiment. So in this paper, we emphasize two original sources in the thought of Father de Lignac: Malebranche philosophy and his collaboration with Réaumur.

Husbandry, alchemy, and technologies of ameliorating nature in the works of Gabriel Plattes

Matei Oana, Vasile Goldis Western University of Arad, Romania

Dealing with the concept of growth both in a chemical and moral way, husbandry was considered in the mid seventeenth century England, the key to salvation, providing solutions for ameliorating as well the economic estate of the nation and the fallen estate of human being. The application of chemistry to practical problems (such as agricultural, medical, educational) has origins traced to Paracelsus and alchemical tradition. But the moral dimension entailed in this process of growth, aiming to ameliorate the fallen condition and to restore the qualities lost in the Fall, is inherited from Bacon. Also, the translation from one domain (such as the vegetal domain easy to explore) to another one (such as the human soul, difficult to explore) points to the Baconian methodological extensions allowed by *experientia literata*.

In this paper I will investigate Gabriel Plattes' view on husbandry. Inspired by the Baconian tradition of experimentation, sharing the same unified vision upon the universe and using the same methodological analogies, Plattes reformulates the view on husbandry, promoting a new type of 'integrated science' able to cultivate the land and the human soul as well. Apart from other tracts on husbandry published before, Plattes used the alchemical tradition but, as Bacon, committed the application of chemistry to a moral end. He developed his own experimental view on husbandry, placing at the very core of amelioration the idea of technological advancement (a project based on transmutation experiments and cyclical chemical change). Plattes' contribution rests in providing a number of 'technologies of amelioration' for the material of Creation (soil, plants, human beings), technologies of salvation compatible with both economic advancement and religious salvation.

The Watchmen of the Body: How Early Moderns Gained an Education in the Physiology of the Eye

Buckle Karen, Clarkson University, USA

In the eighteenth century, learned readers were well acquainted with the tenets of physico-theology espoused by Fontenelle, Derham, and afterward made famous by the naturalist William Paley. Building upon traditional body politic rhetoric and a sensory hierarchy that prized vision as the prime source of worldly knowledge, it is not surprising that Paley and those before him should select the example of the eye to evidence the existence of a divine creator.

Detailed knowledge of the eye was not, however, widespread in the early modern medical profession, nor among the public at large. In the mid-eighteenth century, Thomas Gataker of the College of Surgeons candidly acknowledged the medical and surgical professions' lack of contribution to training in and treatment of the eyes, attributing the flourishing of quack oculists in the city to their failure in this area.

Against this backdrop, this paper examines the way that medical men and the enquiring English public did gain their knowledge of the anatomy and physiology of the human eye. It does so by exploring the contributions made by those practitioners that Gataker sought to dismiss – those oculists and operators who made a living treating the distempers of the eyes, couching cataracts, and, not infrequently, performing their surgeries before audiences of the elite and members of the medical establishment, as well as their day-to-day clientele. It was through their endeavors to carve out a livelihood that oculists ultimately shaped both public and medical understanding of the wonders of the eye.

History and Philosophy of Life Sciences, 17th-18th century B (submitted papers)

Charles Georges Leroy and Enlightened Ethology

Martínez-Contreras Jorge, Universidad Autonoma Metropolitana, Mexico

Charles Georges Leroy has been one of the forerunners of Ethology, in the XVIIIth C. Being a hunter and a keeper of the King's hunting domains in France, he did observe the behavior of several animals, both predators and their game. The thought we shared with non-Human animals the same sensibility. He tried to explain animal behavior based on our shared natural feelings. Some of his ideas may announce some of the principles of an evolutionary Ethology, like mate selection by females and territoriality. Leroy had a great influence in the XIXth C., especially in philosophers like Come and others. His work must be reviewed according our actual knowledge on animal behavior.

Charles-Georges Leroy and Auguste Comte on cooperation in animals and altruism

Bourdeau Michel, IHPST & Université Paris 1 Panthéon-Sorbonne, France

Comte had a high idea of Leroy's contributions to biology and his followers, like Jean-François Robinet, went on drawing attention to his work. Such an appraisal is mainly grounded on methodology. According to positivism, a sound understanding of life has to take account of two elements: not only the organism, but also its environment. Leroy shared the same approach: against Buffon, he argued that the study of animal behaviour had to rely upon observations made in their natural environment. Furthermore, his work is also relevant for sociologists, in as much as the comparison of man to other animals is an important part of the sociological method.

Among the various insights we can gain from Leroy in this last respect, I shall focus on what he says about cooperation and innateness of altruism. Comte, who coined the term altruism, credited Leroy for giving " a definite refutation of metaphysical egoism " (*Système de politique positive*, III 589). I shall review some of Leroy's observations on cooperation in animals, for instance in hunting, as well as what he says about altruistic behaviour, in order to see how far it supports Comte's claim I just quoted. I shall also show how Comte develops Leroy's ideas, and where he disagrees from him.

History and Philosophy of Life sciences, 19th-20th century (submitted papers)

Progress, Adaptation, and Organism-Environment Interaction: Spencer's Criticism of Lamarck

Morganti Federico, Sapienza Università di Roma, Italy

The paper aims to elucidate Herbert Spencer's attitude towards the evolutionary thought of Jean-Baptiste Lamarck. According to a common misunderstanding, Spencer's view of evolution, in its endorsement of the inheritance of acquired characters, was nothing but a different form of Lamarckism. Such a description, while stressing a relevant feature of Spencer's perspective, still impoverishes his view by forcing it into an inadequate interpretative framework: the clash between Darwinians and Lamarckians. The quarrel between these two schools of evolutionists, not only was subsequent to the development of Spencer's thought, but was also confined to a limited number of biological concerns which by no means exhaust the extent of Spencer's philosophical evolutionism, whose aspiration was to explain not merely organic evolution but the whole cosmic development. Moreover, even considering solely the biological side of the matter, there are two aspects of Spencer's perspective which render it quite irreducible to Lamarck's. Firstly, while Lamarck had founded his own account of evolution on the particular features of living beings, Spencer referred evolutionary change to the fundamental transformations of force, matter and motion, thus explaining evolution in physical terms. Secondly, while Lamarck had seen in life an inherent tendency to advance towards more complicated forms, Spencer explicitly rejected such hypothesis reducing all evolutionary progress to a form of adaptation. Nonetheless, in order to avoid a seemingly theologically-oriented conception of evolution, he embraced the equally slippery view based on the idea of a growing ‘harmony' between organisms and environments. The paper will focus on the explanation of these two main points.

Elan Vital Revisited: Bergson and the Thermodynamic Paradigm
Difrisco James, Institute of Philosophy, KU Leuven, Belgium

Bergson's concept of *élan vital* has been often disparaged as a classic expression of vitalism, a charge which has contributed to the relative neglect of his thought in contemporary philosophy of biology. The first part of this paper argues against the vitalistic interpretation of Bergson's *L'évolution créatrice* (1907) in favor of an interpretation based on his often-overlooked reflections on entropy and his ongoing engagement with the energeticist physicists of his time (e.g., Faraday, Kelvin, Duhem). It is shown that Bergson's view of evolution and living organization resonates deeply with more contemporary approaches belonging to the "thermodynamic paradigm" of theoretical biology (Brooks and Wiley, 1986; Wicken, 1987) in different aspects, including the critique of selectionism, the critique of adaptationism, and—more generally—the promotion of a "metabolism first" conception of the origin of life and of the minimal living system. Viewed in light of this thermodynamic interpretation, together with Bergson's radical process metaphysics, it becomes clear that *élan vital* is not a "vital force" distinct from physical forces, and that *élan vital* and matter are opposed not as static substances but rather as energetic processes of organization and degradation.

After having shown these connections between Bergson and more contemporary work, the second part of the paper will examine one challenge Bergson's philosophy of life poses for us today. This is to conceptualize how the thermodynamic-energetic condition of organization—*élan vital*—is intrinsically coupled to the living system's particular duration (*durée*), or the way its existence in time is organized.

History and Philosophy of Medical Practice (the 19th century-today) (submitted papers)

Disease Avatars: the epistemology of cell reprogramming-based disease models
Testa Giuseppe, European Institute of Oncology, Italy
Germain Pierre-Luc, European Institute of Oncology, Italy

Since the landmark derivation of induced pluripotent stem cells (iPSC) from somatic cells in 2006, cell reprogramming has been framed as a revolutionary development not only for the prospects of regenerative medicine but also, and likely in a shorter timeframe, for our capacity to understand human genetic diseases through cellular models. In principle, cell reprogramming makes it possible, for the first time in the history of medicine, to make human genetic variation experimentally tractable through the creation of genetically matched cell lineages on which to decipher and target pathology, biological stand-ins or 'avatars' of ourselves, as recently proposed.

In this work we present a historical and epistemological analysis of this momentous development in biomedicine, asking how these cellular avatars are reconfiguring the normal and the pathological, and through which resources, both material and conceptual. To this end, we bring into relief the following salient epistemological shifts through a combination of discourse analysis and empirical confrontation with laboratory practices: i) the mutual reclassification of in vivo cell types and in vitro developmental milestones, with the vindication of Canguilhem's intuition that pathology grounds physiology; ii) the explicit investment of reprogrammed cells with clinical features in a bidirectional flux that conflates research and treatment; and iii) the transition of cellular avatars from representational models to measurement devices of physiopathological differences. This epistemological dissection allows then to explain the innovation of reprogramming-based disease modeling in terms of an iterative biomedical platform in which the patient becomes both a source and a target of extrapolation.

Why so long to abandon bloodletting, and why the relative lack of influence of the work of P.C.A Louis on its use? Reflections on whiggish queries in the history of medicine and biology

Hook Ernest B., University of California Berkeley, USA

Physicians use bloodletting today to manage a few rare disorders. But on the basis of different physiological views about the body, many, not all, earlier "schools" or "systems" of western medicine used it frequently, some promiscuously, up to about the mid 1800s, when sharp expressions of skepticism markedly increased. Usage then diminished but did not disappear. From today's perspective, bloodletting would seem to have had little clinical value, indeed often been dangerous, e.g. notoriously, in treatment of the dying George Washington. Why then did widespread use of this therapy last as long as it did? A specific query arises with regard to influence of the work of P.C.A. Louis (1787-1872) and his published reports (1828, 1835). Historians cite the "father of clinical epidemiology" as the first to undertake analytical investigation, to find no evidence for any benefit of bloodletting, and imply his work had great influence on usage. But Louis claimed his results *did* show bloodletting shortened the course of lobar pneumonia and endorsed strongly its use for "inflammations which are severe and are seated in an important organ." And those on either side of the issue later in the 1800s cited his work in support of *opposite* views. I suggest, rather than Louis' work, that the emergence of new views of the physiology of the body, the pathology of disease states, especially those termed "inflammations", and perceived inadequate "rational" reconciliation of these with therapeutic practices such as bloodletting, accounted for the end of the widespread use of the procedure.

Cancer as a complex disease and a transdisciplinary challenge: ontological, epistemological and sociological implications

Valadez Blanco Edgar, UNAM, Mexico

The genetic paradigm of cancer have been proven to be inadequate due to its reductionism. This model does not consider the various levels of biological organization, the environmental factors and the complex social impact involved in cancer. In this context, cancer has been redefined as a complex disease that require models and theories which incorporate such factors. In this paper, I analyze the main discourses and practices as regards the complexity of cancer through a framework of metascientific and sociological categories (models, paradigms, research styles and inter-and transdisciplinary fields). Such strategy allows to classify and relate the diversity of the epistemological, ontological and sociological aspects involved in cancer research. With this framework it is possible to distinguish at least three paradigms related to the complexity of cancer: the first one defines and explains cancer as a disruption or modification of complex systems through mathematical and computational models; the second defines cancer as a complex disease and uses statistical models and epidemiological data to elucidate the social and environmental causes of cancer; the third consist of the practices and theories that focus on cancer patients, where intervention lie in the uniqueness of the person who suffers the disease.

The relationships between these paradigms can be sociologically understood as the emergence of an inter- and transdisciplinary field. In this field, each discipline possess its own style of research, paradigm and model; and at the same time, the different disciplines are closely intertwined, thus consolidating a new and promising cancer research field.

History of Science in Science Education (submitted papers)

The History of Science as a tool for teaching metascience: an assessment of changes in pre-service biology teachers' conceptions

Prestes Maria Elice, University of São Paulo, Brazil

The introduction of disciplines that include themes of History of Biology in undergraduate courses is quite recent in Brazil. This deployment motivates new fields of research that leads to the improvement of teaching units and strategies of learning. In this sense, our presentation will discuss the results of research conducted among students of an elective discipline offered to pre-service biology teachers of the University of São Paulo. After pointing out the historical components and metascientific objectives of the discipline, it will be presented the students' perceptions about some aspects of the nature of science. The survey instrument used was the questionnaire VNOS-A, developed by Lederman and O'Malley (1990) for this level of teaching. The questionnaire was administrated at the beginning and end of the semesters of 2010 and 2011, to 8 and 13 students, respectively. Qualitative analysis of data was performed, consisting of the construction of *a posteriori* categories. It will be discussed students' responses to questions 1, 3 and 7 of the questionnaire devoted to investigate their opinion about the mutability, or not, of scientific theories, the distinction between scientific laws and theories and the elements that can lead scientists to defend rival theories to explain the same phenomenon. The final results show little change in the opinions of students, while indicating greater precision and sophistication of the arguments that sustain their views. Based on the survey results, changes were introduced in the syllabus for enabling explicit broaden discussions about these and other aspects of nature of science.

The origin of electric organs: can that Darwin's special difficulty contribute to the teaching of Evolutionary Biology?

Jensen Gerda, University of Sao Paulo, Brazil

This communication presents a Teaching Learning Sequence (TLS) focusing on Evolutionary Biology to be applied to Brazilian High School students. That modality in the country lasts three years and concentrates on learners generally aged from 15 to 17 years old who have finished elementary school, nine year duration modality .The implementation, development and evaluation of this sequence is based on the active participation of students in discussions about the idea of the transformation of species focusing on electric fishes as biological material. That theme is part of the author doctoral research. The next stage of this study consists in the application of the TLS to students enrolled in a public school in São Paulo, action already scheduled. The History of Biology “add-on approach” teaching is the central theme of this TLS and addresses the fact that the electric organs of certain types of fish were considered by Charles Darwin (1809-1882) as one of the special difficulties within his theory of natural selection, according of his work *On the origin of species* between 1859 and 1876. Based on the review of excerpts related to the biological evolution from textbooks and Brazilian biology education official archives, it was chosen the strategy of conducting an integrated study of that evolution and, in parallel, articulate explicit discussions about the characteristics of Science and its historical development. The TLS focus of this communication is composed by a variety of instructional materials based on selected excerpts from original sources which are considered the most reliable ones.

Darwin in the classroom: replication of historical experiments to assist in the understanding of the evolution theory

Silva Tatiana, Universidade de São Paulo, Brazil

The theme of the evolution of living beings and the evolution theory of Charles Robert Darwin (1809-1882) are part of the syllabus of Biology courses of middle schools, in Brazil. The nuclear role of evolution in the organization of biological thinking and contemporary Biology, by one side, and the difficulties to its effective integration in the curriculum, by another, motivated the development of a Teaching Learning Sequence based in the hands on approach of History of Science in teaching. This presentation discuss the results obtained in a research that promoted the elaboration, validation, application and evaluation of a Teaching Learning Sequence centered on the replication of Darwin`s experiments about seeds dispersion and consequent plausibility of common ancestry of living beings. The Teaching Learning Sequence had the purpose of facilitate the learning of scientific contents, in the case, the common origin of living beings, by means of explicit discussions about the construction of scientific knowledge. For this, instructional materials were produced and different teaching strategies were used. The empiric study was applied in two classes of 11th grade of a private school, in the city of São Paulo, in the first semester of 2012. Between the results we find, among students, a demystification of the historical character of Darwin, discussions about the nature of science and the evolutionary theory and discussions about the role of experiments as only one of the sources of scientific evidences.The diversity of activities proposed, focused on practical activities, showed play one important role for the apprenticeship.

History and Philosophy of Science and how they relate to Science Education: Teaching for Conceptual Change in Evolutionary Theory

Kampourakis Kostas, University of Geneva, Switzerland

In the science education literature, conceptual change in science has often been described as similar to a Kuhnian paradigm shift. Students are supposed to undergo conceptual change when they are appropriately taught about evolutionary theory and to shift quickly from their (mostly Lamarckian) preconceptions to Darwinian concepts. However, particularly in the case of evolutionary theory, conceptual change neither took place at once as soon as Darwin's theory was published, nor did it involve a simple shift from a pre-Darwinian to a Darwinian worldview. Darwin's influence was enormous and much more complicated than a simple paradigm shift. Furthermore, research has shown that students do not hold Lamarckian preconceptions but ones that often stem from deep intuitions, which make evolutionary theory seem counter-intuitive and conceptual change difficult to achieve. Students of all ages and adults tend to intuitively provide teleological explanations for the features and properties of organisms. In this paper I will argue that a careful study of history and philosophy of science, in particular of Darwin's own conceptual change and of the structure and content of teleological explanations, can provide valuable tools for designing science instruction aiming at conceptual change in evolutionary theory.

Hodgiana A

Buffon and Darwin after Hodge: the case for extremism

Hoquet Thierry, University Jean Moulin Lyon 3, France

It is a commonplace of intellectual life that admirers often take good ideas further than their originators approve or appreciate. In this talk I shall reflect on two ways in which my own work represents just such an apparently unwelcome -- but, in my view, nevertheless appropriate, and ultimately irresistible – taking to extremes of themes introduced in Jon Hodge’s challenging and enlightening writings. The first concerns Buffon as a “historical thinker”. In Hodge's view, the question of Buffon’s historicism must not be decided anachronistically. I agree, but, in my “ultra-Hodgean” fashion, have come to disagree with Hodge himself about what conclusion to draw. For Hodge, only Victorian prejudice can lead someone to classify Buffon’s writings as non-historical. But for me, Buffonian history has to be seen as part of the tradition of natural history, from the Greeks onward – a tradition emphasizing, not a certain stance on time, but an effectively timeless stance on empirical knowledge. The second set of issues concerns Darwin, in particular the argumentative structure of the *Origin of Species*. Here I have argued that, while Hodge's assimilation of the *Origin*'s structure to the three stages of a good "vera causa" argument is persuasive as far it goes, it leaves some chapters – notably the chapter on variation (ch. 5) – less well accounted for. Here are puzzles that emerge most forcefully, not for Hodge, but for the ultra-Hodgean.

From germs and cells to species and trees of life... and beyond: Jon Hodge's articulation of Darwin´s Generation Theorizing into its wider frames

Lopez-Beltran Carlos, UNAM

Synthetic and overloaded with interpretative nuances and erudite details as it is, M.J.S. Hodge's epochal paper "Darwin as a Lifelong Generation Theorist" (1985) remains to this day a landmark in many ways. Confronting in the same move what he calls the "Franciscan view" (for Francis Darwin) and some 1970´s "modified Lovejoyian" views of Charles Darwin theoretical developments, Hodge managed in this paper to provide us with a rich exemplar of how to avoid both "vertigos" (to use Pereda's expression). In this presentation I will connect Hodge's skillful highlighting of the Grantian "Generation Program" Darwin adopted as a young man (and it's well known achievement: Pangenesis) with its broader historiographical frameworks, with special attention to the cultural emergence of the modern concept of Heredity. I will show how Hodge's Darwin (that carefully connects Darwin's physiology of organismic reproduction with his origin of species) has been instrumental for many achievements in the history of biology, and that many lingering interpretative misunderstandings stemming from both the "Franciscan" and the "modified Lovejoyian" should be definitely put to rest.

Against "Evolution"? Non-Darwinian Theorizing and the Hodgean Historiography of Biology

Bowler Peter, Queens University Belfast, UK

Jon Hodge is well known for his work on Darwin and the later development of Darwinian theory, but he has also worked on pre-Darwinian evolutionism, especially the ideas of Lamarck and Chambers. Here he has emphasised the importance of not treating these figures as forerunners of Darwin, because they conceptualized the development of life in a completely different way, invoking mechanisms of predetermined development and parallelism. Hodge has also emphasized the continued use of these mechanisms in later periods, a point I developed in my own study of the eclipse of Darwinism. He argues that the gulf between these theories and the Darwinian conception of common descent is so wide that we should not use the term 'evolution' to denote them. I want to challenge this argument by suggesting that the wide appeal of these ideas in later periods makes them an integral part of what was called the evolutionary perspective, so from this wider perspective we must be careful not to create the impression that they exist in a world apart.

Hodgiana B

How Hodge's History of Biology and Philosophy of Biology Fit Together

Radick Gregory, University of Leeds, UK

Jon Hodge is a historian of biology's historian of biology. But he is nevertheless someone whose teaching and writings have been philosophically informed and engaged to an unusual degree. How, within the Hodgean oeuvre, does this integration work? I want to explore this question by looking at affinities between one of his recent historical projects and one of his recent philosophical projects. The historical project is to describe the way Darwin understood his analogical argument for the causal efficacy of natural selection and how he came to develop that argument. The philosophical project is to defend a causal interpretation of the theory of natural selection against those – "statisticalistas", he calls them – who see Darwinian explanation not as causal but as mathematical. Of course, one could understand Darwin on natural selection as Hodge does and yet side with the statisticalistas in the present-day debate. But in Hodge's case, the causalist enthusiasm spreads across the history-philosophy divide – not, I will suggest, because he thinks Darwin was right, but because, for Hodge, the Darwinian biological tradition, from Darwin forward to Fisher and Wright and beyond, is a fundamentally causalist tradition, and traditions have origins and integrities that need to be reckoned with.

Hodge's Paradigm-Making Thinking about the Population Geneticists

Ruse Michael, Florida State University, USA

Compared to the period around the Origin, the history of evolutionary theory around the coming of the Darwin-Mendel synthesis in 1930 is very much an undermined field. However, thanks to the daughter of Ronald Fisher, Joan Box, and the indefatigable labors of Will Provine, we do have a basic understanding of the work of the early population geneticists, especially Fisher and Sewall Wright. I shall argue however that it has been Jon Hodge who has taken the discussion to a much higher level of historical sophistication, particularly with his seminal discussion of the religious and eugenical factors driving Fisher. After Hodge's work, no one could possibly think that what was going on in the man's mind was simply an attempt to map nature. Fisher had a very strong driving set of external factors or aims. If immodestly I might say that I was able to do much the same for Wright, showing the overwhelming influence of Herbert Spencer on his thinking, I would be the first to agree strongly that I was motivated only because the revolutionary scientist Hodge gave us the paradigm, leaving puzzles for normal science inquirers like myself. If there was sauce for the English goose, then there simply had to be sauce for the American gander. In this discussion, I shall present the various moves made by or inspired by Hodge's deep insights, and then look at his more recent thinking on these topics.

Responses and reflections

Hodge Jon, University of Leeds, UK

I am profoundly grateful to all those who have organized and will be contributing to this discussion. Looking ahead to the occasion itself, our main aim will be to clarify the historical, philosophical, social and biological issues themselves, and to do so not just for ourselves, the session participants, but for everyone in the room. To keep discussion of misunderstandings to a minimum, I am going to be sending commentators some published and unpubished items designed to do just this. That way we can focus on the primary issues and also let the discussion range all the way to those religious, political and other questions which so often enliven and enhance ISH conversations in and between the scheduled sessions.

Holism and organicism: conceptual consensus or historical typologies?

Holism, organicism and the risk of biochauvinism

Wolfe Charles, Ghent University, Belgium

Since Gilbert and Sarkar's reflection on the need for an 'umbrella' or 'organizing' concept to convey the new vitality of systemic or holistic concepts in biology (Gilbert and Sarkar 2000), seconded by Laubichler's paper proclaiming the return of the 'organism' as such an organizing concept (Laubichler 2000), some scholarly work has been done which dispels earlier prejudices and gives us a more useful, nuanced sense both of these concepts in biological science and their possible pertinence today (see e.g. Huneman and Wolfe eds. 2010, and Cheung 2006 on the history and theory of organism; Wolfe 2011a, b on forms of vitalism and Normandin and Wolfe eds. 2013 on the relation of vitalist themes to mainstream science). In addition, there has been some sustained work on these concepts in current biology. To name three recent examples, (1) in theoretical biology, the effort to articulate a model in theoretical biology of "organizational systems", in Moreno and Mossio's research (see Moreno and Mossio, forthcoming and earlier, Ruiz-Mirazo, Etxeberria, Moreno & Ibáñez 2000). A question arising in reaction to this research is the extent to which philosophically it is committed to a non-naturalistic concept of organism as organizing centre, as a foundational rather than heuristic concept – or possibly a "biochauvinism," to use Di Paolo's term (Di Paolo 2009). (2) In biochemistry, Kirschner et al.'s research paper in *Cell* (Kirschner et al. 2000) on what they called "molecular vitalism": they suggested that, faced with the limitations of genomics, researchers should investigate what the authors "whimsically" termed the "vitalistic" properties of molecular, cellular, and organismal function: "the organism has fashioned a very stable physiology and embryology. . . . It is this robustness that suggested 'vital forces', and it is this robustness that we wish ultimately to understand in terms of chemistry. We will have such an opportunity in this new century" (87). (3) In evolutionary biology, Pepper and Herron's 2008 paper suggests that organisms define a category that evolutionary biology cannot do without.

My aim in this paper is to conceptually clarify the forms of holism and organicism that are involved in these cases (and I acknowledge that the study of early 20th-century holisms [Peterson 2010] indicates that not all of them were in fact 'organicist' or 'biologistic'). I suggest that contemporary holists are still potentially beholden to a certain kind of vitalism or "biochauvinism"; but that when they reduce their claims to mere heuristics, conversely, they risk losing sight of a certain kind of organizational "thickness", a "vital materiality" (Wheeler 2010) which is characteristic of biological systems (Bechtel 2007, 2013). And I ask if it is possible to articulate a concept of biological holism or organicism (whether it is located in systems biology, theoretical biology, evolutionary biology or a philosophical reconstruction of several of these) which is neither an empirical 'biochauvinism' nor a metaphysical 'vitalism'?

Cabanis's Living Systems

Cheung Tobias, Max-Planck-Institute for the History of Science, Germany

Cabanis's *Rapports du physique et du moral de l'homme* (1802) was a treatise on the systemic relations between, first, organic units, second, organs and intellectual operations, and, third, the entire organized body and its outer world. Within this conceptual framework, I will focus on the role of "reaction centers" (*centres de réaction*) and the order of their interactions. For Cabanis, there were multiple "reaction centers" within one "living system", like organs or nerve nets. Through stimuli-reaction-schemes, "reaction centers" interacted with each other and with the regions or worlds that surrounded them. "Living systems" thus maintained their inner order through complex interactions between different inner and outer inside-outside-interfaces. Further on, "reaction centers» were agents within processual hierarchies that determine the influence of each "center". Finally, the acts of "reaction centers" did not only maintain and reproduce the "living systems" in which they occur, but also modify their inner organization.

Coming to Terms with Holism: Minimalistic Conceptual Tools for Describing and Explaining Holistic Systems in Biology

Toepfer Georg, Zentrum für Literatur und Kulturforschung Berlin, Germany

In my contribution, I will focus on some of the most important general concepts in recent discussions of organisms as holistic systems, namely "interdependency", "(causal) cyclicity", "(functional) coherence", and "(organizational) closure". All these concepts emerged within causal models of the organization of the living. I shall characterize these concepts in their presuppositions and implications and discuss their theoretical relationship to each other. For each of these concepts I will emphasize the crucial role of the relationship between the parts (or sub-processes) that together constitute the whole.

I shall further argue, that, to be united in a holistic system, the parts must (1) exert a causal influence on each other, (2) mutually depend in their existence from the influence of the other parts, and (3) be determined by their effect on the other parts. The three aspects refer to causal, ontological, and epistemic levels respectively. Terminologically, these three levels might be called "interaction", "interdependence", and "interdetermination". On this terminological basis, I shall discuss typical kinds of integrated dynamical systems in nature, organisms and other systems, for example, the water cycle, chemical reaction systems, and regulatory devices within the inorganic world. In discussing the relationship between holistic systems and teleology, I will argue that it is at least partly for contingent reasons that some types of dynamic wholes in nature are always described in functional terms (organisms) whereas others are not (e.g. the water cycle).

Holism in biology: a restatement and defence

Mossio Matteo, Université Paris 1 & IHPST, France

The aim of this paper is to offer a conceptual characterization of holism in the biological domain, and to advocate its relevance as a scientific framework.

In accordance with an increasing number of contemporary studies in theoretical biology and philosophy of biology (Kauffman, 2002), I will submit that the distinctive trait of holism consists in taking *organization* as the fundamental notion in biology, in the light of which all biological phenomena should be understood. From a holistic perspective, what must be explained are, first and foremost, the principles of biological organization (Bertalanffy, 1962). In particular, I will suggest that holism, by shifting the focus on biological organization, opens new research lines to account for the stability that biological systems exhibit in spite of their variability, at both the ontogenetic and phylogenetic scales. This implication is especially relevant in a moment when traditional explanations of stability in molecular biology, framed in terms of genetic information, are being questioned, also because of the increasing evidence of stochastic phenomena at the molecular level (in relation to gene expression and molecular interactions, see e.g. McAdams & Arkins, 1999).

I will conclude by arguing that, more generally, holism provides a coherent naturalized framework to understand central biological dimensions such as, in particular, normativity, functionality and agency.

Immunology and Individuality

Doing Biographical Work: The "Self" of Immunological Theory and the "Self" of Autoimmune Disease

Anderson Warwick, University of Sydney, Australia

While Macfarlane Burnet and others were elaborating on the idea of the immune 'self', patients with autoimmune diseases were doing their own 'biographical work', tending to the self of chronic illness. Burnet was aware that any theory of antibody production must explain pathologies of immunity such as autoimmune disease. Certainly, clinical immunologists came to see autoimmune disease as the pathology of self-recognition. But through the 1960s and 1970s, the clinical hegemony of the immune self was limited. Patients with autoimmune diseases such as SLE, multiple sclerosis, rheumatoid arthritis, to name just a few, rarely imagined their illness as a form of immunological hyper-reactivity to self. Yet at the same time, they were engaged in a related form of biographical work, incited by the experience of chronic illness. For many, chronic illness found expression in a language of loss—in particular, the loss of self—a language more meaningful, if less elegant conceptually, than the discourse of self and not-self articulated in immunology. While clinical immunologists sought to restore the integrity of the body, to lessen self-reactivity through suppressing immune responses, patients tried through social means to restore a sense of self, to reclaim a self displaced by chronic illness.

There was thus a congruence of thought styles between immunologists and sufferers of chronic illness, with both groups favouring a physiological rather than an ontological mode—without apparent intellectual contact. Using Burnet's archive and selections from patient records and literary studies, I will discuss the pathos of these uncoordinated 'selfs'.

Individuality and Immunology's Theories of Cognition

Tauber Alfred, Center for Philosophy and History of Science, Boston University, USA

Notions of individuality in the immunological context typically begin with a given distinction of self and other, and from that dichotomy conditions of identity are built. Given that the 'immune self' is defended by the immune system, protection of this agent requires a cognitive capacity by which the self and the foreign are perceived and thereby discriminated; from such information, discernment of the environment is achieved and activation of pathways leading to an immune response may be initiated. Despite the wide-spread use of a terminology supporting the so-called cognitive paradigm (e.g., 'perception,' 'recognition,' 'learning,' and 'memory'), the philosophical character of such functions has not been explored. When different formulations of cognition are considered, immunology's conceptual infrastructure shifts: 1) extensions of folk psychological understanding of representational cognition based on a subject-object dichotomy support notions of autonomous agency, and 2) an 'ecological' theory of perception dispenses with representations for a model where direct environmental presentation offers an alternative to the predicate structure dominating current immune theory. Reviewing the historical development of immunology, these two understandings of perception – representational and ecological (associated with J.J. Gibson) – are discussed as offering competing views of immune cognitive functions, which in turn provides a critical perspective on the assumptions of a science based on individuality as its governing precept.

The Individual, the Organism, and the Immune System

Pradeu Thomas, Paris-Sorbonne University, France

In this paper, I explore the exact role of the immune system in shaping the individuality of an organism, and in particular in the delineation of its boundaries. A long tradition, in biology and philosophy of biology, has questioned the organism as a legitimate biological category. Yet this tradition tends to focus exclusively on evolutionary biology, and to ignore key biological domains that may contribute significantly to the understanding of biological individuality at the organism's level. Among these domains, which often pertain to what can be broadly defined as "physiology," immunology plays arguably a decisive role. Across phyla, the immune system ensures the cohesion of the organism through the integration or elimination of entities. This "surveillance" activity includes, but is not limited to, what has sometimes been described as "policing" mechanisms (e.g., Michod 1999, Godfrey-Smith 2009). As every organism is heterogeneous, that is, made of many initially foreign entities (especially symbiotic bacteria), it is crucial to understand how the immune system interacts with these heterogeneous constituents, and thus contributes decisively to unifying this plurality of entities (Pradeu 2012). Therefore, the immune system plays a key role in the constant construction of the organism, through the constant unification of heterogeneous constituents, and the contribution of immunology to the understanding of individuality cannot be overlooked.

Individuality and the Division of Labor

Debating Division of Labor in European Ethology. An Epistemological Analysis of the Pardi-Deleurance controversy about the Organization of Wasp Societies in 1950.

Caniglia Guido, Arizona State University, USA

In March 1950, during the international meeting Structure et Physiologie des Société Animales in Paris, an important controversy exploded about the mechanisms that underpin the organization of wasp societies. The main actors of the controversy were a young Italian ethologist, L. Pardi, and a well established French neurophysiologist, E.P. Deleurance. In his work from the 1940s, Leo Pardi had provided a new conceptual framework for the understanding of social life in Polistes wasps that pivoted around the idea of Social Dominance. He had also shown that ovarian development underpins the hierarchy relationships that characterize social dominance. In his intervention at the Paris conference, Deleurance vehemently attacks both results of Pardi's research causing the young entomologist to abandon the field of study of social research for about 20 years. The idea of Social Dominance, according to Deleurance, was a typical example of the anthropomorphic fallacy; also, the occupancy of empty cells in the nest rather than ovarian development was the mechanism underpinning division of labor. Relying on the analysis of archival material, published papers and interviews, in my talk, I show that the Pardi-Deleurance debate went to the heart of our understanding of division of labor in insect societies. I argue that, by focusing on this historical case, we can highlight important and controversial patterns of reasoning that characterize the way scientists investigate and explain division of labor in animal societies even in contemporary science.

Individuality and the Division of Labor in the Nineteenth Century
Nyhart Lynn, University of Wisconsin-Madison, USA

In 1826, the French zoologist Henri Milne-Edwards famously mooted a “physiological division of labor” within the individual organism. Over the next sixty years or so, the division of labor concept became deeply entrenched in European biological discourse. Most historians' treatments have focused on the use the division of labor for understanding the hierarchy of complexity in the organic world (as a way of marking out “progress”), or the transformation that Milne-Edwards' idea underwent in Darwin's hands. By contrast, in this paper I stress how the concept was entangled with ideas about the nature of individuality itself, as it played out in discussions of polymorphism, the meaning of sex, the alternation of generations, and—yes—evolution, as the context for these discussions changed before and after the publication of *Origin of Species*.

Modularity and division of labor: from theory to experimental evolution
Rebolleda Gómez María, University of Minnesota, USA

Division of labor requires high levels of cooperation. Extreme cases, like erythrocytes, have given up any possibility of passing genetic information, but their function is essential for the survival of the organism as a whole. From an evolutionary perspective this degree of cooperation posses two problems: first, how could some cells have evolved to sacrifice their reproductive success for the benefit of the organism? Second, cellular differentiation requires the evolution of a complex regulatory pattern, in which all cell types have to develop in a precise way from a single (or a few) totipotent cell(s). The question is then, how could such a complex pattern of expression evolve in the first place? The aim of this work is twofold. First, I argue that modularity is a useful concept to understand the evolution of division of labor. Second, I use this framework to explore the evolution of cellular differentiation using a simple and tractable experimental system. Multicellular individuals that develop via mother-daughter adhesion evolved from a unicellular ancestor (a *Saccharomyces cerevisiae* strain) in the laboratory as a result of a selection experiment. Using this recently evolved multicellular organisms as a system; this work explores the experimental conditions favoring the evolution of cellular differentiation.

Information and Plasticity

Genetic, Epigenetic, and Neural Memory Systems

Godfrey-Smith Peter, City University of New York, USA

Memory can be understood as communication between temporal stages. This idea is no more than a vague metaphor in the absence of a rigorous and widely applicable theory of communication, but now we have one. Recent developments of "sender-receiver" models, especially by Skyrms, have made it possible to develop a detailed functional account of memory in communicative terms. I will outline a view of this kind and then use it to compare several natural systems that have memory-related functions. This will include a treatment of "genetic information," and comments on the general problem of understanding semantic properties from a naturalistic point of view. I will also briefly discuss Randy Gallistel and Philip King's recent challenge to current treatments of memory in neurobiology.

Plasticity and selection in synaptic populations

Cao Rosa, New York University, USA

How can collectives in the brain coordinate their activity to produce behavior appropriate to changing circumstances? Functional plasticity has traditionally been understood as an adaptive process operating at the level of *neurons*. But another way of seeing plasticity is as the consequence of *selection processes* acting on populations of *synapses*. In many cases, the function of a given collective – from aggregating sensory information to producing motor output or predicting rewards for the organism – is determined by the nature of the selection processes facing its members (as well as by gross anatomical constraints). How likely it is that a synapse will persist (and in what form) depends in part on its activity level, which in turn depends on modulatory influences in its vicinity. Modulation can serve as a mechanism to enforce cooperation between synapses. Prominent types of modulation include feedback effects responsible for phenomena such as gain control through synaptic homeostasis and feedforward effects responsible for pathway consolidation during development.

The Evolution of Vagueness

O'Connor Cailin, University of California Irvine, USA

The phenomenon of learning generalization - where an organism repeats behavior learned in response to one stimulus when presented with a perceptually similar stimulus - has been well documented in a variety of animals. I argue that evolutionary game theory can help explain the prevalence of this type of learning behavior by showing how and when generalization can outperform other strategies in situations where there are payoff similarities between states. Jäger (2007) introduced Sim-Max games, a variation of the standard Lewis signaling game where the state space is endowed with a metric that captures a similarity relation over states of the world. This added structure is manifested in payoffs that reward behavior in both the ideal state for that behavior as well as similar states. A modification of this game can be used as a good model to explore the success of learning generalization in single organism situations.

I show that in these games learning generalization can sometimes outperform simple reinforcement learning. However, it does not do so in all cases. My results highlight an interesting tension. The strategies developed by generalizing learners are necessarily imprecise, and thus perform less well than ideal strategies in these games. However, learning generalization allows actors to develop a fairly successful strategy very quickly. I show that generalization can be expected to evolve in cases where organisms need to learn how to act in many different states over a short time scale.

Is Race Real? (*Interdisciplinary session*)

Race, Slavery, and Polygenism: Edward Long's History of Jamaica
Seth Suman, Cornell University, USA

This paper explores the racial theories of Edward Long, the West-Indian planter and slave-owner who published his *History of Jamaica* in 1774. Long's polygenism, I argue, looks strikingly different from that we are more familiar with from nineteenth-century sources. The reason for the difference, I suggest, is two-fold. First, although Long was willing to buck Biblical orthodoxy, he balked at materialism, a position that gained traction in racial studies following the successes of the phrenological movement in the early nineteenth century. Second, Long presents us with a (rare) case of an eighteenth-century writer on 'race science' with political sympathies toward a part of the world that was both outside the bounds of the European metropole and which also contained a majority black population. As a result, one finds a fundamental ambivalence in his writings on race, an ambivalence that stemmed directly from his desire to manage social relations and political systems in a slave society. Metropolitan figures who believed in the fixity of race (regardless of the question of origin) made a cornerstone of their position the essential identity of newly arrived African slaves and their descendents. For Long, however, the difference between 'salt-water' and 'creole' Negroes was to be the solution to the most pressing social problem of the sugar islands: slave insurrection. This understanding of the (potential) political and social differences between generations of slaves, I argue, required a physical corollary: Long's polygenism presumed less fixity than the monogenism of a figure like Immanuel Kant.

When We Say "Race is a Social Construction", What Are We Saying?
Jackson John, University of Colorado, USA

It is an academic cliché that race is a social construction. Following Ian Hacking's work on social construction, I will trace three lines of argument in pre-World War II discourse about race that underpin this claim: The first is *contingency*: the world does not have to look the way it does. The second is *nominalism*: The world does not have joints at which we can carve it, the joints are completely products of our choosing. The third is *stability*: The world appears stable because of social factors, not because nature is providing the stability. In the development of claims about race's social construction we can see all three arguments at various times. All these arguments were framed by the rhetorical tactic of shifting probative obligations onto those who would maintain the existence of race. In other words, the critique of existing racial classifications was coupled with arguments that shifted the burden of proof onto those who would maintain the existence of race as a biological category--a burden that they would ultimately fail to meet.

I will focus on writers such as African-American activist/scholar W.E.B. Du Bois, the Polish-born French philosopher, Jean Finot, the German/Jewish-born American anthropologist Franz Boas, and the French/American literary polymath, Jacques Barzun. I argue that by focusing not just on the evidence they produced, but on the way they framed that evidence in a system of probative obligations we gain a better understanding of what it means to say race is a construction.

Concepts of Race among U.S. Biologists and Anthropologists
Morning Ann, New York University, USA

Sociological literature often claims that academics across the disciplinary spectrum have converged on a common understanding of race as socially constructed rather than biologically anchored. Yet this claim has received little empirical scrutiny. In this presentation, I report the results of over 40 interviews with academic biologists and anthropologists at four universities in the northeastern United States. Contrary to sociologists' expectations, racial constructivism is revealed to be a minority viewpoint. Moreover, this research shows that the usual "constructivist" versus "essentialist" dichotomy is a blunt tool with which to characterize scientists' concepts of race; a third perspective—"anti-essentialism"—must be taken into account. Recognizing anti-essentialist discourse calls for a reevaluation of prior research that emphasizes sociodemographic status and professional affiliation as key influences on interviewees' concepts of race; this project demonstrates that such factors do little to distinguish essentialist from anti-essentialist thinkers. Instead, I argue that scientists' boundary-marking attempts—especially their efforts to champion their concepts of race by emphasizing these ideas' scientific and moral worth—offer a more promising clue for understanding why some "experts" maintain that race is biologically real, and others disagree.

Why the Usefulness of Race Is Useless

Kopec Matthew, University of Colorado Boulder, USA

The Pragmatist tradition holds, roughly speaking, that the meanings of scientific terms are cashed out through their use and that the reality of the entities labeled with such terms can be determine by the usefulness of employing them. This tradition, although once marginalized, has been making a comeback. For example, biologists and philosophers of biology are increasingly comfortable with pragmatic answers to metaphysical questions concerning taxonomic groups like various species and subspecies. To defend her claim that group X is a genuine subspecies, a biologist today might cite how the group is useful for conservation purposes. And, over the past decade, authors in a range of disciplines have claimed that the common sense human races must be real given that the corresponding racial categories (Asian, European, African, etc.) are useful for various purposes, including medical diagnosis, ancestry tracking, and forensics analysis. This paper aims to show that this Pragmatist tradition, at least in the case of the common sense races, is mistaken—the current usefulness of common sense racial categories is irrelevant to the metaphysical reality of the races. I show that biologists deal with similarly useful groups in the animal world all the time, and yet they don't treat those groups as genuine biological units. I then offer examples of useful groups that we would never believe are anything more than merely socially constructed groupings. I argue that biologists and philosophers have been making unwarranted exceptions for the human races.

Issues in Biological Modeling – Mechanisms, Simulations and Target Systems

Trading Fiction for Performance: How to Understand Computer Simulations of Ecological Systems

Miller Shawn, University of California, USA

Biologist Steven L. Peck has recently argued that computer simulation models of ecological systems present philosophers of biology with "deep interpretive problems" owing to their complexity ("Agent-based Models as Fictive Instantiations of Ecological Processes," *Philosophy and Theory in Biology*, March 2012). He proposes analyzing such models as fictive instantiations, employing the hermeneutics of Hans-Georg Gadamer. I advance a critique of fictionalism about ecological simulation models, arguing that (1) deflationary views, i.e., claims that models are *mere* fictions, are uninformative, and (2) non-deflationary views that rely on particular theories of fiction break down when applied to ecological simulation models, i.e., generate disanalogies that thwart the interpretive understanding that Peck seeks.

I propose an alternative conceptualization of these models drawing on notions of performativity developed in the medical ethnography of Annemarie Mol. On this view, models are constructed, historical entities with genealogies that are best understood by attending to their particular parts and manner of their making. So conceived, ecological simulation models are not postulated fictions, but rather things that scientists *do*. A case study of an invasive species model serves to illustrate.

What is the Target of a Generlized Model?
Elliott-Graves Alkistis, University of Pennsylvania, USA

The logistic growth model in ecology is a generalized model, because it represents a class of phenomena instead of particular instantiations of a phenomenon, yet scientists use it to learn about particular populations, such as Vancouver Island marmots or Canadian horseweed. How is this possible? Weisberg (2013) tries to avoid the problem by arguing that generalized models represent *generalized* target systems. On his view, generalized targets are either composed of the common features of a number of specific targets, or they are more abstract than the model which represents them. In the latter, more complex cases, the scientist must restrict the scope of the model to the more general results which are compatible with the generalized target.

In this paper I will argue against the view that generalized models represent generalized targets. I will provide a unified account of the relation between generalized models and target systems, where the targets are always aspects of instantiated phenomena in the world. I will show that the simple cases of so-called generalized targets are directly derivable from specific targets. Also, the so-called complex cases can be given a simpler characterization. An additional merit of this view is that it is better supported by scientific practice, as scientists often apply these models pluralistically, at different levels of abstraction (e.g density dependence in plants results in the -3/2 power law).

Issues Raised by Synthetic Biology (submitted papers)

Synthetic biology and the almighty fixers
Fisher Susie, The Open University of Israel, Israel

The entrepreneur Craig Venter has made a significant contribution towards the sequencing of the human genome; he has since added synthetic biology to his scientific repertoire. He founded the J. Craig Venter institute (JCVI) and is building the first carbon-neutral laboratory facility in the world. At the lab "designer" bacteria and other organisms will be produced by mixing bits and pieces of DNA. The organisms will be designed to remove oil pollution, to clean up toxic waste and to fight global warming. Apparently, what man has (inadvertently) broken in his use of nature and technology to better human's life, man can fix. Consequently, one should not be overly concerned with today's environmental crises and should not fear for new ones, in particular, those that may be the result of producing artificial organisms.

The idea that man can “fix” the world (improve it) or can fix what he has broken is shared by many in the western world: scientists, politicians and the public in general. In this talk I will present Eric Katz’s "restoration theses." Katz, an environmental philosopher, offers a critique of the “fix” idea hoping that his argument may be of use to environmental activists in their efforts to set limits to land use. Here, I will examine whether this theses can serve as a warrant for action in the public domain as regards synthetic biology.

Is the Creation of Artificial Life Morally Significant?
Douglas Thomas, Oxford University, UK
Powell Russel, Boston University, USA
Savulescu Julian, Oxford University, UK

In 2010, the Venter lab announced that it had created the first bacterium with an entirely synthetic genome. This was reported to be the first instance of ‘artificial life,' and in the ethical and policy discussions that followed it was widely assumed that the creation of artificial life is in itself morally significant. We cast doubt on this assumption. First we offer an ontological account of the creation of artificial life that distinguishes this from the derivation of organisms from existing life, and we clarify what we mean in asking whether the creation of artificial life has moral significance. We then articulate and evaluate three attempts to establish that the creation of artificial life is morally significant. These appeal to (1) the claim that the creation of artificial life involves playing God, as expressed in three distinct formulations; (2) the claim that the creation of artificial life will encourage reductionist attitudes toward the living world that undermine the special moral value accorded to life; and (3) the worry that artificial organisms will have an uncertain functional status and consequently an uncertain moral status. We argue that all three attempts to ground the moral significance of the creation of artificial life fail, because none of them establishes that the creation of artificial life is morally problematic in a way that the derivation of organisms from existing life forms is not. We conclude that the decisive moral consideration is not how life is created but what non-genealogical properties it possesses.

Functions in Biological Artifacts

Holm Sune, University of Copenhagen, Denmark

Scientific research and rapid advances in technology is accelerating our ability to manipulate biological systems. The core aim of the emerging field of synthetic biology is to enable the design of living systems with new functions that do not exist in nature and the redesign of already existing functions. A recent book on synthetic biology and its promises and perils (Carlsson 2010) proclaims that biology is technology: Organisms and their constituent parts are engineerable components of larger systems, and the possible products of synthetic biology are commonly described as *living machines*. While these locutions are extremely effective when it comes to proclaiming and communicating the engineering aspirations of synthetic biology, they are also philosophically perplexing. However, little investigation has been focusing on the status of the products that synthetic biologists announce that they will construct. In this paper I explore the ontological nature of synthetic biology products. The question concerns how to conceive of synthetic biology products and what to make of their status as technology or machines. In particular I examine the notion of a biological artifact in relation to theories of function in biology and technology. I will focus on *the organisational account* (OA) developed by Mossio et al (2009) and Saborido et al (2011), which arguably accommodates the central features of proper functions and grounds them in the current capacities of the system to which the function bearers belong.

From rational to random re-composition: two design principles in synthetic biology

Ijäs Tero, University of Helsinki, Finland

Synthetic biology is a growing post-genomic research field which aims to construct artificial biological components and systems. In this paper, I analyze different design principles which synthetic biology uses to re-compose and construct synthetic components and devices. I focus especially on two design principles called *rational design* and *evolutionary engineering*. Rational design uses computer simulations and fabrication to reduce complexity and create well-defined standardized synthetic components and devices. This principle is mostly championed by those researchers who argue that synthetic biology should use same kind of heuristics as engineering and treat biological systems with the same criteria as man-made systems (cf. Endy 2005). In turn, *evolutionary engineering* aims to create random mutation and variation on constructed devices and systems to optimize and find novel functional solutions (Dougherty & Arnold 2009). By some synthetic biologists, rational design is considered as an ideal design principle and evolutionary engineering's use of ‘messy' processes is seen as ‘ad hoc' solution for rational design principle's current limitations (cf. Brent 2004). I elaborate how these two design principles use different heuristics and abstraction. I analyze how these design principles take different stances towards complexity of biological phenomena, cellular context, robustness and modularity. Finally, I will argue that both design principles provide unique tools to understand biological systems and their dynamics, and successful research should continue using them complementarily.

Issues with causation in Biology

Prospects of recommending management interventions on the basis of formal population viability analysis with scarce data

Anderson Wes, Arizona State, USA

One problem in conservation biology is the calculation of the probability of quasi-extinction times, given some interventions, for all times of concern. Formal population viability analysis (PVA) is taken to have as one of its tasks just this sort of calculation. In the textbook models of quantitative conservation biology, moreover, it is encouraged that conservation biologists use classic models such as exponential or logistic growth models with error terms as the basis of PVA when data is scarce. Indeed, this is encouraged over relying on more informal methods of PVA such as asking experts for their opinions, for example. I ask whether such formal PVA, in general, can generate the required probability calculations when only scarce data is available. Ultimately, I think the prospects for such PVA are dim. The point can be made in two ways. First, in general, there is simply not enough data to expect reasonably accurate parameter estimates. Second, because certain demographic and environmental causes of quasi-extinction time – other than population size – are not taken into account, error in predicting the effects of hypothetical interventions will typically be unbounded. Following the arguments for these claims, I examine some counter-arguments and find them to be lacking.

Integrating proximate/ultimate causation

Otsuka Jun, Indiana University, USA

Ever since Mayr's formulation in 1961, the distinction between proximate and ultimate causation has had a great influence on the practice and interpretation of evolutionary biology, suggesting an incommensurable "division of labor" within biological sciences. Although such a complete division has been challenged by recent works in Evo-Devo that aim to integrate developmental and evolutionary processes, no similar attempts have been made in evolutionary genetics – the stronghold of ultimate causation – whose basic framework dates back to the modern synthesis.

In this talk, I set forth a theoretical framework that incorporates proximate or developmental causal relationships into a mathematical model of evolution. The new framework not only shows how selective pressures (i.e. "ultimate causes" of evolution) propagate through "proximate" causal relationships among phenotypes, but also enables us to predict their short-term evolutionary consequences. Furthermore, it is shown that models that fail to address such phenotypic networks may result in an incorrect or misleading picture of selection and evolution.

There are several conceptual consequences of this proposed theoretical framework. First, it highlights the possibility or even necessity of integrating proximate causation into the study of ultimate/evolutionary causes. Second, it offers a novel perspective on evolution where selection acts on a whole network of phenotype-genotype mapping, rather than on just one level such as genes (as in population genetics) or phenotype (as in quantitative genetics). Implications for other philosophical issues such as units of selection will also be discussed if time allows.

Population Size, Type Number, and Evolutionary Outcomes

Glymour Bruce, Kansas State University, USA

It is often supposed that population size is, by way of drift, connected to such evolutionary outcomes as the probability of fixation, heterozygousity, the number of polymorphic loci, and the number of alleles per loci, among others. Discussion is complicated by at least three issues:

the nature of the ‘connection' between population size and outcomes (causal, nomic or conceptual); the proper precisification of drift vis-à-vis that connection (does population size cause or quantify drift); and the way in which drift itself is conceived (process or product) and its paradigmatic instantiations categorized (see e.g. Beatty, 1984; Reissman and Forber, 2004; Millstein, 2006; Guildenhuys, 2009; Matthen, 2010). In this paper I attend to a particular subset of ‘drift-like' phenomena, distinguished by the fact that population size influences the probability distribution over the difference between offspring frequencies and their expectation. Having done so, I use simulated data from individual based models to investigate the causal dependence relations between population size, type-population size, type frequencies, expected reproductive success, variance in reproductive success, the probability of arbitrary deviations from expectations, and fixation rate. The results bear on discussions in philosophy of biology, and also on certain features of biological practice. In the one case, conditional support is offered to those who interpret ‘drift' as a cause, but only modulo some important caveats about variable selection, while in the other, the results inspire some critical reflection about the theoretical and empirical role of measures of effective population size.

A Longue Durée History of the Cell

Restricted individuality. Individuals and supra-individual order in German Naturphilosophie

Lettow Susanne, Universität Paderborn, Germany

Within the historiography of the cell theory the question of how the relation of primordial, elementary living beings to supra-individual orders has been conceived, has been widely discussed. In particular, the political articulations of the relations of individuals to a ‚higher order' have been scrutinized. With regard to theories that pre-dated the cell theory, Georges Canguilhem has compared Buffon's theory of ‘organic molecules' that form an organism by association to Lorenz Oken's hierarchical view that borrowed much from the *Naturphilosophie* of Friedrich Wilhelm Joseph Schelling. In my presentation I will discuss different articulations of the relation of living individuals to supra-individual orders within German *Naturphilosophie*. In addition to Oken, I will focus on Schelling and Carl Friedrich Kielmeyer who proposed a multi-level model of the integration of individuals to the ‚life of the species' and the ‚life of the organic world'. In contrast to Schelling and Oken who presupposed a homogeneous circular time, Kielmeyer conceived of an interaction of different forms of temporality. In addition, he avoided an overtly sexualisation of living beings whereas Schelling and Oken – albeit in different ways – were heavily preoccupied with sexual difference. Schelling's and Oken's understandings of sexual difference and temporality, I argue, contributed much to an epistemic fascination with ‘higher order' and the subordination of the individual – which in Schellings words is ‘contested' by Nature.

Latent Life of Organisms and the Cell Scale During the XIXth Century

Tirard Stéphane, Université de Nantes, France

The phenomenon of latent life was identified and studied during the XVIIth century, notably by Lazzaro Spallanzani. It concerns some invertebrates Tardigradas, Rotifers, seeds or numerous others organisms, which are able to stop their activity under certain extremes conditions.

During the XIXth century very active works and discussions took place in France on the possibility of absolute stop of metabolism in organisms in latent life. After Henri Dutrochet's studies on Tardigradas and Rotifers (1812), the Louis Doyère's thesis (1842) was an important moment in the description and analysis of the phenomenon. Doyère insisted on the necessity of preservation of the microscopically structure of organisms during the latent life phases.

The second important time was the debate initiated by the Société de Biologie. It opposed, in 1859, Felix Pouchet, who denied this possibility of the stop of metabolism, to several biologists who supported it.

Eventually, in 1878, the French physiologist Claude Bernard gave an important place to latent in his *Leçons sur les phénomènes de la vie communs aux animaux et aux végétaux*. He presented it as the first form of life and explained it at the cell and protoplasmic scale.
Therefore, during the XIXth century, latent life was a very accurate question about limits of metabolism and the most intimate scale of the matter of life. The goal of his paper is to study, during these three periods of this history, the complex relationship between the empirical and experimental approaches of the phenomenon and the philosophical considerations of scientists on life.

Exploring the History of the Cell from a Transnational and Local Perspective

Thomas Marion, Université de Strasbourg, France
Vienne Florence, Technische Universität Braunschweig, Germany

In 1936 and 1959, the Strasbourg physician and researcher Marc Klein (1905-1975) published two studies on the history of the cell theory. They have been largely remained unnoticed by historians of biology, although they contain fascinating aspects and questions. Taking Klein as a starting point, we aim at exploring further the work of early nineteenth century French and German naturalists on “cells”, “globules” or other elementary units, and show how central notions of the cell theory like that of individuality, autonomy, universality as well the analogy between organism and the state emerged before respectively Schwann's and Virchow's late 1830s and early 1850s cell theories. Secondly, by looking at medical textbooks and examining the research work of nineteenth century century Strasbourg and Parisian physicians, we want to investigate further Klein's statement of a different reception of the cell theory in Strasbourg and Paris, and retrieve not only epistemological but also political factors to explain it. This contribution is part of an upcoming joint research project, which aims at shedding a new light on the development of the cell theory in the nineteenth century century in France and Germany. Last but not least, by combining a transnational and local perspective, this project intends to provide new insights into the intertwined links between cell-theory and politics.

Stem Cell Research and the Embryo. Conceptual and Practical Shifts in the 1970s

Brandt Christina, Ruhr University Bochum, Germany

In this paper, I will trace the research problems that scientists dealt with in developing embryonic stem cell research in the 1970s and which led to the first isolation of so-called ‘embryonic stem cells' from mouse embryos in 1981. The paper aims at analyzing the shifts in research practices that guided the work on embryos and related cell cultures at that time. In particular, the paper will analyze the developments at the intersection of research on mouse *chimera* and research on cancer, especially work on murine cell lines derived from a very specific tumor that appears in the gonads of mice: the so-called ‘teratocarcinoma'. In the 1970s, a rapidly developing new research field emerged from this conjunction: the widespread use of then so-called teratocarcinoma *stem* cells as promising models for the study of embryogenesis *as well as* carcinogenesis. Their material properties shaped the concept of an *embryonic* stem cell because they became an implicit reference model for materially identifying those cell cultures that were isolated directly from the developing embryo and which were named *embryonic stem cells* not earlier than 1981. Finally, the conceptual shifts of the notion of a “stem cell” (that were related to these developments) will be discussed against a broader historical context that goes back to the late 19th century when the term “stem cell” was coined.

Macromolecules and Molecular Biology (submitted papers)

Rosalind franklin and the DNA double helix: historiographical accounts
Silva Marcos, University State of Londrina, Brazil

The history of the model for DNA, proposed in 1953 by Watson and Crick, has deserved by the historians an attention in what concerns to the experimental work of Rosalind Franklin with x-ray diffraction of DNA. Since that this work has provided the fundamental empirical evidences to the building of the model, is questioned why Watson and Crick weren't very excited with Rosalind's participation. To Watson, she wouldn't have any theoretical keen to the DNA helical representation; while to Crick, Rosalind was not a very imaginative scientist, and her methodological choices blocked her from trying to discover something about the DNA's. However, some biology historians didn't accept this treatment and questioned Crick and Watson's considerations from three distinctive argumentative lines. The three arguments are emphatic about Rosalind's contributions to the DNA's *structure*. However, this was not the only problem concerning to the DNA, given that the DNA deserved more than just a treatment about its structure, but also about its genetic *function*. Thus, I have as a purpose to argue that on the opposite of what happened to the problem to the DNA's structure, there was not a such dispute regarding to the problem about the DNA's function, since Rosalind didn't share with to Watson and Crick, any interest on the implication of DNA to genetics.

Molecules in Biology Before Molecular Biology
Liu Daniel, University of Wisconsin-Madison, USA

Since the 1970s *molecular biology* been an umbrella term to describe a set of techniques and core ontologies for studying genes and proteins, holding both kinds of objects as both three-dimensional objects whose functions are largely determined by a one-dimensional code. However, Warren Weaver in 1938 did not originally use the term “molecular biology” only in relation to genetics and protein synthesis. This paper will argue that by 1938 many biologists and biochemists were quietly set on “molecularizing” the cell and its functions, well before the blockbuster discoveries of the structures of macromolecules in the 1950s. The cytologists, plant physiologists, and general physiologists who began exploring molecular structures did so with firmly biological concerns for explaining the *aggregate* structures and functions of living cells and protoplasm. Such a perspective came directly from biology's wholesale adoption of colloid physical chemistry in the 1920s. Rather than an immediate “overthrow” of colloid chemistry some time during the Second World War, the newer ontology of biomolecules and repeated monomers complemented the descriptive language of colloid chemistry up through the 1950s. However, as techniques for examining cellular structures became finer and more sophisticated, cell studies split into detailed research on individual parts — mitochondria, cell cell wall, membrane structure — at the expense of understanding cell structure as a whole.

Rendering the dynamic static: examining how x-ray crystallography constructs investigation into protein function
Gandier Julie-Anne, University of Toronto, Canada

In this paper I will examine the values and thought patterns embodied in the practices of x-ray crystallography and the ways this imaging method constructs a ‘static' approach to protein functions.

In the late 1950s, X-ray crystallography revolutionized the way in which we visualize biological macromolecules. It allowed us to resolve and construct the image of the complex irregular structures of proteins captured within a crystal. This approach continues to influence our understanding of protein function and interaction fueling drug discovery. These crystal structure representations, however, construct a very specific concept of proteins. They encourage us to view proteins as static, rather than as the dynamic macromolecules they often appear in solution.

Specialists in more applied fields, such as chemical engineering, often treat these models as a black box, relying on the positions of the atoms in the model to investigate and/or engineer function. These structures, however, are visualizations of average positions and their 'static' appearance is an artifact of the technology. This project explores the values embedded in imaging technology that help shape the discourse of protein function in the wider scientific context. I will examine how the "static" methods of X-ray crystallography have shaped subsequent interpretations of what a protein is by addressing 1) how it has changed the way structural biologists interpret and resolve the spectrums produced to obtain a protein structure; 2) how these models are then applied not only by structural biologists but by the scientific and engineering community at large.

Making Modern Developmental Biology

From Embryology to Developmental Biology: The Diversification of a Biological Field.

Dietrich Michael, Dartmouth College, USA
Crowe Nathan, Arizona State University, USA

Embryology and Developmental Biology: Is there a difference between the two? Developmental biology gives the impression of encompassing more than simply the study of embryos; however many problems such as limb regeneration have been studied by embryologists for decades before the term developmental biology became fashionable in the 1950s. Historians Tim Horder and Paul Weindling propose that around the time of the Second World War the study of development underwent a transformative change from a narrow set of issues associated with embryogenesis and experimental embryology to a much more diverse set of topics and issues associated with process of development and so called developmental biology. Richard Burian and Denis Thieffry described the transition in terms of the integration of molecular biology into the traditional study of embryos. Jane Oppenhiemer rooted this transformation in late 1930s, where Donald Brown claims that developmental biology was an "intellectual backwater" until the full integration of molecular biology in the 1980s. We seek to paint a new picture of the transition of embryology into developmental biology with a much broader canvas. Using the surveys of worldwide embryological research conducted for the General Embryological Information Service from 1950 to 1963, we will provide a description of the how topics of research identified as embryology and developmental biology by practitioners in the field changed in the post-war period.

Molecularising mammalian development: gene transfer, recombinant networks and the making of transgenic mice

Myelnikov Dmitriy, University of Cambridge, UK

Knowledge of development was increasingly molecularised in the 1980s, with specific genes, RNAs and proteins invoked to explain the progression from fertilized egg to complex organism. Though reconstructed in part for the Drosophila and C. elegans communities, this historical shift remains otherwise largely obscure. The case of genetically modified ('transgenic') mice, one of the earliest kinds of genetic engineering in higher organisms, illustrates the exchanges and boundary crossings by which molecular biologists expanded into higher organisms and developmental biologists increasingly exploited molecular tools. This talk will explore how in the late 1970s, scientists from five different laboratories in the USA and Europe, driven by different questions, independently combined the practices and agendas of mouse developmental biology and gene transfer research to produce a new kind of animal technology. The earliest attempts had relied on viruses and even the acknowledged successes were achieved before the techniques of recombinant DNA were widely disseminated or standardised; there was no 'bandwagon' yet. However, as I will argue, the infrastructure and research questions born out of this new set of tools made the required exchanges more straightforward and advantageous to all. The key players had access to a small network of academic centres where new genes were being purified, introduced into cells and exchanged. By analysing cross-disciplinary collaborations, the talk seeks a more nuanced account of the role of recombinant DNA in the 'molecularisation' of developmental biology'.

Communicating Reproductive Biology: Claims to Human In Vitro Fertilization

Hopwood Nick, University of Cambridge, UK

The 2010 Nobel Prize in Physiology or Medicine recognized the achievement of a human birth following in vitro fertilization (IVF) as one of the most significant innovations of the reproductive sciences. Now more than ever, the dominant histories trace a ‘path to IVF' culminating in the work of the British team that delivered Louise Brown in 1978. Yet though she made global news as the first ‘test-tube baby', she was far from the first to be announced. Repeated claims between the 1940s and the 1970s provide an opportunity to explore communication in a prominent and controversial science. How did researchers seek to convince their colleagues that they had done what they claimed, and that this was new, significant and should be allowed? How did reproductive scientists set and revise criteria as they assessed claims? What interplay was there between publication in media ranging from specialist journals to newspapers?

Mechanistic Explanations A (submitted papers)

A Salmonian Approach to Mechanistic Explanations

Roe Sarah, University of California, USA

Mechanistic explanations are abundant throughout the biological sciences. Here, I sketch a new approach to mechanistic explanation. By utilizing and enhancing Wesley Salmon's work, I argue that mechanisms are just causal processes propagating through space and time that may intersect with other causal processes. This new way of understanding mechanistic explanation may better handle some types of biological phenomena. In an attempt to illustrate this, I offer a case study in breast cancer research. Drawing from new research, I show how scientists are utilizing findings in porcine lactation to explain breast cancers within the human population. I argue that they are indeed utilizing Salmonian mechanisms to provide a biological explanation for breast cancer. I conclude that a Salmonian approach to mechanistic explanations fits well with scientific practice, and may provide a much needed explanatory pathway for some types of biological phenomenon.

Abstract Models, Generic Mechanisms

Stinson Catherine, University of Tübingen, Germany

Abstraction is necessary in modeling, for epistemic as well as practical reasons. A model that abstracts the right things away is better than one that shows irrelevant details. Too much detail obscures the features of the model that are most important. The literature on mechanistic explanation stemming from Machamer, Darden & Craver (2000) reflects this in its emphasis on mechanism schemas. Truncated, abstract representations are what scientists are usually interested in.

Given the central role of schemas, it is curious that when at least M and C of MDC turn to talking about explanation, the details of the mechanism are suddenly very important. Craver (2006) emphasizes that ‘how-actually' explanations have to get the details of the mechanism right, and argues that generalizations do not explain. Bogen (2005), who convinced Machamer (2004) to drop regularity of functioning from the MDC definition of mechanism, further

entrenched the view that singular causal chains are what should count as explanations.
My aim is to resolve this tension between the necessity of abstraction in mechanistic modeling, and the constraint that mechanistic explanations should reveal the actual causes that bring about explananda. I introduce generic mechanisms, defined as things in the world qua a type which the fully-elaborated mechanism instantiates. Generic mechanisms are in-the-world counterparts to mechanism schemas. They abstract away unnecessary details from instantiated mechanisms, just as schemas do for representations of mechanisms. This allows for general explanations that are still 'how-actually' explanations. I illustrate this with examples from neuroscience.

Understanding the "machine metaphor": organizational similarities and differences between machines and living beings

Marques Victor, Pontificia Universidade Católica do Rio GRande do Sul, Brazil
Brito Carlos, Universidade Federal do Ceará, Brazil

The aim of this paper is to analyze the concepts of organism and machine, and identify if there are irreconcilable incompatibilities between them. To put aside superficial differences, we investigate them as natural systems, in order to highlight possible similarities and differences in the constitution, organization and functional dynamics. In doing so, a certain parallel becomes obvious: as physical entities, both organisms and machines are heterogeneous systems, internally differentiated, and composed of a large number of microscopic particles, which are arranged in functional components, thereby allowing a description of behavior based on general notions such as operation and coordination. As Robert Rosen points out, what machines and organisms have in common is that they are material systems that admit relational description, and that is precisely why Maturana and Varela define organisms as "autopoietic machines".
Howard Pattee famously utilized the concept of 'constraint' to base the relational representation of dynamical systems. More recently, authors such as Deacon, Moreno and Mossio are reclaiming the idea of constraint to explain the specificity of life itself. It is at this level of abstraction that an essential difference between organisms and machines appears: while the organization of the machine is defined from the outside, with externally enforced constraints, in organisms just the opposite happens, for their constraints are permanently established and regenerated as a result of the very dynamics of the system - there is not, as in the first case, a split between the system´s activity and its own production process.

Conflicting Results for Natural Selection and the NPM

Matthews Lucas, University of Utah, USA

Natural selection offers prima facie conflicting results for the New Philosophy of Mechanism (NPM). On one hand, the NPM is often held to an accurate representation of actual scientific practice. Thus Robert Skipper and Roberta Millstein (2005) challenge the NPM on the grounds that it fails to accommodate natural selection, which biologists refer to as a mechanism. On the other hand, the NPM is often held to a claim about the value of mechanistic methodology to successful scientific practice, such as the search for and discovery of mechanisms. Thus, Millstein (2006) appears to strengthen the NPM by arguing that "finding a mechanism is a crucial piece of the natural selection story." To exacerbate the situation, Skipper and Millstein's (2005) contribution has sparked an ongoin debate – the so-called, 'Natural Selection as a Mechanism' debate, which sets the stakes high for an assessment of the NPM against natural selection (Robert Skipper and Roberta Millstein, 2005; Benjamin Barros, 2008; Phyllis McKay Illari and Jon Williamson, 2010; Joyce Havstad, 2011; Jon Matthewson and Bret Calcott, 2011; and Daniel J. Nicholson, 2012). This paper resolves the conflict and argues that the two contributions bear on distinct NPM theses (developed by Arnon Levy, 2012). I argue (1) that Skipper and Millstein (2005) most evidently problematize Causal Mechanism (CM), a metaphysical thesis regarding the causal structure of the natural world and (2) Millstein (2006) bolsters Explanatory Mechanism (EM) and Strategic Mechanism (SM), which represent descriptive and prescriptive theses regarding actual scientific practice. The philosophical upshot recommends an informed perspective for future assessments of the NPM against novel cases of scientific explanation.

Mechanistic Explanations B (submitted papers)

Mechanistic Explanation & Evo-Devo

Mc Manus Fabrizzio, National Autonomous University of Mexico, Mexico

It has been argued that *Mechanistic Explanation sensu* MDC (2000, see also Craver, 2007), although notoriously important in many areas of biology, faces two significant limitations: on the one hand, it fails to characterize what evolutionary biologists call *evolutionary mechanisms* (Skipper and Millstein, 2005) and, on the other hand, it is too restrictive when applied to *developmental mechanisms* (Mc Manus, 2012). Insofar these criticisms are accepted, this would imply that *Evolutionary Developmental Biology* will constitute a dual challenge for this approach. It might even be that Evo-Devo cannot be integrated within the mosaic unity of neuroscience, at least not through an integration mediated by mechanisms, and so it would be a serious limitation on the scope of the entire mechanistic account. Some philosophers of biology have actually embraced this possibility and have sought to describe Evo-Devo as a *trading zone à la Galison* (Winther, forthcoming).

But Evolutionary Developmental biologists seem to consider developmental mechanisms central to their research in topics such as (i) constraints, (ii) the explanation of form, and (iii) considerations regarding homology and function, thus calling into question the idea that Evo-Devo is merely a trading zone in which mechanisms, homologies and evolutionary explanations only interact tangentially. In this talk I track the source of these deficiencies to the Cumminsean notion of function that underlies the Craverian understanding of mechanisms and advocate a different characterization of what mechanisms are in Evo-Devo, a characterization in which mechanisms can be homologous and so not entirely describable in Cumminseans terms.

Explanatory frameworks in molecular oncology: the case of the gene p53

Maugeri Paolo, European Institute of Oncology, Università degli Studi di Milano, Italy
Blasimme Alessandro, Faculté de Médecine Inserm, France
Germain Pierre-Luc, Università degli studi di Milano, European School of Molecular Medicine, Italy

What has been called the new mechanistic philosophy conceives of mechanisms as the main providers of biological explanation. This talk draws on the characterization of gene p53 in molecular oncology, to show that explaining a biological phenomenon (cancer, in our case) implies instead a dynamic interaction between themechanistic level—rendered at the appropriate degree of ontological resolution—and far more general explanatory tools that perform a fundamental epistemic role in the provision of biological explanations. We call such tools ‘‘explanatory frameworks''. They are called frameworks to stress their higher level of generality with respect to bare mechanisms; on the other hand, they are called explanatory because, as we show in this paper, their importance in explaining biological phenomena is not secondary with respect to mechanisms. The talk will illustrate how explanatory frameworks establish selective and local criteria of causal relevance that drive the search for, characterisation and usage of biological mechanisms. Furthermore, the talk will show that explanatory frameworks allow for changes of scientific perspective on the causalrelevance of mechanisms going beyond the account provided by the new mechanistic philosophy.

From Cyborg to Replicant: The Historical Transition from Mechanical Transplants to Digital Genetic Intervention. The Heart Case

Guevara-Casas Carlos, Escuela de Periodismo Carlos Septién García, Mexico

Since Descartes, the primary way to view the human body, and particularly the heart, has been mechanistically. In 1958, Kolf and Akutso placed an artificial heart inside of a dog, and Jack Steel coined the term *Bionic* to indicate the technological imitation of biological structures. Two years later in 1960, Manfred and Kline proposed the term *cyborg* to refer to the fusion of organic and mechanical parts.

At the same time a new perspective analyzing life in terms of the flow of information was emerging. This view came from Wiener, Shannon, Bigelow and Rosenblueth´s works in the early 1940s. The discovery of restriction enzymes in 1970, use of genetically modified cells in medicine, and the Human Genome Project (HGP) allowed for research into cardiac tissue regeneration with stem cells and genomic medicine.

There has been a transition from a macroscopic, mechanistic view of human body to a genetic, mechanistic view with linguistic and digital explanations. An example of new representation of organism is in the film Blade Runner (1982) based on the novel by Philip K. Dick (1968) *Do Androids Dream of Electric Sheep*? Dick's Androids seem to be mechanical, and in Scott's movie they are clearly genetic. These changes in perspective on the human body and heart indicate new ways of thinking about the human body that I explore in more detail in this presentation.

Statistical Learning as a Mechanism

Betzler Riana, University of Cambridge, UK

Philosophers of science have offered various definitions of mechanism, most of which derive from biological or neuroscientific roots. In this paper, I consider whether these definitions apply equally well to cognitive science -- and whether cognitive science is, as Abrahamsen and Bechtel state, “more than anything else, a pursuit of cognitive mechanisms” (“Phenomena and Mechanisms: Putting the Symbolic, Connectionist, and Dynamical Systems Debate in Broader Perspective.” In R. Stainton (Ed.) *Contemporary Debates in Cognitive Science,* 2006). I examine this question by looking at the example of statistical learning, which has been called a domain-general learning mechanism in the cognitive scientific literature. Though the term “statistical learning” applies to several broadly related attempts to account for the “problem of inference” in human and machine learning, I focus in this paper on one specific instance of statistical learning -- that thought to be involved in parsing continuous perceptual input into individuated units (e.g. Saffran, Aslin, & Newport, *Science*, 1996). This focus allows me to hone in on the cognitive scientific level of research rather than more recent attempts to fill in the neuroscientific details of this process. I evaluate the statistical learning “mechanism” under four conceptions of mechanism in the philosophy of science -- those of William Bechtel, Stuart Glennan, Jim Woodward, and Carl Craver. Ultimately, I argue that the concept of mechanism described by these philosophers of science does not translate directly from neuroscience and biology to cognitive science but that it nonetheless provides a useful construct that facilitates the process of cognitive scientific research.

Metaphors and Models in Evolutionary Biology

Why is Metaphor like a Model? Epistemic and Cognitive Uses of Scientific Metaphors

Lamm Ehud, Tel Aviv University, Israel

Simply put, modeling involves studying one system - primarily via the ability to manipulate it – as a means for studying another. I argue that manipulability is the hallmark of models, which are meant to provide a way for studying modeled systems via the manipulations of their models rather than by manipulating the original system. Manipulability requires that the model have an organized, ideally well-specified, articulated fine structure. Literary metaphors, as well as scientific metaphors invoked merely to rhetorical effect, need not exhibit the structure required in order to support internal manipulability. But sometimes they do. I will explore several rich metaphors, in science and literature, particularly those used by Richard Goldschmidt to articulate his theory of the gene, and argue that they are best understood as models. Viewing them as models provides the best way to understand the function of the metaphors. Seeing what viewing them as models entails helps adjudicate differing accounts of what models are. In particular, similarity between a model and the modeled system is required by some accounts of scientific models, but the notion is fraught with difficulties (Goodman; Suarez). Metaphors are typically too ambiguous and open-ended to establish a robust similarity relation. On the alternative account I endorse the relationship between model and system is reflected, or even constituted, by the manipulations the model permits. This relationship is one of exemplification (cf. Elgin). My account explains why metaphors, even those appropriately understood as models, are typically only weak models.

Metaphor and the Evolved Mind: The Case of Darwin’s “Tree of Life”
Priest Greg, Stanford University, USA

From “natural selection” to the “war of nature” to the “tree of life,” Darwin's *On the Origin of Species* teems with metaphors. There are, no doubt, many reasons Darwin was so free with metaphorical figures in the *Origin*. They served a rhetorical function, assisting him to persuade his audience of the truth of his theory. In many cases, the metaphors had been central to how Darwin had developed his own ideas about evolutionary change, and so came naturally to hand as he sought to articulate his ideas. Without denying the importance of these uses of metaphor, I want to explore a different use to which Darwin put metaphor in the *Origin*. Darwin believed that human mental capacities were evolved traits. In consequence, the human mind is not a perfect engine of deductive logic or inductive inference but an evolved bodily system with characteristic capacities and infirmities. Just as human eyes can perceive certain wavelengths of light and not others, human minds are good at dealing with and understanding certain kinds of facts about the world but are apt to misperceive others. Darwin believed that the limitations and weaknesses in evolved human mental capacities make complete comprehension of evolutionary processes unachievable. In this paper, I explore how Darwin's understood those limitations and weaknesses, and how he deployed his metaphor of the “tree of life” to provide his audience with what he believed to be a limited and imperfect, and yet meaningful, understanding of evolutionary processes.

Microbes as model systems

Beyond Tractability: Microbes as Model Systems
O’Malley Maureen, University of Sydney, Australia

Tractability is a good reason to use microbes as model systems in evolutionary and ecological experiments. It is not the only reason, however, and I will explore in this talk other reasons – several of which should be of particular relevance to philosophers. Microbes are the most numerous, ancient and physiologically diverse forms of life on the Earth. The ways in which they survive, reproduce and evolve are multiplicitous. Often, when philosophers discuss general properties of living systems, they begin with multicellular organisms and work backwards from them, with the consequence that large organisms become the exemplars of units of reproduction, selection, evolution and biodiversity. I will take three such cases and compare what happens when the analysis starts with microbes against what happens when it starts with macrorganisms (specifically animals). The three cases are the notion of organism (including modes of reproduction), multicellularity (with relevance for developmental processes), and evolutionary transitions (specifically the evolution of eukaryotic characteristics such as sex). In all three cases, I will suggest philosophers at least are better off starting with microrganismal consortia than they are starting with macrorganismal ‘individuals'.

What microbes can model
Bolker Jessica, University of New Hampshire, USA

We can learn much from microbial models. They are a powerful tool for studying evolution and ecology, because they enable studies of large populations over thousands of generations, and correlation of changes in ecological roles, individual phenotypes, and genomes. Microbes can model developmental phenomena that occur at cellular and intercellular levels within more complex organisms. Microbes can be selected or engineered to exhibit specific behaviors or functions that take place naturally in embryos; these phenomena can then be analyzed in a simpler, more accessible context. Finally, *in vitro* populations that represent naturally-occurring microbial communities (especially those of clinical significance) offer a substrate for experiments that enhance understanding of natural microbiota. What we learn about these populations in the laboratory can inform clinical strategies to monitor and manipulate microbial communities with key roles in health and disease. Each of these cases highlights specific questions about how we use models in different contexts; microbial models thus offer tractable, powerful systems not only for biological research, but also for framing epistemological issues common to all model-based science. One is the balance between tractability and representation: although the simplicity of microbial models makes them tractable, it constrains their ability to represent the full complexity of larger-scale organisms and ecosystems. Microbes' predominantly clonal reproduction offers practical advantages, but limits their power to model evolutionary processes that entail sexual reproduction. Exploring the tradeoffs between tractability and representation in microbial systems can yield generalizable insights: microbes thus serve as models for epistemological as well as biological research.

Experimental Evolution of Multicellularity
Travisano Michael, University of Minnesota, USA
Ratcliff William, University of Minnesota, USA

The evolution of development (evo-devo) has been the focus of intense interest for over three decades, and important conceptual, theoretical and empirical advances have been made. These advances, however, have not been based upon direct observation of the evolution of development, because the appropriate model systems were absent. Experimental evolution and new appreciation of microbial model systems now provide tools to investigate the evolution of development as it occurs. An abundance of new studies into evo-devo using microbial selection experiments are underway. Using Baker's yeast, we are observing rapid evolution of complex development during an evolutionary transition from a single celled organism to a multicellular form. The evolution of juvenile and adult life history stages, stochastic differentiation, changes in cell shape and increased hydrodynamic morphologies are all readily observed within a single year of selection. These results challenge current thinking on the tempo and mode of the evolution: developmental complexity can easily evolve under appropriate conditions.

How general is social evolution?
Velicer Gregory, Eldgenössische Technische Hochschule Zürich, Switzerland

Social microbes have been promoted in recent years as powerful model systems for empirical investigations into basic principles of social evolution. Microbes exhibit many traits that are demonstrably or putatively social in character and which range in complexity from the simple production of individual extracellular compounds that act as public goods (or semi-private goods in the case of compounds that remain attached to the producing cell's surface) to genetically and behaviorally complex traits such as aggregative multicellular fruiting body development. The reach and limits of microbes as models for social evolution in animals will be considered, particularly with reference to the myxobacteria, which exhibit some of the most sophisticated cooperative traits found among prokaryotes.

Models & Mechanisms: Extending the Framework

How-kind-of actually Models

Glennan Stuart, Konrad Lorenz Institute for Evolution and Cognition Research & Butler University, USA

It is a common practice in the biological sciences to study the behavior of mathematical models and computer simulations that contain highly unrealistic assumptions about the system that the model is supposed to represent. Can such models explain? A common suggestion is that such models should be thought of as how-possibly models. If, however, explanation requires that explanantia refer to the actual causes of some phenomenon, then such models cannot explain unless they bear some actual resemblance to the explanatory target. This means, to the extent that such models can be explanatory, they must be how-kind-of-actually models. I shall illustrate the use of such models by reference to agent-based models in ecology.

Causal Order & Two Kinds of Robustness

Levy Arnon, Van Leer Institute, Jerusalem, Israel

Machine analogies play a prominent part in proximate biology. But their specific content is often left under-specified and so is the relation between machines and mechanisms. I suggest an account of what makes a system machine-like, relying on a notion of causal order. Orderly systems have parts with distinctive and interdependent roles, and their internal dynamics are relatively predictable. On this way of thinking, some mechanisms are more machine-like than others, because they exhibit more underlying order. Machine-like systems are more amenable to decompositional explanation and to related cognitive-epistemic methods.

Thinking in terms of causal orderliness isn't only of conceptual significance. It can also help us explore empirical questions. I will illustrate this by looking at one important attribute of biological systems – robustness. Two kinds of robust behavior will be distinguished: one consisting of orderly causal interactions, the other disorderly. Orderly robustness utilizes feedback loops and certain modes of backup. Disorderly robustness consists in aggregative stability, arising from numerous interactions amongst stochastically independent elements. There are reasons to expect these two forms of robustness to differ in their characteristic developmental timing and in their evolutionary potential.

How mechanisms work, how they change, and how the way they work affects the way they change

Calcott Brett, Austalian National University, Australia

Work on mechanistic explanation in philosophy has focused primarily on proximate biology: explaining how the parts, processes, and organisation of a biological mechanism produce some phenomena of interest. A related project, which has received far less attention, is examining explanations for how mechanisms change over time. Such explanations appear frequently in evolutionary developmental biology and evolutionary systems biology. I show how a key tool for exploring the structure of such proximate mechanisms—the notion of difference-making—can be equally applied to understanding change over time in mechanisms. I then use a model of evolution in gene regulatory networks to demonstrate how paying attention to difference-making both at-a-time and over-time provides a strategy for investigating the evolution of evolvability.

Mechanisms, Models, and Explanatory Autonomy
Polger Thomas, University of Cincinnati, USA

In this paper I argue that, contra initial reports, mechanistic modeling as an explanatory strategy in the mind and brain sciences is not good news for advocates of the explanatory autonomy of those sciences. The reason is that the autonomy-enabling features of mechanistic models arise only in those that lack other features important to understanding the mind and brain sciences.

It is commonly thought that mechanistic explanation is more descriptively adequate to the mind and brain sciences than the standard nomological approaches that have dominated thinking about the special sciences since the early 1970s. But at the same time, the mechanistic approach is widely interpreted as also delivering some of best features of the nomological approach. In particular, it is claimed that explanation in terms of mechanisms secures the multiple realizability of cognitive and psychological entities or regularities by neuroscientific entities or regularities. Consequently the strategy of mechanistic explanation is seen as vindicating the explanatory autonomy of the special sciences in general, and of the mind and cognitive sciences in particular.

The trouble for those who wish to defend the autonomy of the mind sciences on the basis of the mechanistic approach is that it is entirely unclear whether the apparent autonomy arises because of the multiple realizability of mechanisms, or because mechanistic models tend to be highly idealized (Klein; Haug; Piccinini and Craver). And this is a problem because idealization tends to undermine other more realist disiderata that are valued by philosophers of the mind and brain sciences.

More About Darwin and Wallace A (submitted papers)

Evolution without Natural Selection: Darwin's Domain of the Useless
Robert Thomas, Université de Genève, Switzerland & University of Calabria, Italy

Darwin is often reduced to a single book, *On the Origin of Species*, and to its main thesis: descent with modification by means of natural selection. Such an emphasis on natural selection leaves aside several issues fruitfully treated by the naturalist. Animal behaviour is one of them. However, in both his manuscripts and his later works, such as *The Descent of Man* and *The Expression of the Emotions in Man and Animals*, Darwin develops a peculiar ethology based on anecdotes expressed in anthropomorphic terms. The study of Darwinian ethology makes appear a domain of the useless, in which the significance of non-adaptative and anti-adaptative structures and behaviours is recognised. Expressive movements, sexual and social behaviours are paradigmatic example of the domain of the useless. Far from being isolated phenomena, useless structures and behaviours have transformative power over the Darwinian transmutationism in general and over natural selection in particular: animals are complex beings and cannot be limited to their adaptive features; natural selection cannot be considered as an active, creative principle but has to be redefined as being purely negative, eliminative. In short, the study of the domain of the useless leads to recognise that Darwinian ethology is not conformed to the realist-Cartesian paradigm still applied in mainstream ethology and makes appear the necessity of an evaluation of the centrality of natural selection in the context of the Darwinian transmutationism.

Modus Darwin Reconsidered
Helgeson Casey, University of Wisconsin, USA

Modus Darwin is the name given by Elliott Sober to a form of argument that Sober attributes to

Darwin in the *Origin of Species*, and to subsequent evolutionary biologists who have reasoned in the same way. In short, the argument form goes: ‘Similarity, ergo common ancestry’ (i.e., species X and Y are similar, therefore they evolved from a common ancestor). In the present paper I review and critique Sober’s analysis of Darwin's reasoning. Sober’s project is part exegesis, part epistemology: How did Darwin argue?, and Was it a good argument? In this paper I bracket the exegesis and focus on the epistemology. I argue that modus Darwin (as Sober understands it) has serious limitations that make the argument form unsuited for supporting Darwin’s conclusions. In short, my criticism is that in rigorously spelling out ‘similarity’, Sober employs a system of character correspondences that, at worst (1) begs the question by presupposing common ancestry, and at best (2) registers ‘similarity’ in a way that illegitimately biases the subsequent inference in favor of shared ancestry. Thus, either Darwin argued badly (he gave bad reasons for a true conclusion), or he didn’t use modus Darwin.

More About Darwin and Wallace B (submitted papers)

Hair-raising observations: Darwin and Crichton Browne on piloerection and insanity

Adriaens Pieter, University of Leuven, Belgium
Pearn Alison, University of Cambridge, UK

One of the main aims of Darwin's *Expression of the Emotions* was to document and to detail the many commonalities between humans and other animals in expressing emotions. Examples of such commonalities include the raising of the eyebrows in surprise, the baring of the teeth in rage, and the erection of the hair (piloerection) in fear and anger. In this paper I trace back Darwin's ideas on piloerection to his correspondence with the young psychiatrist James Crichton Browne. More particularly, I reveal how Darwin's initial doubts about the analogy between erection of the hair in animals and in psychiatric patients were eased when studying a photograph of one of Crichton Browne's patients, Ruth Lockwood, whose mental condition was supposed to reveal itself in the bristling of her hair. Remarkably, very few commentators have challenged the analogy in question, even though a) Darwin's evidence for it was at best anecdotal, and b) his correspondence shows that he lost his belief in the documentary value of psychiatric photography soon after the publication of *Expression*. I conclude with some general observations about the role of psychiatric photography in the early development of evolutionary theory.

Darwin and the decline of Ancient Greece: a problem or a shining example for his theory?

Lefkaditou Ageliki, University of Leeds, UK

In *The Descent of Man* (1871), Darwin devoted several pages to discussing the effects of natural selection on civilized nations. By developing a rather complex argument, he concluded that in the cases such as that of ancient Greeks “continued progress depends in a subordinate degree on natural selection” and went on to offer several reasons for the apparent paradox of a superior civilization going into decline. Darwin's discussion reaffirmed his conviction in natural selection as a force acting only conditionally but is also telling with respect to the Victorian fascination with Ancient Greece. The *Descent* passage was a direct response to W.R. Greg's 1868 article “On the Failure of ‘Natural Selection’ in the Case of Man” but the Greek case had been puzzling him for quite a long time, as his correspondence with Charles Lyell reveals. This paper will try to explore Darwin's views of those “wonderful people”, and the persistence of the classical heritage more generally, with the help of his notes and letters to Lyell, Galton and Greg.

Charles Darwin as Historical Methodologist; The Role of Scottish Conjectural History in the Origin of Species

Herter Cosima, University of Minnesota, USA

The importance typically granted to the Scottish literati on Charles Darwin's work has been based primarily on the assessment of their works in political economics. But this does not convey the full magnitude of their influence. I will argue that the Scottish philosophes need to be regarded first and foremost as *historians* with regard to how their work impacted Darwin when he wrote the *Origin of Species*, and that it is from their works that Darwin derived a model for his own historiographical methodology. This also suggests a new way to think of Malthus' influence as not simply a political economist, but as an historian. Furthermore, it suggests a new source of uniformitarian methodology (especially in the actualist sense) championed by Lyell. The uniformitarianism stressed by Lyell was very much in line with scientific principles for understanding historical development that were developed and advocated by the Scottish Conjectural historians. I view Malthus' work as a continuation and clarification of the Scots' civil histories; indeed, the computational insight Darwin earned from Malthus gave deeper substantiation to the scientific thrust Darwin gained from Scottish historical principles. I will argue that Scottish Enlightenment historiography is the strong thread that weaves together the influences of both the geologists and Malthus. I hope to demonstrate that seeing Darwin's historiography as drawn from Scottish speculative history offers us some insight into the rhetorical rationale he used to develop his "long argument," and the nature of his historiographical methodology more generally.

More About Darwin and Wallace C (submitted papers)

The Charles Darwin-Wyville Thomson Debate: deep sea crinoids, scientific evidence, and the adjudication of Darwinian natural selection

Alaniz Rodolfo, University of California, USA

By the late-nineteenth century, the deep ocean floor had become "Darwin's laboratory," a place to test the "direct action of external conditions on organisms." According to dominant Victorian marine biology, the deep sea was an eternal, unchanging biogeographical space. There, and only there, could naturalists investigate how organisms evolved without the influence of changing environmental factors. Consequently, marine invertebrate specimens from the ocean floor played a large role in the formation of evolutionary theory throughout the nineteenth century. This presentation explores the 1880s dispute between Charles Darwin and Sir Wyville Thomson regarding natural selection as the culmination of a half-century of conflict over deep sea invertebrates and biological evidence. Marine invertebrates, according to some naturalists, were uniquely suited to the philosophical study of organismal complexity. Other naturalists focused on the much-anticipated discovery of Darwin's "living fossil" dredged from the sea floor as proof through consilience. Sir Wyville Thomson, on the other hand, was certain that his deep sea crinoids offered no proof of evolution by natural selection, thereby offering a serious challenge to Darwin's theory. As naturalists fought over how to apply the valuable deep sea specimens to the theory of natural selection, the crinoids themselves were also squabbled over as physical objects to be collected, routed, and eventually controlled. The use of biological specimens in the Darwin-Thomson debate illustrates the complex interactions between expertise, evidence, and rare natural objects in the history of Darwinian evolution.

From The Malay Archipelago: Alfred Russell Wallace's Scientific Contributions

Matykiewicz Emily, Florida State University, USA

This paper is a contribution to our understanding of Alfred Russell Wallace, for whom this year marks the 100th anniversary of his death. I seek to explore Wallace's scientific contributions that resulted from his eight years' residence in the Malay Archipelago and his impact on theoretical biology. Wallace's enthusiasm for natural science and cheerful fearlessness made him well suited to exploring the equatorial archipelago. His field notes and specimen collection alone added monumental data to the understanding of our natural world, the sum total of his Malay Archipelago collection is 125,660 specimens. Focusing on Wallace's most notable contributions to the development of biological theory, including his letter to Charles Darwin on natural selection and his influence on the study of biogeography, I argue that his time in this fertile region yielded depth and breadth of knowledge that has catalyzed sustained scientific advancement in theoretical biology, proving Wallace's worth in the history of science.

Contribution to the methodology of reception studies: considerations regarding the study of Darwin in Portugal (1910-1974)

Fonseca Pedro, Pereira Ana, Pita João all at University of Coimbra, Portugal

The presentation deals with methodological issues concerning reception studies. It is largely based on the four-year Ph.D. research programme on the reception of Charles Darwin (1809-1882) in Portugal between 1910 and 1974 carried out by Pedro Ricardo Fonseca at the University of Coimbra, under the supervision of Ana Leonor Pereira and João Rui Pita. The main objective of the cited research was to evaluate the influence of Darwin's biological theory upon Portuguese biologists. Thus, we carried out an extensive analysis of the scientific production of some of Portugal's most prominent 20th century botanists and zoologists. However, to obtain a more comprehensive understanding of the influence of Darwin in Portugal during most of the 20th century, other research lines had to be pursued. For example, we analyzed all of the Portuguese translations of Darwin's works and gathered relevant information about the translators and publishers. This effort was complemented by the identification of alternative sources through which Portuguese readers could access Darwin's ideas. In order to better understand how Darwin was (literally) "viewed" in Portugal, we did a historical-iconographic study of Darwin in Portugal. We also started a large-scale bibliometric study of Darwin's works available in Portuguese public libraries. Besides its more quantitative component, this study also informs us of the type of work that was most available (English original editions, Portuguese translations, other foreign translations) and of the year that a certain work became available at a certain library.

The Nature of Cellular Complexity (Interdisciplinary session)

Mechanicism vs. Organicism: Two Views of the Cell

Nicholson Daniel, Tel Aviv University, Israel

In accordance with the mechanicist tradition in experimental biology (inaugurated by Descartes in the seventeenth century), it has become customary to regard living systems as intricate pieces of machinery, different to man-made machines only in terms of their superior complexity. Today, this mechanicist ontology serves to justify the belief in the sufficiency of explanatory reductionism in molecular biology, and it also lies at the heart of the theoretical appeal to design charts and circuit diagrams in systems and synthetic biology. In cell biology, mechanicist conceptions have been buttressed by the traditional methodologies used. Much of what we know about cells was derived from static snapshots of fixed or stained biological structures generated by conventional microscopical techniques. The interpretation of these snapshots favoured an understanding of subcellular architecture in terms of clockworks and molecular machines. However, the introduction of novel methodologies, such as fluorescence-based *in vivo* imaging techniques, is leading to the accumulation of experimental data inconsistent with the machine conception of the cell. In this talk I argue that a new view of the cell is emerging which calls into question our intuitive adherence to mechanicist tenets like determinism, reductionism, and the reliance on design as an explanatory principle. This new view of the cell requires us to adopt an alternative ontology of living systems, such as organicism, capable of making theoretical sense of the self-organizing nature of the cell and the inherent stochasticity and non-linearity of subcellular processes.

The cell: between constraints and stochasticity
Kupiec Jean-Jacques, Ecole normale supérieure, France

Since the beginning of molecular biology, it has been postulated that genetic information is transferred to proteins via their tri-dimensional structure, allowing them to interact specifically with other molecules. Molecular specific interactions are in turn thought to be the basis for the formation of molecular networks (protein, gene or metabolic networks) underlying cellular processes. In contrast to this prediction, data obtained over the last forty years show that interactions between biological molecules lack specificity and are immensely varied, with one molecule able to interact with a large number of partner molecules. As a consequence, instead of forming specific networks, molecular interactions are subject to large combinatorial interaction possibilities and to extensive stochastic variability. Taking this aspect into account modifies our understanding of biological organization. Molecular networks are not the cause but the result of cellular processes because these latter restrict the stochastic variability of molecular interactions. The making up of an organism, instead of being a simple bottom-top process in which information flows from genes to phenotypes, is both a bottom-top and top-bottom process. Genes provide proteins, but their stochastic interactions are sorted by selective constraints arising from the cell and multi cellular structures.

Demonstrated, predictable, information-rich: why biologists should not be afraid of stochasticity in gene expression
Gandrillon Olivier, Université Lyon 1, France

Stochastic gene expression (SGE) is a phenomenon receiving an ever-growing attention because it exerts a strong influence on many important normal or pathological processes. SGE means that in a population of clonal cells (all harboring the same genome) placed in the same environment, SGE causes a visible and measurable heterogeneity in the patterns of gene expression. This has now been clearly demonstrated in a large number of experimental settings. The controversy therefore now shifts in two directions:

- Since noise is frequently (and wrongly) equated to unpredictability, biologists wonder how " order emerges from chaos".
- Two opposing view on the biological role of noise (including SGE) are in the balance: for some, noise has to be suppressed as much as possible for it is a nuisance to the cell or, for others, noise can be beneficial since it can be used by organisms, for example during the commitment of cells to different differentiation pathways.

We would like to propose that what can actually be seen at the cellular level is the microscopic molecular noise that is " filtered out " (or regulated) by macroscopic structures that have been selected by evolution, precisely because of their ability to "encapsulate" or regulate the amount of SGE, and to make it beneficial for living organisms. This makes SGE both predictable, and a very rich source of information regarding the biophysical processes at stake. This last part will be illustrated from a recent study where one deduced microscopic parameters from macroscopic measurements, with the use of a dedicated gene expression model.

The role of cell environment in controlling stochastic gene expression through the metabolism
Paldi Andras, Inserm, Ecole Pratique des Hautes Etudes, France

The fundamental question of how cell fate decisions are made is in the heart of stem cell biology.

According to the prevailing view in biology cell fate decision is considered as a coordinated change in gene expression patterns in response to external signals. However, the strictly deterministic model of cell differentiation is contradicted by experimental evidence (see J.J. Kupiec's talk for review and criticism of determinism). In addition, the strictly deterministic view fails to explain how the cell deals with the pervasive molecular fluctuations considered as a simple " noise ".

According to the alternative model fluctuations of gene expression play central role. It considers biological processes as fundamentally stochastic that are subjected to selective constraints. Whether a cell undergoes phenotypic differentiation or not is determined by the balance between the fluctuations and stabilizing constraints.

The living cell is an open thermodynamic system far from the equilibrium. A stable cellular phenotype is only possible if it can ensure the permanent energy flux essential for the cell's survival. As a consequence, if the energy flux is substantially modified by a change in the concentration of the metabolic substrates in the environment, the cell is expected to increase the fluctuations in gene expression and promote phenotypic change. Indeed, expression of new proteins capable to metabolize new substrates is the only way the cell can adapt to the environmental changes and restore the required flux of energy.

Here I show that this hypothesis is fully compatible with our present knowledge: the cellular metabolism can directly impact on the stochastic fluctuations of gene expression through well-known so-called epigenetic mechanisms. These chromatin-dependent biochemical reactions are tightly linked to the central metabolism and provide a mechanistic explanation of how the cell can modulate the level of fluctuations in response to environmental changes.

The Nature of Living Systems (submitted papers)

On minimal regulation in biological systems

Bich Leonardo & Moreno Alvaro, University of the Basque Country, Spain

The aim of this paper is to provide a theoretical model to address the issue of regulation in living systems, in particular in the context of the origins of life and of the characterization of proto andminimal living systems.

The appeal to the notion of regulation is widespread in biology. This property is usually ascribed to phenomena involved in the persistence of a living system, such as the passive or active compensation of internal and external perturbations, in strict relation to ideas like homeostasis, feedback and adaptation. Yet, this notion is still not well defined and very dissimilar types of phenomena are gathered under this label. In fact, regulative roles are usually ascribed to processes, components, and subsystems whose behaviors and contributions to the functioning of living systems are qualitatively different.

In our paper we provide a basic framework and a minimal set of requirements for regulation, based on the theory of biological autonomy. By characterizing regulation as an adaptive property - *the capability of a system to mediate the effect of a perturbation by acting on its own internal dynamics through modulation or selection between distinct available internal regimes* - we distinguish it from forms of stability (structural and dynamical) that, on the contrary, entail a passive response of the perturbed system and are shared by a wider class of natural systems. From this standpoint we argue that phenomena like feedback loops and homeostasis are characteristic of systems exhibiting dynamical stability and, therefore, are not necessarily equivalent with regulation.

The ontophylogenetics of J.-J. Kupiec. In between historicism and determinism of the surroundings

Gutierrez Privat José Carlos, Institut d'Études Politiques, France

Epigenetic phenomena constitute an interesting field of current biological research, since it forces us to reconsider the nature of certain mechanisms of life and to reformulate a biological philosophy. Precisely because this research postulates hereditary mechanisms independent of the genetic model (the transmission of a coded instruction), it rekindles the debate on biological determinism, the extension of Darwinism to microscopic phenomena, and, even more broadly, it allows us to consider the conceptual ground in which the division amongst a functional and evolutionist biology – following Michel Morange's distinction – could be overturned.

In this presentation, I will focus on discussing J.-J. Kupiec's ontophylogenetic theory which seeks to be both a new explanation of biological order and a new philosophical approach on the living thing. Kupiec puts forth an ontology in which the " being does not carry internal determination and is not active in itself. It constructs it 'here and now', in its confrontation of the world ". In opposition to interpretations which claim that order is imposed either " from above " (emergentism) or " from below " (genetics), he suggests an order that is historically constructed from the continuous confrontation with its surroundings.

My presentation will ask in which sense a being in confrontation with the world, can also be inactive in itself. In other words, can the historicism of the living thing be reduced to the history of the restrictions imposed by its surroundings? Furthermore, do we then risk postulating a new form of determinism?

The problem of time in theories of organic selforganization and self-maintenance

Güell Francisco, Universidad de Navarra, Spain

This paper aims to deal with a common problem underlying contemporary theories of the nature of living systems: the consideration of time as an extrinsic variable. Broadly speaking, most of these theories define the living being as a system engaged in a relationship with the environment and focus on activities of self-organization and/or self-maintenance. In other words, they all presuppose a concept of the living being as a stable structure that needs to maintain its stability.

However, it is necessary to realize that the living being is not a " structured reality " but a reality on its way to becoming structured. For this reason, time belongs intrinsically to the living being. From this perspective, the aforementioned theories all fall captive to their aprioristic understanding of life, and are limited by their own model. To correct this oversight, the paper introduces the constitutional paradigm as a new approach to the study of living processes, which takes as its starting point the living being as " structuring reality ".

New Directions in the Study of Inheritance

Pluralistic models of inheritance: toward the reform of a central concept in biology

Pontarotti Gaëlle, IHPST & Université Paris 1 Panthéon-Sorbonne, France

Inheritance refers both to the permanence of forms throughout generations (Jacob, 1970) and to the processes involved in the reliable recurrence of features within lineages (Mameli, 2005; Helantera & Uller, 2010). Although the science of heredity has been dominated by the genetic paradigm for decades, several critics recently asserted the replication and transmission of DNA, which appeared to be the support of heritable characters, are not the sole responsible for intergenerational resemblances, and claim for the integration of pluralistic or inclusive inheritance models in biology (Griffiths & Gray, 2004; Jablonka & Lamb, 2005; Danchin et al., 2011). I will argue the multiplication of resemblance channels may bring about a drastic conceptual reform regarding inheritance and its associated notions. After a brief presentation of non-genetic inheritance (ecological, epigenetic, cultural, etc.), I will show that pluralistic models betray the obsolescence of the *replication* of traits rhetoric and urge scientists to adopt that of *maintenance*. Given the mosaic nature of evolving entities, made up of elements not necessarily able to beget offspring and following unsynchronized recurrence cycles, I will then suggest an inclusive concept of inheritance should be coupled to the notion of *persistence* of entities and conceived, consequently, without reproduction or generations. The multidirectional transmission of many variants and the subsequent upheaval of genealogies may furthermore persuade scientists to consider *lineages* in terms of continuity of functional structures instead of genetic ones. Finally, the fickleness of non-genetic variants may sign the return, after the stable Mendelian inheritance, of a highly dynamic phenomenon.

Why culture evolves without being an inheritance system
Morin Olivier, Central European University, Hungary

Human cultures preserve a lot of information that would be lost if left to the care of biological mechanisms. Is this is enough to treat culture as an inheritance system? This talk argues against that view. Human minds often acquire cultural material in ways that are neither aimed at, nor conducive to, faithful replication. As a result, if we use the Price equation to describe cultural change, most of the change would be captured by the second term on the right hand-side of the equation - that describes changes due to transmission biases rather than selection. The omission of such biases may be the source of some frequent misunderstandings found in the 'gene-culture coevolution' literature. One of them concerns the 'Docility hypothesis' (as defended by Herbert Simon, Pete Richerson, Herbert Gintis, and others). It holds that cultural transmission produces a significant quantity of genuinely altruistic behaviors as a maladaptive by-product. We inherit from society a legacy of norms, know-hows and mores, most of them adaptive. Hidden among them is a set of altruistic norms, which compel us to sacrifice our own fitness for the sake of non-kin group members. This hypothesis stands or falls on the assumption that humans fail to select and transform what they learn from others - so much so that they incur maladaptive consequences. The inheritance metaphor carries many such implicit assumptions, that call for careful scrutiny.

New light on species essentialisms in biology

´Biological species´: a hybrid notion referring to a bundle of essences?
Longy Françoise, IHPST & Université Paris 1 Panthéon-Sorbonne, France

The syncretic essentialism of Devitt (2008) - the essence of biological species is made up of intrinsic properties possibly completed by historical and relational properties - can be seen as a tentative to accommodate the various explanatory expectations of different branches of biology as well as of everyday life. Without contesting the legitimacy of pluralistic essences, I first argue that it is doubtful that a unique sort of essence, be it pluralistic or not, may correspond to the notion of biological species. Then I explore the puzzling idea that a bundle of related essences might correspond to it. I show that the idea is not problematic from an ontological perspective if one intends by essence a real (possibly unknown) cause of unity. The difficulty lies in the semantics. As a matter of fact, a NK term, according to Putnam's and Kripke's semantic theory, is supposed to hook either one NK, i.e. one essence, or nothing at all. Taking some inspiration from the analysis Bloom (2007) offers of the concept of "water", I defend that there is a way out of this difficulty that does not challenge the core of Kripkean semantics of NK terms. Bloom (2007) claims that "water" is a "hybrid concept"(and not two homonymous concepts) referring both to a chemical NK and a related artefact kind. I argue that it is indeed possible to associate a less restrictive condition to NK terms than " one essence or nothing ".

Essentialism, evolutionary theory, and the species concept
Barberousse Anouk, Université Lille 1, France

The proponents of the new versions of essentialism claim that they are compatible with evolutionary theory. However, this theory has been built up precisely *against* ancient forms of essentialism. The aim of the talk is to investigate to what extent the compatibility claim can be defended. My own claim will be that the proponents of new wave essentialism encounter a dilemma:

- either they stick to the compatibilility claim, but then they have to weaken their essentialist position with respect to living species, and transform it into a monist position about the species concept,
- or their essentialism is more than monism about the species concept, but in this case they have to give up the compatibility claim.

In my analysis of the first horn of the dilemma I shall restrict my self to the "biological" and to the "phylogenetic" species concepts, the first one being often referred to by the proponents of essentialism, and the second one being entirely relational.

A meta-analysis of species concepts as units of generalizations in biology
Merlin Francesca, IHPST & Université Paris 1, France

The main role of taxonomic enterprise in science today is to provide kind-membership conditions that define epistemically fruitful groupings of entities allowing inductive generalizations. Philosophers of science are concerned with knowing whether these groupings correspond to the objective carving of the world (i.e., they are "natural kinds") or, on the contrary, are just useful tools in order to investigate it. In biology, the presence of a plurality of definitions of what biologists call "species concept" provokes a variety of reactions in philosophers. Some of them adopt a monist attitude and maintain that biologists should look for a single definition of what a species is (Sober 1984, Ghiselin 1987, Hull 1987). Others are pluralist and argue, in various forms, for a realist (Kitcher 1984, Dupré 1993) or for an anti-realist conception of biological species (Stanford 1995, Ereshefsky 1998). In my talk, I offer a meta-analysis of existing concepts of biological species, which is intended to be a prerequisite to any discussion about biological species realism/anti-realism. First, I will consider the plurality of species concepts in biology and evaluate for each them whether or not it fulfills the epistemic role of being a unit of explanatory and predictive generalizations in biology. Then, I will investigate which kind of generalizations each species concept allows making and, on this basis, whether some species concepts are better suited as epistemically fruitful groupings in biology. I will finally show why the analysis I offer is a precondition for engaging the realism/anti-realism debate about biological species.

How feasible is intrinsic taxon essentialism?
Reydon Thomas, Leibniz Universität Hannover, Germany

The debate on the feasibility of essentialism with respect to species and higher taxa has resurfaced due to the development in the past 10-15 years or so of what has come to be known as the New Biological Essentialism (NBE). NBE, however, is not a homogeneous position. Rather, it is a heterogeneous cluster of views that address different philosophical issues, use different conceptions of essence, differ on the question in which contexts of biological reasoning essences should play a role, and differ on what sort of position essentialism exactly is. Therefore, it is difficult, if not impossible, to assess the virtues and vices of NBE as such and to come up with an overall argument for or against NBE. What can be achieved is at most local arguments for or against particular forms of essentialism in particular contexts of application. The present paper aims to contribute to achieving more clarity about the feasibility and scope of essentialist positions in the philosophy of biology by examining the most recent arguments that have been put forward by, among others, Michael Devitt and Travis Dumsday in support of so-called "intrinsic taxon essentialism", i.e., the view that biological taxa have intrinsic (as opposed to relational) essences. My questions will be whether it is possible to endorse intrinsic taxon essentialism and if so, in which forms intrinsic taxon essentialism is a possible position, and what work these various forms can do for philosophers of biology. My general outlook will be skeptical.

New Models and Approaches in Evolution (submitted papers)

Modelling the Course of an HIV Infection: Insights from Ecology and Evolution

Alizon Samuel, Maladies infectieuses et vecteurs: écologie, génétique, évolution et contrôle, CNRS & Université Montpellier II, France
Magnus Carsten, Institute of Medical Virology, University of Zürich, Switzerland

The Human Immunodeficiency Virus (HIV) is one of the most threatening viral agents. The disease progresses more or less symptom-free for 5 to 10 years. During this asymptomatic phase, the virus slowly destroys the immune system until the onset of AIDS when opportunistic infections can overcome immune defenses. We still have an unclear idea of the role of virus evolution in the progression to AIDS. Mathematical models have played a decisive role in estimating important parameters (e.g., virion clearance rate or life-span of infected cells). However, most models only account for the acute and asymptomatic latency phase and cannot explain the progression to AIDS. Models that account for the whole course of the infection rely on different hypotheses to explain the progression to AIDS. Among the few models capturing all three phases of an HIV infection, we distinguish between those that mainly rely on population dynamics and those that involve virus evolution. Overall, the role of virus evolution remains largely open. We know that the virus evolves but is this a driving factor, an indicator, or something completely independent from the disease's progression. However, the modeling quest to capture the dynamics of an HIV infection has improved our understanding of the progression to AIDS but, more generally, it has also led to the insight that population dynamics and evolutionary processes can be necessary to explain the course of an infection.

Modeling evolution using the probability of fixation

McCandlish David, University of Pennsylvania, USA
Stoltzfus Arlin, National Institutes of Standards and Technology, Institute for Bioscience and Biotechnology Research, USA

Here I will describe, and attempt to explain, the surprisingly complex history of a class of widely used population-genetic models. The distinguishing feature of these models is that they express the rate of evolution as the product of 1) the rate at which a particular mutant originates within the population and 2) the probability that a newly introduced mutant of that type will go to fixation. Although from today's perspective it might seem very obvious to go from a probability of fixation such as 2s (a classical result due to Haldane, 1927) to expressing the rate of evolution as $K=2Nu*2s=4Nus$, in fact such models were wholly absent from the classical literature and only emerged as part of the molecular revolution during the late 1960s. Indeed, I will argue that such models are incompatible with the Modern Synthesis, and in essence formalize verbal models for evolution first proposed by the so-called Mutationists at the turn of the century. I will also describe the subsequent development of these models from the 1980s until today, highlighting in particular a highly parallel structure in which multiple independent literatures reinvented the same basic set of elaborations.

New perspectives on the evolution of human cognition

Bonobos as model of the last common ancestor of humans and apes: the neglected discussion in the evolution of human cognition

Gonzalez-Cabrera Ivan, Austalian National University, Australia

Discussions about the evolution of human cognition usually portray the last common ancestor of apes and humans as a chimpanzee-like hominid. This has long been the prevailing view in both the philosophical and biological literature. Such a view has been challenged only by few researchers - most notoriously Adrienne Zihlman and Frans de Waal. For this minority, the bonobo is a mosaic of traits seen in both *Pan* species. An alternative evolutionary scenario is given by the so-called 'self-domestication hypothesis' according to which the observed differences between both species are due to selection against aggression in the bonobo from a chimpanzee-like common ancestor. In this paper I will argue that we have reasons for being skeptic about the selfdomestication hypothesis, and I will explore a particular version the mosaic model of the common ancestor of human and apes, based on currently available behavioural, neurobiological and molecular evidence. If that picture turn out to be correct, I will argue, many evolutionary scenarios that have been provided for the evolution of human cognition would be either correct but too general to explain the relevant cognitive mechanisms or fairly specific in their evolutionary narrative but plainly false. For that reason in the final part of the paper, I will explore some possible consequences for ongoing debates on the evolution of human cognition -particularly, recent discussions about the evolution of social and moral cognition.

As far as I know. Social learning and the available information

Ferrario Chiara, Victoria University of Wellington, New Zealand
Di Paolo Laura, Università di Roma La Sapienza, Italy

Chimpanzees are able to switch between emulation and imitation in solving goal-directed tasks, depending on the quantity of information available in the environment. Surprisingly, children are not. They stubbornly persist in copying demonstrator's actions, even when these are overtly ineffective or wasteful. Such apparent rigidity, contrasting with the standard of high flexibility observed in human behavior, requires an explanation. Taking our cue from a comparative study of Whiten and colleagues, we propose a different interpretation of their results, drawing from a broader framework on the evolution of human cognition.

On the Expansion of the Modern Synthesis ca. 1960-1979, Session I

A bibliometric enquiry about the Modern Synthesis (1947-2010): results and questions

Gayon Jean, IHPST & Université Paris 1 Panthéon-Sorbonne, France

The paper presents the main conclusions of an extensive bibliometric study of journals focused on evolution. From 1947 (date of creation of Evolution) to 2010 (>60 journals explicitly devoted to evolution), the inquiry shows that:

1. The rate of creation of new journals was approximately constant until 1970, after which it declined until 2000, when it increased dramatically.
2. In all, 22 journals have an explicit disciplinary orientation corresponding to the three main fields typical involved in the original Synthesis: Genetics, Systematics, and Palaeontology, whereas 23 focus on other disciplines. In order of first introduction, these are biochemistry (2), anthropology (6), ecology (9), development (3), molecular biology (8), bioinformatics (2), and applied evolution (1). Except for biochemistry, all journals in this second group were created after 1970.

3. An enquiry into the frequency of certain words in titles and key words shows that the references to Darwin is huge and increased continuously from 1947 to 2010, whereas such terms as " Darwinism", "Neo-Darwinism", and "Modern Synthesis", is rare (esp. those related to "synthesis "). Here also, the years 1970-80 show a reversal of tendency.

These data suggest that 1970 was a turning point with respect to two aspects of the Synthesis as defined in the 1940s - the doctrinal aspect (evolution as dominated by mutation and selection) and the disciplinary aspect. The paper discusses the risk of bias involved in this kind of study and proposes ways to reduce that risk. It also suggests how improved tools could bring this bibliometric inquiry closer to more traditional approaches to the history of evolutionary theory and doctrines.

Going Molecular in Evolutionary Biology: techniques, objects, concepts and theories between 1960 and 1970.

Suarez-Díaz Edna, Universidad Nacional Autonoma de México, Mexico

In this talk, I review the impact of molecularization on evolutionary biology, emphasizing the wider context of the Cold War era. For this purpose I distinguish between the context relevant to *theoretical* discussions in evolutionary biology after the 1950s and the material and technical context relevant to the molecularization of evolutionary biology. John Beatty (1987) has focused on the first of these, locating the classical-balance debate in the context of political debates about the effect of radiation caused by atomic testing in the late 1950s and early 1960s. Here, I open a different window on the Cold War context.

The Neutral Theory of Molecular Evolution (NTME) was not simply a development of the classical-balance debate, for it arose from a broad array of technical and experimental developments (Suárez and Barahona, 1996). By the early 1960s major new molecular techniques were used to study the evolution of organisms. Protein finger-printing, DNA hybridization, and protein sequencing provided surprising evidence about genetic similarities between species and, in the case of sequencing, about their phylogenetic relations. New objects and ideas followed, including, most obviously, the molecular clock and the supremacy of informational molecules over morphological data., The shocking finding of highly repetitive sequences (using hybridization) is especially interesting. All these objects and concepts were encompassed by the NTME, as formulated by King and Jukes (1969).

No obvious political issue, like that which framed the classical-balance debate, was connected to these developments. However, I will argue that the cybernetic turn in the natural sciences, including the use of computers and a new language, were part of larger social concerns with the development of the life sciences.

The Creativity of Natural Selection? Darwin, the Synthesis, and Since

Beatty John, University of British Columbia, Canada

Stephen Gould argued that “the creativity of natural selection” is the “essence of Darwinism.” I agree with his emphasis on the issue of creativity, but would put the point this way: The question as to whether, and in what sense, natural selection is "creative" has been a central theme in the history of evolutionary biology. However, “Darwinians” have answered the question very differently, in ways that reflect important conceptual and empirical developments. Darwin answered it one way. Contributors to the evolutionary synthesis answered it a very different way. And post-synthesis developments occasioned still different responses. I will discuss how the case for the creativity of natural selection shifted from the period of the synthesis, to the 1970s and early 80s. Earlier, the point was to emphasize the importance of selection relative to chance mutation, with the emphasis on mutation. Later the point was to emphasize the importance of selection relative to chance more generally, not just chance mutation but random drift as well.

On the Expansion of the Modern Synthesis ca. 1960-1979, Session II

To what extent – and why – did the Modern Synthesis give Developmental Biology short shrift, 1960-1980?

Burian Richard, Virginia Polytechnic Institute and State University, USA

It is often said that the Modern Synthesis (MS) excluded developmental biology and deemphasized the relevance of developmental processes to evolutionary processes and outcomes. This (supposed?) exclusion provides proponents of evolutionary developmental biology (and others) with a major ground of criticism of the MS. The allegation of exclusion is not entirely correct. For example, Theodosius Dobzhansky (and some of those he influenced) envisioned an important role for development in shaping evolution, albeit redescribed in population genetic terms (see Depew 2011). Yet, when one considers the reaction of many architects of the MS to such figures as Goldschmidt and Waddington, there is at least a grain of truth in the criticism.

I will examine the extent to which development was excluded from the MS and the extent, and the ways in which, developmental biology influenced changes in the MS ca. 1960-1980. In doing so, I will consider the role played by the resistance to Lysenkoism and Lamarckism (as it was then understood) in shaping evolutionary orthodoxy among leading (Western) evolutionary theorists, resistance that was greatly strengthened by considerations stemming from the Cold War. The importance of this issue raises the difficult and inescapable question of the extent to which ideological preoccupations influenced the "narrowly scientific" arguments that led to the dominance of the MS in evolutionary theory.

The Changing Ideological Context of the Modern Synthesis

Depew David, University of Iowa, USA

This paper will discuss, cautiously with respect to causal hypotheses, the changing ideological context of the Modern Synthesis. In the 1940s and 50s, the Synthesis showed, and to some extent was formed to show, that advanced evolutionary science could put to rest the racism and eugenics that had embarrassed, challenged, and in some cases compromised geneticists and evolutionists. By the early 1960s it had succeeded in taking these themes off the table by treating culture, in anthropologists' sense, as the genes' finest product. The ideological advantages of this theorem may have played a role in placing the burden of proof onto Muller's classical view of population structure and in creating a presumption for Dobzhansky's balancing view in spite of its empirical weakness. With this consensus achieved, the Synthesis turned to the evolution of lifecycles, relationships among species in islands (seen as quasi-laboratories), and behavioral ecology. Research programs in these areas used calculi developed to facilitate wary cooperation in Cold War nuclear brinksmanship. They interacted with each other in this larger context. Trouble only occurred when use of these calculi was viewed by some as threatening the concept of culture that had been allaying the old worries. Not surprisingly, the old worries came back during the ideologically hypertrophic Viet Nam period.

Best-behaved ethology? Behavioural ecology and the modern synthesis

Cezilly Frank, Université de Bourgogne, France

Although 'classical' ethologists advocated an evolutionary approach to animal behaviour, most of them actually failed to incorporate new advances in population genetics and evolution into the study of animal behaviour during the sixties. For instance, one important step during the consolidation phase of the modern synthesis was the determination of appropriate levels of selection, resulting in the progressive predominance of gene-centred views. Still, reference to group selection persisted among ethologists, long after the concept was abandoned by most evolutionary biologists. Partly in reaction to this, the development of behavioural ecology was clearly an attempt to relocate the study of animal behaviour within the framework of contemporary evolutionary biology. The attempt was particularly successful, as empirical support for key concepts in modern evolutionary biology, such as, for instance, evolutionarily stable strategies, extended phenotype, optimization, selfish gene, and sexual selection, largely comes from the behavioural ecology literature. Recent developments in behavioural ecology suggest that the study of animal behaviour will continue in the future to provide both empirical support and challenges for evolutionary theory.

Organisms, Individuality, and Personality A (submitted papers)

Immune tolerance as a developmental process – innate immune system and gut bacteria interactions

Schneider Tami, Tel Aviv University, Israel

I discuss the implications of the symbiosis between the innate immune system and gut microorganisms to the concept of evolutionary individuality.
The immune system is one of the key players in gut symbiosis being the first to respond to commensal bacteria. In this encounter the immune system is able to tolerate the commensal bacteria introduced to the body at birth and continues to tolerate other kinds of microorganisms throughout life. Moreover, the commensal composition can change as a result of environmental or diet changes. I explore the concept of *immune tolerance* as an active process of the immune system that is active throughout the life of the host. The immune reaction to new species of microorganisms is a vital function for the host's survival due partly to its role in maintaining gut homeostasis. Tolerance is thus a dynamic and flexible process involving interactions with gut microorganisms. These interactions lead to immune development as well as affecting the development and variation in the microbial communities. I suggest a framework which situates the innate immune tolerance in the gut as system that establish and monitor the symbiosis with microorganisms contracted from the environment. From this perspective the innate immune system's relationship with the biotic environment is collaborative not simply antagonistic. This notion conceptualizes the symbiosis of the innate immune system and gut bacteria as a dynamic developmental system which develops during the individual ontogeny.

Ecosystems Unto Ourselves: the concept “organism” in the age of individualized medicine, targeted therapies, and the microbiome.

Tuma Julio, University of Pennsylvania, USA

Queller & Strassmann (2009) argued for a variable concept of "organismality" and Pepper & Herron (2008) suggested a plurality of potentially useful organism concepts, specifically arguing that the feedback between natural selection and functional integration leads to an "organism syndrome." But what causes this feedback and how is it altered by particular, micro-ecological differences? An accurate response is critical to many evolutionary relevant concepts (e.g., variation, fitness, and selection). Useful immunological answers [e.g., Pradeu & Carosella (2006), Pradeu (2010)] begin to address these difficulties by locating control of variation of lower-level phenomenon at the level of the heterogeneous organism. However, recent studies on the human microbiome demonstrate that "control" may be too strong a requirement. The bacterial, viral, and fungal components of the microbiome, both on and within humans, are far more numerous than previously thought, creating unique ecosystems that vary by individual. More importantly, the microbiome interacts with the human genome in dynamic ways where control is difficult to identify. To the extent that these billions of microbes work in concert or in competition with our own human genome, we differentially thrive or suffer (e.g., via allergic and autoimmune diseases). A clearer understanding of the dynamics of boundaries (including immunological and microbialecosystem ones) at work in constructing and maintaining an organism is necessary in order to assess: 1) whether immunological control is critically important at the level of heterogeneous individual organism, or 2) whether regular and persistent interspecies interactions may be the more relevant higher-level of selection.

From cohesion to collaboration: how to define biological individuality

Hutter Thiago, Université de Montréal, Canada

Recent works in contemporary philosophy of biology such as Pradeu's *The Limits of the Self: Immunology and Biological Identity* (2012) examine the definitional slides that have occurred between three different categories: organism, living thing and biological individual. The consequences that have arisen from this mishap in definitions constitute the privileging of organisms when reflecting about biological individuality in general. However, more recently, certain difficulties have imposed themselves in regards to this biased privileging. On the one hand, Dupré and O'Malley, in their article *Varieties of Living Things: Life at the Intersection of Lineage and Metabolism* (2009), focus on the collaborative aspect of the processes of life in order to argue that a large diversity of things other than organisms is alive. On the other hand, Haber, in his article *Colonies Are Individuals: Revisiting the Superorganism Revival* (2013), emphasizes on the notion of cohesion and maintains the inexistence of a paradigmatic biological individual by holding that organisms may comprise marginal cases of biological individuals. In this presentation I try to show that Haber's position is not only compatible but also complementary to Dupré and O'Malley's by arguing that the concepts of collaboration and cohesion highlight similar properties. By doing so, this analysis renders explicit the limitations of the concept of organism in biology as well as philosophy.

Organisms, Individuality, and Personality B (submitted papers)

Autonomy and Multicellular Organisms

Arnellos Argyris, University of the Basque Country, Spain

From an organizational perspective, unicellular entities are considered as autonomous organisms exhibiting a particular kind of functionally differentiated and integrated organization, which plays a fundamental causal role in the generation of those constraints that ensure its maintenance and reproduction. Could this concept of 'basic' autonomy be applied to a multicellular (MC) organization? This is quite challenging, because all MC systems exhibit a degree of functional integration, and most MC systems show, at the global level, forms of functional differentiation and various degrees of inter-dependence.

In this talk, I shall suggest key aspects regarding the *organizational* conditions required for the formation of organisms at the MC level. More specifically, I shall propose a general theoretical scheme that integrates developmental and evolutionary characteristics of biological organisms, and according to which a MC organism should be capable of regulating and controlling the developmental dynamics of its own collective organization. The ontogenetic development of several MC systems is investigated in detail from the point of view of their capacities and characteristics for self-construction. I shall argue that a specific type of functional integration among the cells of a MC group, i.e. a special type of 'regulatory control system' operating on a new organizational/hierarchical level and consisted in several different intercellular mechanisms that modulate the developmental process, is needed to qualify a MC system as organism. Finally, I shall argue why a MC system exhibiting this type of organization should be considered as a second-order autonomous system, and some implications for its agential capacities will be discussed.

Bacteria Cognition and Natural Agency

Fulda Fermin, University of Toronto, Canada

Recent research on bacteria cognition has exposed the inherent capacity of these systems to respond appropriately across a wide range of conditions. But is the attribution of cognition warranted? This tendency, I argue, is predicated on two Cartesian assumptions: First, goal-directed behavior implies intentionality hence the representation of goals (desires) and means (beliefs). And second, intentionality is a kind of causal organization (e.g. computational architecture) that demarcates intentional from mere 'automatic' systems such that bacteria are, categorically, one or the other. However, a dichotomy arises between a mechanistic and an intellectualist conception of bacteria, neither of which captures their distinctive purposive responsiveness. I propose an alternative framework according to which, goal-directedness is a gross behavioral capacity of a natural agent to reliably respond to its conditions of existence as permeated with significance, that is, as a system of 'affordances' or opportunities for attaining its goals. Agency, thus conceived, is not a kind but a robust emergent pattern of adaptive interaction between a goal-directed system and its affordance-landscape. On this view, furthermore, *agency* is a prototypical concept that allows for degrees relative to a system's affordance-landscape. Hence, there are no necessary and sufficient conditions for demarcating agents so no dichotomy arises. All natural agents, I claim, have biological goals and hence are constrained by the demands of survival and reproduction. But cognitive agents are only those with the capacity to act irrespective of whether their goals are biological. Bacteria, I conclude, are biological *agents* (against mechanization) but not *cognitive* agents (against intellectualization).

Does plant genetic diversity shed light on plant individuality?

Gerber Sophie, INRA-Univ Bordeaux, France

The notion of individual was originally built with animals, and more precisely with the eumetazoans characteristics. Considering non-eumetazoans results in problems with the definition of individuality. Among them, plants are particularly neglected regarding individuality considerations. One of the main criteria generally related to individuality is genetic homogeneity. However plants were always considered to be different from animals for this criterion and were supposed to be heterogeneous in nature because of, among other traits, their particular cells, modularity, long lifespan,... In this paper we will first review how different philosophical studies concerned with individuality pointed out plant particularities (and especially intra-individual diversity) in different ways. We will use current scientific knowledge on plant genetic diversity to question the way plants are considered in philosophical studies. Our aim is to use a scientific perspective to shed light on the philosophical question of plant individuality.

The Organism Problem between Life Sciences and Philosophy of Nature around 1800

Schelling, Oken and the Problem of Animal Classification

Gambarotto Andrea, Université Paris 1 Panthéon-Sorbonne, France

In the last thirty years several studies have been concerned with the meaning of German romantic life sciences for the emergence of modern biology. However, these endeavors are often characterized by interpretative errors or too vague arguments. Even the best ones, although they satisfactorily account for Darwin's main intellectual references, fail to address the most important question: which are the respective roles of German life sciences and philosophy of nature in the emergence of the conceptual framework that rendered biology as a science (and thus Darwinism) possible? Most scholars have worked out the problem using Imre Lakatos' vocabulary and referring to an alleged Kant-Blumenbach research program. The paper argues that this notion cannot be used for the analysis of pre-paradigmatic sciences and that, instead, the main ground for a scientific biology is to be sought in the conceptual shift involving the notion of organism from "general form of order" to "individual living entity". Especially in the German context, this shift is expressly connected to the notion of vital force. Kielmeyer was the first one to use it in order to analyze the relationship between physiological functions and animal classification, while Schelling's and Oken's philosophy of nature displays an effective development of this idea. This framework constitutes an important link between romantic biology and the British tradition of comparative anatomy, the background on which Darwinism was elaborated.

Blumenbach: Teleology and the Laws of Vital Organization
Duchesneau François, Université de Montréal, Canada

Blumenbach's physiology and natural history are grounded on a complex theory of vital forces. These forces correspond to a hierarchy of dynamic principles that include the *Bildunsgstrieb* as the proper sufficient reason for sequences of epigenetic processes. From an epistemic viewpoint, these dynamic principles are presumed to stand for the concealed causes of constant and regular physiological effects. But in light of Blumenbach's methodology would not such a system of specific forces point to the project of formulating laws of vital organization that would be ultimately irreducible to physical and chemical laws? Presuming that such is the case, what kind of constitutive or regulative use of teleology was supposed to fit into the formulation and justification of those laws? Assessing the methodological and epistemic profile of Blumenbachian physiology might throw some light on the experimental pattern of *Entwicklungsgeschichte* that became a prominent feature of early 19th century German biology.

Hegel’s Theory of Organism
Illetterati Luca, Università di Padova, Italy

The contribution highlights the key features of Hegel's theory of the organism emphasizing the importance Hegel assigns to externality with regard both to the environment and to other individuals. Moreover, it will be shown how the structure of the organism implies for Hegel the apparently contradictory connection of lack and completeness: the organism is itself only as far as it is unfulfilled and there is life only as long as there is a lack. For this reason, in very general terms, living beings can thus be defined as the activity of a lack. In this respect, life itself displays for Hegel a reflective structure. The second element that will be emphasized is the emergence of the notion of freedom in the field of living nature, which seems to be particularly relevant with regard to the contemporary discussions on naturalism: although the idea of a "natural freedom" may look like like an oxymoron, it is what allows to think of the sphere of freedom as not opposed to that of nature.

Origins of Life

Flying Mother Nature’s Seed Into a New Home Near the Sun
Orlic Christian & Baker Kevin, Michigan State University, USA

Francis Crick and Leslie Orgel proposed a radically different theory to explain the origins of life in 1973. They suggested that life on Earth had been intentionally seeded on Earth. This theory of Directed Panspermia was presented as a valid alternative scientific theory which Crick continued to advocate and support until 1981. Crick argued that every step in his theory of directed panspermia was scientifically plausible. He defended his theory in journals, letters, articles and even a book (Life Itself). I argue that directed panspermia was not a joke (as has been argued by others) but rather it was presented as a genuine alternative hypothesis.

Furthermore, I argue that other scientists took it as such. Lastly, I seek to place Cick and Orgel's directed panspermia in both the context of concurrent investigations into the origin of life (as well as an interest in extraterrestial intelligence) and Crick's persona.

What is the driving force for life's emergence?
Pascal Robert, Institut des Biomolécules Max Mousseron, Université Montpellier I & II, France

This year marks the 60th anniversary of the publications in 1953 of both the double helix structure of DNA revealing the nature of genetic information and of the Miller-Urey's experiment showing that organic building blocks of life can be formed abiotically. But there is still no accepted scientific view to account for the origin of life process. Jacques Monod in "Chance and Necessity " proposed that the origin of life was an intrinsically improbable contingent event. But is it scientifically acceptable to give up researching considering that life originated from a violation of the 2nd Law? The presentation will be dedicated to show that inanimate matter and the living beings are not, in principle, separated by an impassable border, but are both manifestations of a world that is understandable through the laws of physics and chemistry and open to scientific investigation.

On the origins of autonomy: protocells as the first forms of functional integration
Murillo Sánchez Sara, Ruiz-Mirazo Kepa, University of the Basque Country, Spain

Maturana and Varela's work on the theory of autopoiesis in the seventies and eighties lead to a conception of life as a certain form of *organization*, by which each living entity recursively produces itself, including the boundary with its local environment (i.e., the cellular compartment). In more recent times, we have applied a similar idea, 'basic autonomy' (Ruiz-Mirazo and Moreno 2004), to design a research agenda in the field of origins of life, proposing it as an intermediate bridge between complex self-organizing phenomena and 'genetically-instructed metabolisms' -- i.e., minimal but already full-fledged living organisms, capable of open-ended evolution (Ruiz- Mirazo et al. 2008). For historical reasons (that we will not go into in this contribution), the autopoietic school avoided the use of the term 'function' or 'functional' in their theory. However, a physiologically well grounded naturalization of this fundamental concept for biology could be approached in the context of prebiotic research on protocellular model systems (Moreno & Ruiz- Mirazo 2009). In fact, function can be understood from an organizational perspective (Mossio et al. 2009), as a very reasonable alternative to etiological accounts of it, and provides a good theoretical framework for our approach here. Starting from a relatively simple theoretical model of a protocell (Ruiz-Mirazo & Mavelli 2008) we are trying to implement empirically this first or minimal form of autonomous organization, which would involve functionally integrated components. The 'in silico' simulation model includes a semipermeable membrane (made out of simple amphiphilic self-assembling molecules - e.g., fatty acids or related amphiphilic compounds) where precursor transport mechanisms would be anchored (peptides and oligomers), helping the system to overcome problems like the accessibility of substrates or the regulation of osmotic imbalances, and allowing it to host a proto-metabolic reaction network. The 'in-vitro' approach of this model, dealing with real biomolecules and thermodynamical behaviors, will surely reveal additional difficulties but, at the same time, will hopefully bring about a more realistic understanding of the organizational principles that could have been at play in this origin of life scenario.

Going Live: The Origin of (Artificial) Life
Pennock Robert, Michigan State University, USA

The problem of determining when life originated on earth may be seen as a special case of the problem of detecting when life presents itself for the first time in any previously lifeless environment. If one wanted to build a scanner that would detect lifeforms, what properties should it key on? The design of such a scanner is not merely a scientific or technical problem. The conceptual questions that are involved in adjudicating scientific disputes about the origin of lifeforms on earth are equally at issue when thinking about the possibility of alien lifeforms on other planets. Assuming that one had successfully designed a scanner that could work in both terrestrial and extraterrestrial environments, would that be sufficient for it to also work for the possibility of artificial lifeforms so one would be able to detect when a new lifeform was successfully created? Artificial life research falls into three broad categories -Wet, Hard and Soft- which attempts to simulate or synthesize life with different kinds of components (organic molecules, mechanical parts, or software, respectively). I have previously argued that explicating the concept of life may be facilitated using theoretical insights from Darwin and Wittgenstein. Here I consider what are the advantages and limitations of this approach for solving the scanner design problem for the detection of the origin of artificial life.

Outsourcing biomedicine

Buy-ology: kits and knowledge in molecular biology

Stevens Hallam, Nanyang Technological University, Singapore

Over the last twenty-five years, the use of commercial 'kits' has grown increasingly common in molecular biology. Such kits - usually consisting of standardized reagents along with instructions for use - can be used for hundreds of different laboratory assays, preparations, and experiments. They range in price from a few dollars to hundreds of dollars.

This paper uses interviews with molecular biologists, advertisements, and online discussion forums to interrogate the consequences of this form of ‘outsourcing’. By making laborious and complicated laboratory procedures routine, kits have the potential to generate speed and efficiency in biological work. On the other hand, this routinization means that such work requires very little knowledge of underlying biological or biochemical processes. Such ignorance could lead to poor experimental design, misinterpretation of results, or an inability to innovate.

Both the speeding up and the deskilling of biology point to the emergence of two distinct kinds of labor. The consumers of kits are usually only interested in them so far as they can speed up their own problem solving. Kits are often perceived to give lab workers more time to concentrate on 'real' scientific problems. But the production of kits in commercial setting requires attention to different kinds of problems: standardization, robustness, and quality control. These kinds of knowledge and labor are often elided in accounts of biology. Interrogating the origins and usage of kits provides an opportunity to show how these alternative forms of labor also participate the making of biological knowledge.

Outsourcing in anatomical visualization. Atlas production and the politics of visual cultures in early 20th century Vienna

Nemec Birgit, University of Vienna, Austria

When Julius Tandler in 1910 took over the First Anatomical Chair in Vienna he was asked by a renowned publishing house in Leipzig, CW Vogel, if he would be interested in editing his own anatomy textbook. The project promised to be prestigious. The publishing industry was still living well from the prosperous decades of the late 19th century, when it boosted the rise of the Viennese medical university to a leading place for medical education and research worldwide. Tandler and his publisher agreed on content and material aspects of the volumes; the crucial work of image production, however, was finally outsourced to an academic artist who Tandler insisted on. Neither Tandler, a powerful social-democrat politician, nor Vogel or the financially stricken artist Carl Hajek could know the project would take them almost three decades to finish, marked by ongoing negations and disappointments on all sides.

In my talk I will examine practices of outsourcing in anatomical atlas production. How were preparations and sketches transformed into working models and final images? What epistemic processes are linked to the single working steps? How could the artist's work be directed in order to meet an anatomist's assumptions about the normal human body, health and society on the one hand, and publisher's aesthetic and financial expectations on the other hand? And finally, what role did outsourcing play in transformations of knowledge, political, social and symbolic orders, related to anatomical image production in early 20th century? I will compare the case of Tandler's project to the second important atlas in Vienna, the Toldt/Hochstetter, and to a Heidelberg based book, the Merkel/Kallius. This allows us to take a closer look at how urban structures, local milieus and their international networks influenced (standards of) outsourcing in anatomical atlas production.

The Vertical Integration of American Paleontology

Rieppel Lukas, Northwestern University, Singapore

During the 1870s and 80s, American paleontologists such as Othniel Charles Marsh and Edward Drinker Cope acquired most of their specimens from freelance collectors based in the American west. Among other things, the practice of negotiating for the purchase of rare and valuable fossils over long distances required solving a problem of trust. What was to stop a freelance collector from selling a specimen under false pretenses for their own personal gain? The deception and fraud made possible by the vast expanses of space that separated collectors from learned naturalists threatened to undermine both the economic viability of acquiring specimens by purchase and the epistemic credibility of the knowledge produced by learned naturalists. In this paper, I will describe some of the practices that paleontologists such as Marsh developed to establish control over freelance collectors out in the field. I will then use the example of Henry Fairfield Osborn to argue that around the turn of the 20th century, a new generation of paleontologists largely abandoned the practice of outsourcing specimen collection. Rather than continue to purchase their fossils, early 20th century paleontologists preferred to integrate backwards by sending museum curators and their assistants into the field. However, internalizing the market for fossils did not solve the problem of trust on its own. As such, museums continued to develop increasingly sophisticated means to maintain oversight and control over the actions of their employees out in the field.

Open Source, Outsourced: Synthetic Biology in the Age of Biological Taylorism

Roosth Sophia, Harvard University, USA

Synthetic biologists are a community of bioengineers who seek to standardize genetic parts, applying principles borrowed from electrical and mechanical engineering to biological substance. As this paper reports, their project extends to standardizing labor practices as well. Entering the lab of a Boston start-up company that built what members termed a biological "assembly line" following the principles of Taylorism, I compare it to a much larger for-profit synthetic biology company in the Bay Area, in which the corporate ethos is suffused by management theories emphasizing efficiency. Scientists in both companies subscribe to the "Toyota Way" production cycle forged in Japanese factories and popularized in American manufacturing philosophies such as General Electric's "Six Sigma". Touring both labs, I observed the deskilling of PhD benchwork in favor of undergraduate labor in one company and short-term manual laborers manning robots in the other. Biological labor is being outsourced and routinized, first from academic laboratories to companies, then from humans to machines. Comparing these two companies, I reflect on how engineers have imported not only technical principles of manufacture (such as standardization and abstraction) into biology, but also the labor relations and forms of alienation that underwrite mass production in late capitalism.

Parental Effects I: Historical, Sociological, and Medical perspectives (*Interdisciplinary session*)

The Origin and Operationalization of Fetal Programming Science
Waggoner Miranda, Princeton University, USA

David Barker, a U.K. physician, began an intellectual trend in the 1980s with an epidemiological idea known as the "fetal origins hypothesis". Based on observational data that linked low weight at birth and the incidence of chronic disease in adulthood, Barker theorized that in utero conditions and exposures during early human embryonic development may relate to epigenetic modifications in the fetus that determine outcomes in later life. In his writing, Barker began to use the metaphor of "fetal programming" to explain potential mechanisms at play in the developmental origins of health and disease. As it precipitated novel research inquiries across a range of fields, from biology to demography to economics, the metaphor of programming was operationalized in both animal and human population sciences, thus moving from rhetoric to practice. This paper maps and traces the flow, evolution, and standardization of the idea of fetal programming within and across scientific disciplines, focusing especially on its uptake in animal and human population studies. Drawing on the professional scientific and medical literature as a public forum in the formation and dissemination of scientific knowledge, I examine how scientists understand and interpret phenomenological effects vis-à-vis impacts on the womb. Tracing this knowledge course around diverse mechanisms of environmental imprinting and parental effects, from initial epidemiological hypotheses and metaphors to animal experiments to modeling population health and disease, this paper will reveal how a scientific idea travels and how scientific knowledge and scientific practice are co-constituted.

Maternal Effects and the Twentieth Century Sciences of Heredity
Sarah Richardson, Harvard University, USA

This paper explores the complex location of maternal effects research within the twentieth century sciences of heredity. In research on Mendelian inheritance, maternal effects were primarily recognized as a source of error to be controlled for in experimental manipulations. Molecular biologists similarly minimized maternal effects as they advanced a vigorous gene-centric vision of biological development governed by DNA. In contrast, critics of the gene-centric program seized upon observations of maternal effects to build a counterdiscourse to the hereditarianism they perceived in genetic research. Through studies of "maternal effects" on the offspring during fetal development and early life, researchers sought to prove the intuition that more is inherited by offspring than just DNA, and that DNA itself can be altered or overridden by other factors. Maternal effects research became one important empirical pillar of the argument, increasingly embraced today, that "it's not all in the genes". Yet against this polarized narrative of contestations around maternal effects in the twentieth century life sciences, the literatures of early- and midtwentieth century agricultural breeding, eugenics, antenatal medicine, and reproductive physiology situated maternal effects firmly within a hereditarian, gene-centric framework. Reclaiming, schematizing, and historically situating these conceptions of maternal effects within the twentieth century sciences of heredity, this paper brings maternal effects research into relief as a critical and multivalent arena for theorizing the nature of heredity in the twentieth century.

A biomedical perspective on parental effects
Gluckman Peter, Liggins Institute, New Zealand

Studies from the 1930s had shown that fetal growth itself was subject to maternal non-genetic influences but it was not until the recognition of developmental teratogenesis and the development of experimental fetal physiology in the 1960s that it was accepted that the human fetus was not fully isolated from its maternal environment. Studies in the 1960s-1980s led to the recognition of long-term metabolic and physiological consequences of alterations in the fetal environment. While popularized by Barker in important studies, there were antecedent observations and arguments. While a limited adaptive argument focused on intrauterine growth retardation was suggested by Barker and Hales, a broad range of developmental environmental influences can have subsequence phenotypic effects. These may occur within the normative range of fetal development. Molecular epigenetic studies suggest that their contribution to disease risk by altering the sensitivity to altered environmental conditions can be considerable. Predictive adaptive mechanisms have been suggested to underlie the consequences of the variation within the normative range and where fetal nutrition is poor. The evolutionary novelty of maternal obesity may operate through different mechanisms. The consequences of gestational diabetes may reflect a mechanism that was adaptive in more nutritionally constrained pre-modern environments. An evolutionary perspective combined with molecular epigenetics is allowing greater dissection of the sequelae of maternal effects which, as a result of modern demographic (smaller family size, etc) and environmental change, appear to be of greater importance than is generally recognized.

Parental Effects II: Philosophical and Scientific perspectives (*Interdisciplinary session*)

Parental Effects: Development, Heredity, and Evolution

Uller Tobias, University of Oxford, UK

Parental effects mean different things to different biologists - from developmental induction of novel phenotypic variation to an evolved adaptation, and from epigenetic transference of essential developmental resources to a stage in ecological inheritance. This diversity of perspectives comes from the fact that parental effects combine aspects of development, heredity, and selection. This makes parental effects research central for evaluating the need for an extended evolutionary synthesis. Here I outline the challenges of parental effects for standard evolutionary theory and show how these are conceptually related to similar discussions in the literature on developmental plasticity, non-genetic inheritance and niche construction. This analysis clarifies the evolutionary implications of parental effects and suggests the need to rephrase heredity and selection in developmental terms.

Different interpretations of parental effects and their implications our understanding of development, heredity and evolution

Stotz Karola, University of Sydney, Australia

The varied ways in which to view parental effects allow one to focus on different aspects of how they provide a link between development, heredity, and evolution. Parental effects (PE), through mechanisms that promote the transitions for young and adult species-typical development, provide a link between the generations. Their study enables a deeper understanding of developmental dynamics of life cycles and their role in evolution. PEs as the context-dependent transgenerational transmission of phenotypic strategies have been interpreted as developmental plasticity at the intergenerational level. They allow organisms to be as ecologically open as possible. Some PE may be predictive adaptive responses of offspring to subtle variations in parental behaviors as a forecast of the environmental conditions they will face in the future. PE as the non-genetic transfer of developmental resources shows that evolution has trusted an exogenetic system to transmit information vital to the reconstruction of the next generation's life cycle. Reliably re-occurring PEs support the faithful reconstruction of the developmental niche for successive generations, while more context-dependent PEs participate in the modification of developmental niches, and hence the creation of environmentally induced and developmentally regulated, phenotypic variation. Some PEs highlight the hereditary/evolutionary significance of aspects of experience, either through the transfer of parental experiences or the reliable provision of affordances for learning necessary for species-typical development. This paper will discuss these different interpetration of PEs and their implications for our understanding of heredity and evolution.

Perspectives on Extinction

The unextinct: Living fossils and their place in evolutionary theory
Turner Derek, Connecticut College, USA

There are many well documented living fossils, from Darwin's example of South American lungfish (*Origin*, first edition, p. 107), to the chambered nautilus, the coelacanth, ginkgos, and the wollemi pine tree (a.k.a. the "dinosaur tree"), not to mention the recently discovered singlecelled "sea grapes" living on the ocean floor near the Bahamas. These examples show that in some cases, evolutionary history is characterized by long stretches of morphological stasis. Living fossils provide a good test case for thinking about two issues in evolutionary theory: (1) The first issue concerns natural state models and the burden of explanation. Is extinction the expected (or "natural") fate of every lineage, such that a failure to go extinct requires some special explanation? Or is persistence the default expectation, and extinction the phenomenon that needs explaining? (2) The second issue has to do with levels of explanation, and with the so-called hierarchical expansion of evolutionary theory. Some of the mechanisms proposed to explain stasis (e.g. stabilizing selection) would operate at the population level. There might also be differences among whole lineages that help explain differential persistence vs. extinction, raising the question whether a macro- vs. a micro-level explanation is more appropriate. Without addressing these philosophical issues concerning levels and direction of explanation, we will not have a good story to tell about the place of "the unextinct" in evolutionary theory.

Extinction and the Value of Diversity
Sepkoski David, Max Planck Institute for the History of Science, Germany

As a number of authors have observed, biodiversity has come to be seen as an intrinsic scientific and cultural value. In other words, biological diversity -the sheer multiplicity and heterogeneity of living things - is now understood to have an inherent value that is not reducible to the utilitarian or aesthetic worth of any particular individual species: the value of diversity is diversity itself. Extinction plays a central role in this understanding of biodiversity, since diversity is something that is understood to be fragile and tenuous, constantly endangered by the threat of loss. Whereas most historians who have examined this phenomenon have placed the modern biodiversity movement in the context of a history of conservation biology and endangered species protection, I want to frame it in a new perspective. This talk will examine the influence of biological theories about the nature and dynamics of extinction - and especially mass extinction - on the current valuation of biological diversity. I will focus particularly on the ways that paleobiological analyses of global historical diversity patterns during the 1970s and 80s have contributed to a new understanding of extinction as an often catastrophic phenomenon with significant and permanent ecological and evolutionary consequences. I will argue that this new model of extinction has played a prominent conceptual and rhetorical role in debates surrounding the current biodiversity crisis, which I will examine in critical historical perspective.

Once upon a Time: Construction and Realism of K-T Mass Extinction Data
Tamborini Marco, Ruprecht-Karls-Universität Heidelberg, Germany

David Jablonski (1996) argues that two basic problems lie at the base of the mass-extinction debate: a) Limitation on fine temporal scale; b) The scarcity of simple cause-effect relation. My talk aims to sketch out the degrees of construction of the paleontological data involved in the study of Cretaceous-Tertiary mass extinction, thus posing a philosophical reflection upon this event. I will start by problematizing Cleland's asymmetry of causation and time (Cleland 2001, 2002, 2011). If on the one hand the research of (non) smoking guns seems to fit into the actual praxis of the historical reconstruction (Keller 2005), on the other the asymmetry of time can be overcome, i.e. stabilized, only by modelling a working version of the past. Models are indeed able to describe the effects of extinctions. They are a narration of diversity through time, extremely important to understand the history of biodiversity through deep time. Nevertheless, they lack a precise dimension of time, exactly as every narration does. On the contrary, biostratigraphical correlation provides a finer chronology. This finer scale, however, is based upon insufficiently elaborated data. It therefore generates an asymmetry of time and the great expectation syndrome (Ager 1993; Tsujita 2001). I will conclude my talk by arguing that paleontology should primarily concentrate on the description of selective patterns, since it is the only way to overcome the problem of local underdetermination.

Ecosystem functioning and species extinctions
Delord Julien, Independent Researcher

I would like to propose an epistemological typology of the different explanations relating species extinctions to ecosystem functioning. Indeed, the evaluation of biodiversity effects on ecosystem services such as gas regulation, food and fiber supply, soil regeneration, relies on the impact attributed to species or population extinctions on the functioning of ecosystem. This major research program in ecology, sometimes called the "Biodiversity-Ecosystem Functioning (BEF) paradigm", aims at predicting the effect of species richness and characteristics on ecosystems and at backing new conservation strategies on scientific evidence.

Considering the extinction problem, the loss of species can affect the functioning of the ecosystem and on the reverse, a disturbed ecosystem can cause the extinction of some of its constituting species. This reciprocal relationship needs to be studied on an homogeneous epistemological background. I show that three main paradigms allow to conceive ecosystemic and populational dynamics on a par in the BEF paradigm: probabilism, mechanicism, and organicism. I then discuss the limits of this approaches regarding the predictions of extinction dynamics and I suggest that species should be replaced by ecological traits as the focus entities of ecosystem functioning studies.

Philosophical Anthropology I: The Bio-Philosophy of Helmuth Plessner in Context

Keywords in the Conceptualization of Life: Plessner's "Boundary" and Hegel's "Deficiency"
Michelini Francesca, University of Kassel & Humboldt University, Germany

My point of departure is the surprising similarity between Hegel and Plessner on many characters of the living organism - particularly with respect to the notion of "organisation" in plants and animals. The thesis I advocate concerns their general theories of biological individuality and is articulated in the following points: 1) For Hegel and Plessner the difference between plants and animals consists in the different levels of development of the "principle" of the organism's dynamic self-definition. 2) This "principle" is similar for both philosophers, because it is based on two cognate categories, i.e. "boundary" (Grenze) and "deficiency" (Mangel). 3) Hegel and Plessner's basic conceptions of life - often seen as divergent - on close scrutiny have a great deal in common.

Plessner's Conceptual Investigation of 'Life': Structural Narratology

Davis Lawrence, Department of Sociology, Washington and Jefferson, USA

Plessner's theories presented a distinctive opportunity to formulate biological perspectives within cultural anthropology. In organizing the foundations of philosophical anthropology, he resisted a linear or naturalistic placement of anthropology emerging out of biology, but insisted that " the construction of a philosophical anthropology has as a presupposition the investigation of such facts which concentrate around the circumstances of 'life'". This essay will consider Plessner's conceptual investigation of life and suggest ways that its "concrete natural philosophy" involves a structural narratology, suitable for pursuing knowledge in the life and human sciences. Rather than insist on special domains of Geisteswissenschaften and Naturwissenschaften, Plessner proposed unifying the sciences through reconceptualizing how philosophical anthropology reclaims scientific knowledge in narratable construction. By properly conceptualizing life and life sciences, philosophical anthropology includes its own basis for observation.

As Ernst Mayr pointed out, the nature of biological knowledge deals necessarily with individuals rather than types. Such investigations are inherently narrative. This essay will examine several characteristics of contemporary views of biological evolution that are reflected in procedures of narrative analysis, and suggest isomorphisms in analysis of cultural practice parallel these biological characteristics: an instance of using just the same direction to treat the natural world and its human inhabitants, to articulate a philosophical anthropology based on organic nature in the way Plessner imagined. This essay will trace out implications of Plessner's writings for the way anthropology conducts cultural analysis.

The substantive and methodological integration of biology, anthropology, and philosophy in Plessner's *Die Stufen des Organischen und der Mensch*

Honenberger Phillip, Rowan University, USA

Plessner's *Die Stufen* (1928) offers a sweeping, systematic philosophical account of the place of human beings in the natural world - or, as Plessner put it, a "philosophical anthropology" set in the context of a new "philosophy of nature". The central theoretical innovation of Plessner's work is the concept of *Positionalität*, which highlights major structural differences between species-typical forms of organism-environment interaction, and leads Plessner to conclude that human beings' relation to their environments is distinctively characterized by the speciestypicality (for humans) of *mediation* of their organism-environment interaction by non-speciestypical artifactual conditions (*natürlichen Kuünstlichkeit*), and their associated capacity to take an extra-bodily perceptual standpoint (*Exzentrizität*). (For review, see Grene 1974a, 1974b, Fischer 2009, and Honenberger 2012.)

Here I review Plessner's detailed engagement, in *Die Stufen*, with the biological literature of his day – particularly Darwin, Jakob von Uexküll, and Hans Driesch. On the basis of this review, I identify two types of interdisciplinary integration characteristic of Plessner's procedure that (I argue) offer lessons for contemporary inquiries situated at the border of biology, anthropology, and philosophy. The first integration is methodological, regarding the co-operation of biology, anthropology, and philosophy in the theoretical approach to objects of common concern to each.

(In Plessner's account, these objects prominently include nature itself, organic life, plants, nonhuman animals, and human beings, as well as adaptation, nutrition, memory, and similar features.) The second integration is substantive, involving substantive claims about the constitution, distinction, and relation of a number of these objects of common concern.

Philosophical Anthropology II: Applications in Genomics, Human Evolution, and Addiction

Roles for technology in feeding an evolutionary feedforward loop in the human lineage

Blad Sylvia, University of Amsterdam, Netherlands

Repetitive sequences have long been ignored in genome comparative studies because they were thought to be without adaptive significance (e.g. The Chimpanzee Sequencing and Analysis Consortium, 2005). The passive accumulation of duplications, deletions and translocations that can happen in response to reductions in the stringency of natural selection, however, can increase the modularity of a genome (Lynch & Connery, 2003), and highly modular genomes have an enhanced potential for phenotypic adaptive flexibility. If accessible this potential can, in turn, help organisms circumvent selective constraints. Novel epigenetic and behavioral resourcefulness resulting from the creative deployment of increases in genomic modularity can, in principle, help sustain and buffer further increases (Varki, Geschwind & Eichler, 2008).

Hypothetically speaking this situation can cause an evolutionary feed-forward loop in which organisms become more and more 'detached' from explicitly and linearly coded functional genetic information and rely instead on epigenetic ways of accessing 'implicit' functional information in the genome (Moss & Pavesich, 2011; Caporale, 2006). The evolutionary lineage towards human beings shows continual increases in genome modularity and repetitiveness that may indicate that such a loop has indeed come into existence. What roles may the unique technological history of humanity have played in the dynamics of human genome evolution, and in making the modular potential of the genome more accessible as a flexible resource for adaptive deployment in the context of the constructed niches of the *Homo* lineage?

We-Intentionality, Being-in-the-World and Multi-Level Selection: Re-synthesizing an evolutionary account of anthropogenesis by way of the hominid 'super-organism'.

Moss Lenny, University of Exeter, UK

The return of multi-level selection theory as a robust and respectable approach in contemporary evolutionary theory opens up new possibilities for critically and synthetically bringing together, within a plausible evolutionary account, a myriad of empirical and phenomenological insights into "human nature" that did not and do not fit easily into a more narrow individual or geneselectionist account. An expanded and re-tooled account of hominidization by way of the emergence of a 'super-organism' will test itself against the philosophical anthropology of Gehlen, the existential phenomenology of Heidegger and the cognitive psychology of Tomasello.

Advancing Insights from Philosophical Anthropology: Addiction as a Detachment-Compensatory Occupation

Wasmuth Sally, University of Exeter, UK

In this paper I will argue that Gehlen's philosophical anthropology provides a conceptual starting point that brings insight to our understanding of addiction. The term 'addiction' in scientific research has been likened to a set of criteria defining substance dependence, and research has therefore narrowly focused on uncovering neurobiological etiologies to account for problematic drug use. 'Addiction' is seen as irrational, superfluous, and pathological drug use at the expense of the user's well-being. However, if we adopt Gehlen's notion that all humans are underdetermined, problematic, defective life forms (*mangelwesen*) in need of compensatory action, addiction shows up as a function of an already (always) present human need. Addictions are rational attempts (albeit often problematic and unsatisfactory ones) to maintain motivation and life organization. Individuals with addictions have experiences that are organized around the object of their addiction and provide structure and direction for how to act. While Gehlen suggests “institutions” (i.e. customs, conventions, and societal establishments) as means for reducing the arbitrariness of human existence and providing meaning and direction for how to live, the emergence of addictive patterns in work and other conventional realms blurs the distinction between 'healthy' and 'addictive' compensations for human under-determination.

Taking this into account, rather than a disease model with neurobiological etiologies to account for the purported irrationality of addiction(s), what is called for, I argue, is a model that can delineate both the problems/harms and the compensatory gains realized in both addiction and other responses to the human situation of lack.

Philosophical issues raised by Evo-Devo (submitted papers)

Evolutionary Developmental Biology’s Relative Significance Controversy

Craig Lindsay, University of Idaho, USA

The question of the possibility of a theoretical synthesis of so-called neo-Darwinian theory and evolutionary developmental biology (evo-devo) has led to a controversy over the relationship between the two different explanatory frameworks (e.g., Amundson 2005, Laubichler 2010, Minelli 2010, Pigliucci and Müller 2010). Through analysis of the terms of the debate and the arguments employed in it, I argue that there is a relative significance issue (Beatty 1995, 1997) that is missed by the current debate. Indeed, the heterogeneous domain of biological evolution requires both neo-Darwinian theory and evo-devo to account for its different phenomena because the two explanatory frameworks do not and cannot explain the same phenomena. It is my view that the relative significance issue serves as further indication that a theoretical synthesis of neo-Darwinian theory and evo-devo is highly unlikely at best; instead, both are needed to explain different phenomena within the domain of evolutionary biology.

The genetic and the morphogenetic approach in evodevo: rethinking evolutionary causality

Nuño De La Rosa Laura, Konrad Lorenz Institute for Evolution & Cognition Research, Austria

Evo-devo is often reduced to the comparative study of the developmental genetic machinery of different species. However, other authors in evo-devo have denied that either developmental biology or evo-devo can be reduced to the investigation of regulatory genes. What I call the 'morphogenetic approach' attempts instead to unravel the mechanisms of pattern formation and to understand how these mechanisms generate morphological variation. In this presentation, I will compare the genetic and the morphogenetic approaches to evo-devo in the light on the contemporary philosophical debate on causation. I claim that the morphogenetic approach to evolution challenges reductionism in a way that has been poorly explored in philosophy of biology, which mostly revolves around the notion of 'factor'. For example, proponents of Developmental Systems Theory have argued that development and inheritance cannot be reduced to genetic factors, but that other non-genetic (cytoplasmic or environmental) resources need to be equally incorporated in evolutionary explanations. I argue that the morphogenetic approach challenges reductionism in a very different way, by focusing on mechanisms corresponding to different levels of organisation rather than factors.

Theoretical and Methodological Diversity in the 1980s: Early Development of Evo-devo

Yoshida Yoshinari, Kyoto University, Japan

When the development of evolutionary developmental biology (for short, "evo-devo") is discussed, it is often said that in the 1980s, there were diverse movements that rethought the relationship between evolution and development (Love and Raff 2003; Laubichler 2010). The aim of this talk is to point out that some of the movements in the 1980s attempted to and actually did partially integrate methodologies and results of diverse disciplines. Moreover, I argue that they had significantly different positions on the accepted framework of the Modern Synthesis.

For example, some researchers attempted to *include* development *into* the gene-centered framework of the Modern Synthesis depending mainly on results from developmental genetics and also on those from comparative embryology, paleontology, or comparative morphology. (e.g., García-Bellido 1983; Raff and Kaufman 1983). Other researchers, however, *criticized* such a gene-centered and adaptationist framework: They tried to demonstrate the importance of epigenetic mechanisms to evolution by integrating methodologies and results of comparative morphology and experimental embryology (e.g., Alberch and Gale 1985; Hall 1984; Müller and Streicher 1989). Thus evo-devo was formed as the combination of these different interdisciplinary researches in the 1980s, and therefore has included the *opposing* positions on the gene-centered and adaptationist framework of the Modern Synthesis.

Gene Networks in Developmental Evolution: What do Common Developmental Mechanisms mean for Evolutionary Explanations?

Racine Valerie, Arizona State University, USA & University of Western Ontario, Canada

In the Gene Regulatory Network approach to evolutionary developmental biology, phenotypic evolution is considered to be a consequence of modifications of regulatory factors within gene network architectures. By focusing on large parts of the genome as an integrated regulatory system, rather than on allele frequencies of particular gene loci, this approach introduces a distinct kind of experimental and causal-mechanical thinking into the study of evolution. It also suggests a new *manière de faire* for studying evolution: instead of the manipulation of phenotypic characters to study fitness consequences, the design of selection experiments tracking changes in allele frequencies in different populations, or the introduction of mutagens into different population strains, it can proceed by intervening in the genome (and gene regulatory networks) to re-engineer phenotypic changes that have occurred in evolutionary history. In this paper/presentation, I propose to focus on a case study depicting deep homology to delineate the distinctive explanatory framework of the GRN approach in developmental evolution. I consider research on the origin and evolution of beetle horns, which questions whether beetle horns have arisen independently numerous times and, if so, whether they have occurred via the same mechanism (Shubin, Tabin, & Carroll 2009). Recent studies by *Moczeket al.* (2006) show that the potential of horn formation via a common mechanism is widespread in several species of beetles, including hornless species.

I argue that the way in which the GRN approach frames macro-evolutionary inquiry into deep homology can provide explanations that diverge from functional and selectionist accounts of evolutionary history and evolutionary processes. For instance, if the developmental mechanism responsible for the formation of beetle horns in diverse species are highly conserved or deeply homologous, then parallel evolution might be ubiquitous, or at least perhaps more important than convergent evolution, in explaining some phylogenetic patterns.

Philosophical perspectives on and from systems biology

Systems biology and the quest for organizing principles

Green Sara, Aarhus University, Denmark

With the emergence of systems biology the notion of organizing principles has been (re) introduced in the life sciences. I highlight the motivation behind the intensified search for organizing principles and reflect on their epistemic role in scientific practice.

Organizing principles are abstractions that reflect general system properties; possibly signifying what counts for *any* cell, *any* organism or *any* control system. I suggest that organizing principles can be understood as templates for relational and dynamic properties in a double sense; i) as coarse-grained sketches for developing more detailed models of biological phenomena, and ii) as higher order abstractions for understanding general dynamic properties for classes of typified systems. They are investigated within an abstract mathematical framework that facilitates transfer of methods and concepts across systems, levels and even disciplines. Thus, organizing principles are not only templates for arriving at de-idealized mechanisms but also provide an investigative framework for the ongoing search for general features that underpin the organization of biological systems at a higher level of abstraction than much of biological research.

Their role as de-contextualized abstractions at first sight seems to be at odds with the widely accepted view that explanations in biology are descriptions of biologically specific and contextdependent mechanisms. However, the goal of organizing principles is different from mechanistic explanations; it is to signify how a class of systems works "in principle", abstracting from the detailed dynamic features of biological systems. I therefore argue that this approach is complementary to, rather than conflicting with, finer-grained mechanistic explanations.

A standard for dividing labor in systems medicine

De Langhe Rogier, Tilburg Center for Logic and Philosophy of Science, Netherlands
Wolkenhauer Olaf, Universität Rostock, Germany

There is increasing evidence that systems medicine will be required to deal simultaneously with subcellular, cellular and tissue level phenomena in order to explain how biological function at the tissue, organ or whole organism level emerges from the interactions of molecules and cells.

Systems medicine arises from the coming together of large-scale data analysis and high-level network modeling using bioinformatics approaches and few-variable mechanistic modeling using dynamical systems theory. The need for integration of these various types of models confronted biologists with an acute need for reflection on important philosophical questions concerning *scientific virtues* (can a single type of model maximize all virtues simultaneously?) and the division of *cognitive labor* (should all scientists work on the same type of model or should the community hedge its bets?). Richard Levins (1966) offered a glimpse of what such a framework might look like. In this joint paper by a systems biologist and a philosopher of science we extend this framework and apply it to systems medicine. Our aim is to provide a standard for dividing labor in systems medicine. Increased coordination on a common standard for dividing labor in systems medicine has the potential to lead to substantial gains in scientific productivity.

Articulating Mechanisms in Molecular Systems Biology

Richardson Robert, Boogerd Fred, University of Cincinnati, USA

We contrast two broadly different approaches toward developing mechanistic explanations, specifically within molecular systems biology. One focuses on modelling system behaviours, without specific attention to information concerning the composition of the system. The other constructs models based on independent information concerning the parts, processes, and organization present. On the former approach, the development or "articulation" of mechanistic models includes four phases, beginning with an initial adequate description of systemic behavior, and ending with the articulation of an elaborate a causal model. This approach to modelling the behaviour of complex systems has a number of strengths. Most importantly, it emphasizes the idea that we must at least begin with some reasonably robust phenomenon to be explained. So, for example, the characteristic switching behavior exhibited in the growth of micro-organisms under changing nutritional regimes is a phenomenon that is relatively robust and important. It demands a causal and mechanistic model. The latter approach follows a different, more constrained, methodology. These latter models emphasize functional composition rather than functional decomposition, with more detailed structural data, including kinetic data concerning componential behavior, and complex networks. Much of contemporary molecular systems biology offers its allegiance more to the detailed modelling of pathways, given better information about component capacities, and somewhat less to its cybernetic ancestors. We sketch an analysis of heuristics in mechanistic explanation of this latter sort and emphasize the dynamic 'fluid' character involved in the process of articulating and elaborating mechanistic models.

Physiology in the 20th Century

Forged Together: Anglo-American Physiologists and the Structure of War and Post-War Physiology 1935-1955

Casper Stephen, Clarkson University, USA

Historians in recent years have begun examining how relationships between locales in different nations have shaped scientific communities, identities, and research. Using such studies as a springboard, this paper considers the origins and assumptions of a transnational collaboration in basic and applied research that formed among Anglo-American physiologists during the Second World War. At that time, physiologists on both sides of the Atlantic created a powerful network focused on questions of joint defence. Including such figures as E. D. Adrian, John F. Fulton, Detlev Bronk, Henry Dale, and A. V. Hill, these physiologists endeavoured to link governmental policy with research in university and industrial laboratories to create highly efficient joint research ventures that did not replicate work in any of the participating nations. The most famous result from these collaborations was penicillin, yet the questions I wish to pursue in this social history are broader than any story of scientific discovery. Did the transnational nature of physiological research exert an impact on the social, political, economic, and industrial structure of wartime science? And did Anglo-American physiologists play a significant role in the formation of government funded research and did their role stop there or did they serve broader diplomatic roles as well? In short, the answers to such questions, investigated in trans-Atlantic archives, may shed light on how these collaborations began and the way their existence promoted a longer-lasting influence on the organization of international science.

The erythrocyte “has a life span” - erythrocyte aging between experimental and mathematical approaches

Almeida Maria, ICBAS, University of Porto, Portugal

Present paper explores the early twentieth century debate around the life span of the erythrocyte.

Research around this problem is rooted in the clinical realm. Several studies were related to the interest in better understanding the basis of different cases of anemia. The evidence of a normal process of selective removal of old cells has focused attention to the study of the aging process of this specific blood cell and in a way marks the emergence of the aging erythrocyte as a biomedical object. Later, the mammalian cell became a promising experimental model in the study of aging, an idea fully embodied in papers published in the 1980s.

Whether these cells are removed from circulation at random or by age was object of much investigation and debate throughout a few decades. Both experimental and mathematical approaches were extensively used in the study of erythrocyte survival. In the late 1930s, Schiødt locates the discussion between a "theory of longevity" and a "theory of destruction". The isotopic labeling technique developed by Shemin and Rittenberg provided compelling evidence that the erythrocyte "has a life span", as these researchers conclude in a paper published in 1946. This evidence refers to the normal circumstances in humans and the study of survival curves proceeded in different species and conditions.

Here, I will look at the interplay between experimental and theoretical analysis in building broadly accepted knowledge with regards to the erythrocyte survival arguing that both approaches were fundamental in defining erythrocyte aging.

Playing by their own rules: marginality and heterodoxy in modern science

Defining Wild: Japanese Primatology and Monkey Parks

Setoguchi Akihisa, Kyoto University, Japan

Since their encounter with modern science, Japanese scientists have tried to catch up with Western science. However, primatologists at Kyoto University in the 1950s were different. Although they tried to publish their papers in English, for international academics, they willingly distinguished their methods from the Western style. This paper discusses why Japanese primatologists pursued two contradicting paths: internationalization and marginalization. In 1952, primatologists at Kyoto University, led by Kinji Imanishi, succeeded in feeding Japanese monkeys (*Macaca fuscata*) at Koshima and Takasakiyama, which made long-term observation of these monkeys possible. Afterward, some wild monkey parks were designated for public leisure. However, there were some critics against feeding, claiming that it altered the behavior of wild monkeys.

Primatologists defended feeding method, stating that it was the Japanese way of confronting nature, which obscures the boundary between human and animal. Monkey parks entertained a vast amount of tourists until the 1970s when younger generations of primatologists began to criticize them. This paper will show how Japanese primatologists defined a border between artificial and wild nature, using self-orientalism to attract the attention of the lay public and international academics.

Science for gentlemanly breeders? British acclimatisation revisited

Ito Takashi, Kanazawa Gakuin University, Japan

Much has been written on the comparative and global histories of acclimatisation in the nineteenth and early-twentieth centuries. In France, the acclimatisation movement thrived under the leadership of Isidore Geoffroy Saint-Hilaire, who founded the Société zoologique d'acclimatation in 1854. By contrast, in Britain, acclimatisation appeared to be practiced only by a limited circle of gentleman menagerists, failing to evolve into a disciplinary science. The Acclimatisaiton Society of the United Kingdom (1860-4) was indeed castigated as a dining club of epicurean gentlemen. This paper, however, rethinks the trajectory of British acclimatisation by identifying its long-term development and contributions. A variety of breeding experiments began to be conducted with the foundation of the Zoological Society of London in 1826, and in the late 1850s the society tried to collect a breeding stock of Himalayan pheasants in its attempt to acclimatise them in the Scottish Highlands. In the late nineteenth century, acclimatisation remained to be spontaneous and leisurely practices of gentleman breeders. Expertise on nomenclature, breeding and the effect of climatic change on animal physiology was often provided by specialist zoologists such as Alfred Russell Wallace and Phillip Lutley Sclater, secretary of the Zoological Society, both of whom later published on the geographical distributions of animals. The study of acclimatisaiton involved investigating the relationships between the distribution of species and environmental condition: it was the legacy passed on to the emerging field of zoogeography.

‘My sole intention in that country is to obtain a giraffe’ – Science, patronage, and the local merits of an African expedition in Restoration Frankfurt am Main

Sakurai Ayako, Senshu University, Japan

Eduard Rüppell (1794-1884), son of a wealthy Frankfurt banker and merchant, undertook two expeditions to northwest Africa in the early nineteenth century to collect natural-historical specimens for the museum of his native town. The purpose of this paper is to set Rüppell's enterprise against Frankfurt's culture of civic patronage, and to show how a local scientific culture could affect the extent and reception of a scientific expedition.

The first part of the paper will focus on Rüppell's first journey (1822-27), which took him through the upriver regions of Egypt to Sudan. Unusually successful in obtaining the assistance from the Egyptian army, which had just placed Sudan under their control, Rüppell managed to collect specimens in areas previously uncharted by Europeans, most importantly Kordofan, a region of central Sudan lying west of the White Nile. The second part will investigate the reception of Rüppell's journeys at home. The rich spoils from the expedition, including the giraffes from Kordofan, were donated to the museum of the Senckenberg Society in Frankfurt, pushing the institution into the European limelight. By the mid-1830s, the Senckenberg Museum was regarded as one of the top five natural history collections in Europe. The paper will point out that a powerful ideology of patriotic contribution, guiding intellectual practices in contemporary Frankfurt, framed the reception of Rüppell's enterprise. It will go on to suggest that the same ideology determined to a large extent the scope and objectives of the expedition, as well as the institutional strategy of the Senckenberg Museum.

Predictive ecology in a changing world: from data to practices

When the bio-sphere becomes a data-sphere: quantifying nature for big ecology

Devictor Vincent, Université Montpellier II, France

Several scientific disciplines have entered a "data world" following the information revolution, the development of computer networks and Internet facilities. In this talk, I will question whether, how, and why the raise of new techniques of quantifications has changed the perception of nature in ecological sciences. Using concrete examples, I will i) discuss how natural objects are transformed into data, ii) illustrate how a new spatiality and temporality emerge from this transformation, iii) assessed whether this process has created an autonomous data-sphere with its own normative and scientific rules. I will then propose a critical analysis of this transformation to show how it opens a route for new social strategies and uncertainties. Overall, this talk proposes to illustrate how ecology is, to some extent, progressively sharing similarities with what was identified as "big-sciences" and "techno-sciences" in modern epistemology.

The two meanings of "prediction" and their consequences in ecological science

Calba Sarah, Université Montpellier II, Ecole Pratique des Hautes Etudes, France

In this presentation, I will critically investigate the notion of prediction in science, especially in ecology and the consequences of its meanings and usages. I will focus on three complementary main axes: (i) the general definition of the notion of prediction in science; (ii) the epistemological singularity of ecology as a science with respect to predictability; (iii) the consequences of the interplay between ecology and human society on the problem of prediction. I will show that the term "prediction" hides two meanings. Traditionally, prediction is regarded as being central to science because it represents a key step to explanation. Scientists make predictions about observable phenomenon in order to corroborate or to "test" a theory. In this case, the concept of prediction corresponds to an epistemic problem. However, the concept of prediction has recently gained a different meaning. It also refers to an anticipation of the future in the view of action.

Prediction is therefore often considered as a practical tool synonymous of forecast, projection, or scenario. In this case, the prediction in itself is important and does not necessarily relate to a theory testing. I will show with concrete examples how these two meanings (epistemic and practical) have in turn different consequences in ecological science. Indeed, the most pressing environmental problems require scientists to “predict” the effects of global changes. But their models and results will have different implications according to the meaning of prediction they adopt.

The methodological individualism of individual-based modeling in ecology

Justus James, Florida State University, USA

Cross-pollination between biological and economic theorizing has a long and fruitful history. Evolutionary economics and evolutionary game theory are prominent examples, and recent philosophical work has targeted the same confluences. But evolution is only one indispensable part of biology. Ecology is clearly another, yet cross-fertilization of ecological and economic theorizing remains largely unexplored. In particular, connections between methodological individualism (MI) and individual-based models (IBMs) in ecology are underappreciated. MI is a multifaceted set of principles, but a common denominator is privileging the individual-level in explanations of higher-level social phenomena. IBMs embody this perspective in ecological science. Just as actions of individual (putatively rational) agents constitute the preferred level of analysis according to MI in economics, individual organisms function similarly in IBMs. Evaluating the analogy is one task of this paper. Interestingly, recent work establishing links between rational choice theory and evolutionary theory suggests the ecological analogy is also apt. Another task is showing that arguments about MI in social science reveal insights about how IBMs in ecology should be understood. For example, the explanatory priority on the individual MI requires does not require ontological reductionism of population-level properties to the individual-level. Different methods for scaling actions of individual agents to higher-level social patterns also indicate how relationships between rational choice and evolutionary theory might be scaled to the ecology of biological populations and communities.

The Problem of “Race” A (submitted papers)

Remeasuring Man

Weisberg Michael, University of Pennsylvania, USA

Samuel George Morton (1799-1851) was the most highly regarded American scientist of the first half of the 19th century. Thanks largely to Stephen Jay Gould's book *The Mismeasure of Man*, Morton's measurements of cranial capacities of different races is now held up as a prime example of and cautionary tale against scientific racism. Recently, a team of anthropologists reevaluated Morton's work and argued that it was Gould, not Morton, who was biased in his analysis. This paper is a reexamination of the Morton and Gould controversy. It argues that most of Gould's arguments against Morton are sound. Although Gould made some errors and overstated his case in a number of places, he provided prima facia evidence, as yet unrefuted, that Morton did indeed mismeasure his skulls in ways that conformed to 19th century racial biases. Gould's critique of Morton ought to remain as an illustration of implicit bias in science.

The use of the concept of race in biomedicine: the hypothesis of social causes undermines the utilitarian argument

Lorusso Ludovica, University of Sassari, Italy

Nowadays it is generally accepted that the use of racial categories in biomedicine may reinforce social differences among racial categories; however, it has been claimed that this is the price that must be paid in order to reduce the differences in risk of complex diseases among them. In this paper I will show that this utilitarian argument can be accepted only under the “genetic hypothesis” about the existence of genetic differences among races that cause the differences in risk. " Races" used in biomedicine are categories constructed on the basis of selfdeclarations: they are not taxonomic categories but categories depending on personal beliefs about group membership characterized by several social and cultural properties, like having a specific behaviour, sharing a specific environment, eating specific food, etc. Given that, such categories are characterised by strong cultural and social differences that should be considered in causal explanations of differences of risk of diseases: why should the genetic hypothesis be preferred to the "social hypothesis" invoking social differences among races as causes of the differences in risk? I will show that the current biological theories in genome-disease associations support the role of environment in causing predisposition to complex diseases. If the differences in risk of diseases among racial categories are more likely to be caused by social differences than by genetic differences, the utilitarian argument cannot be accepted, since to reinforce social differences would mean in fact to reinforce the causes of the differences in the risk of diseases.

The Last Race Realisms

Barker Matthew, Concordia University, Canada

This paper improves arguments for recent and sophisticated views concerning biological realism about race, but also helps move many of us beyond this issue altogether.

I first argue that if we are going to inquire about whether races are biologically real, we should reconfigure the way this issue has been framed and pursued till now. My new way uses recent work on property clusters to make common but unclear appeals to non-essentialist natural kinds more precise. This allows us to uncover and articulate several distinct and often confounded sorts of biological realism about race, some more interesting than others. I then show how this helps improve on existing reasons to think that *clinal* biological races are unreal in some respects, and in others are real but uninterestingly so. Likewise for *cluster* biological races, and *clade* biological races. More generally the needed innovative reconfiguring more convincingly points evidence in support of the view that each biological realism about race is either false or vacuous.

However I next argue that many of us have less reason than often supposed for inquiring in the first place about whether races are biologically real. For instance, even when a particular biological realism about race is false, any favored anti-realist counterpart is often of less interest than supposed. When race matters practically and theoretically, it is often because of associated claims about causation, intervention, and prediction, the truth-values and justifications of which are not influenced by verdicts about realisms.

The Problem of "Race" B (submitted papers)

Racial Certificates and "Jewish Racial Traits": Otmar von Verschuer and Nazi Racial Policy Practice at the Institute for Human Heredity and Racial Hygiene, 1936-1942

Weiss Sheila, Clarkson University, USA

This paper seeks to make a contribution to our understanding of the specifics of racial policy practice in the Third Reich as well as the racial certification process at Otmar von Verschuer's Institute for Human Heredity and Racial Hygiene. I will focus on a recent and heretofore uninvestigated archival find intricately linked to National Socialist racial policy: 247 racial certificates completed in von Verschuer's research center between 1936 and 1945. An analysis of the racial certificates constructed at von Verschuer's Frankfurt Institute can hence disclose valuable information on the relationship between National Socialist racial policy and practice.

Moreover, it raises the contested issue of whether or not such ancestral examinations based on the concept of "Jewish racial traits" were undertaken according to "scientific criteria" of the day, while simultaneously demonstrating the sometimes subtle, sometimes not-so-subtle, mixture of ideological prejudice and scientific practice as they combined in these examination procedures.

Finally, considering the nefarious collaboration between von Verschuer and his protégé Josef Mengele during the war years and the historiographical preoccupation with their medical offences, it is also worth asking whether von Verschuer and his former student's duties as "racial experts" can help explain why they decided to undertake their notorious investigation of "specific proteins" at the world's most infamous death and slave labor camp.

Survival of the Fittest during the First World War: Herbert Spencer, the French Army, and the Development of La force noire, 1890-1920

Lunn Joe, University of Michigan, USA

In *La force noire*, his influential feasibility study of 1910 about recruiting West African soldiers to defend France in the event of a World War, Colonel Charles Mangin sought intellectual validation for his ideas by invoking Herbert Spencer: "the philosopher...who had conducted the most profound study of the organization of human societies and their development in history." Citing Spencer's *Principles of Sociology*, Mangin embraced the Englishman's theoretical construct of "progressive evolution" and contended that a dichotomy existed between as yet " primitive" but "militant" societies, and their more highly evolved "industrial" counterparts. Referring to the "warrior instincts that remain extremely powerful in primitive races," Mangin concluded that West Africans possessed exactly those attributes that made them ideal for use as " shock troops" by the French in the event of a European war.

Mangin's scheme for expanding recruitment in West Africa for service overseas was not new; indeed, it had been advocated by a series of French Colonial Army officers--including Louis Archinard, Henri de Lacroix, Charles Perreaux, and Marie Audéoud -prior to 1910. His explicit linking of this scheme to Spencer's race theories, however, and their subsequent incorporation into the military organization, language instruction, and tactical doctrine of the Colonial Army between 1914 and 1918, offers an explicit glimpse of the Englishman's institutional influence in France. More broadly, it also provides an insight into the significance of Spencer's ideas for French imperialists, as well as the tragic human consequences of linking race theory to military doctrine during First World War and, indeed, long thereafter.

Do I look Mexican? The Reification of a National Face

Nieves Abigail, Universidad Nacional Autónoma de México, Mexico

About a century ago, Bertillon proposed methodologies based on facial features for identifying criminal suspects. The *portrait parlé* and the mug shot techniques were extensively popularized. They had a strong influence in the procedure to establish individual identity. 20 years ago, three anthropologists from the Institute of Anthropological Research at UNAM in Mexico City started developing a computerized system for personal identification through facial features. This system is now widely used by the Mexican Police Department and represents a landmark for similar systems in Latin America. Stemming from Bertillon's legacy, "Caramex" aims to construct more accurate portraits using a photographic database; a record of pictures obtained by sampling representative regions in the Mexican territory. Assuming a tri-hybrid origin of Mexicans (Indigenous, European and African), researchers looked at the current population to find "the typical physical traits"; in other words, to construct the Mexican face.

In this presentation, I will show how this system of identification imposes a new grid of interpretation on human variation. In the process of defining what a *mestizo* phenotype is, the system reifies a typical biological and national face. In generating a limited set of ears, eyes, mouths, eyebrows, etc., to represent all facial variation found in the country, the system inscribes into the human body notions of common origin and nationality.

The Problem of Species A (submitted papers)

Cohesion and the Individuality Thesis

Neto Celso Antônio, Federal University of Minas Gerais, Brazil

This paper examines the concept of cohesion in the realm of the species-as-individuals thesis. Firstly, we present one main theoretical role it plays on David Hull's account of individuality: cohesion as a synchronic individuating criterion to individuals. Then, we discuss this role in regard of different senses of "cohesion" present in the literature, such as structural, functional, responsive and integrative cohesion (e.g. Hull, 1980; Wilson & Barker, 2010). The discussion seems to show either that cohesion isn't an attribute of all species or that it is something rather trivial. Facing this dilemma, some philosophers choose to relativize the species-as-individuals thesis, whereas others choose to deny it. But there's a way out. One obvious possibility is to refuse the connection between the individuality thesis and cohesion (Ghiselin, 1987, 1997). This option encounters difficulties, at least if we maintain that individuals are synchronically individuated entities. Another possibility is to re-articulate the concept of cohesion. The fruitfulness of such option will be defended at the core of this paper. In particular, we argue for a more relaxing way of treating "cohesion" based on the diversity of biological individuality. If we pay attention to different concepts of biological individuality, we can note different mechanisms that satisfy the theoretical role described above. The cohesive character of biological individuals is diverse, such that no unique sense of "cohesion" can be prescribed to them. So it`s better to take "cohesion" as a complex concept composed of different variables and subject to variation in degrees.

The Perdurantist Implications of the Species-as-Individuals Thesis

Martin August, Leiden University, Netherlands

In this paper, I argue that the species-as-individuals (SAI) thesis has broader and as yet unexamined metaphysical implications in that it entails a perdurantist view of biological ontology. Perdurantism holds that entities "perdure" over time by having both spatial and temporal parts and full spatiotemporal extension. Endurantism, by contrast, holds that entities "endure" over time by having only spatial parts and spatial extension, and existing wholly and completely every moment. The SAI thesis, as its principal supporters agree, is committed to perdurantism. It holds that species are "historical entities" that are "spatiotemporally localized" (Hull 1978). Spatiotemporal location is extension in both space and time, hence Hull's amplified claim that species are "spatiotemporally extended" (1989). Crane (2004) argues that if the SAI thesis is committed to a relational view of species as concrete ancestor-descendant lineages, then it has a four-dimensional view. This is in fact the predominant view of the SAI thesis (Horvath 1997). Because the parts of perduring entities must also perdure, the SAI thesis is committed to viewing organisms, as parts of species, as perduring entities. This implicit facet of SAI is reinforced by Hull's (1978) explicit reliance on Huxley's (1898) perdurantist view of biological entities. The SAI thesis thus extends perdurantism to the entirety of biological ontology. These implications should be carefully considered because the metaphysical issue of persistence is contentious and perdurantism is not universal in philosophy of biology.

The Idea of Neo-Biological Species Concept -A new approach to responding the old debates

Lai Bo-Chi, Da-Yeh University, Taiwan

In Biology, "Species" is a very fundamental and controversial idea, and philosophically, "Species " is a relatively distinct grouping of individual organisms. Both extend into our understanding of human nature. The "Species" problem arisen by the worries of the realism and pluralism (debates of Claidge and Misheler in 2010). Nevertheless, there were dozens of species concepts have been being proposed, and there are the Biological Species Concept (BSC, proposed by E. Mayr), the Hennigian Species Concept (HSC, by R. Meier and R.

Willmann), the Phylogenetic Species Concepts (PSCs, by both B. D. Mishler/E. C. Theriot and Q. D. Wheeler/N. I . Platnick) and the Evolutionary Species Concept (ESC, by E. O. Wiley and R. L. Mayden) will remain being discussed mainly in this century (Wheeler and Meier, 2000).

In this article, I will construct a species concept named Neo-Biological Species Concept (Neo-BSC), which is an alternative of Mayr's BSC with reproductive isolation mechanism, based on the signal-communication theory, which is a model of "individuality" demonstrated by biological relationship of the *Volvox*. I will illustrate my Neo-BSC, and try to reveal the followings: (1) How my Neo-BSC can be both theoretical and practical applications to the biological need; (2) How my Neo-BSC can be developed from Mayr's BSC, and responds the critiques of HSC, PSCs and ECS; and (3) The Neo-BSC can be constructed and treated as the definition of the "individual " deduced by the signal-communication theory.

A Process-Focused Approach to the Species Problem

Skillings Derek, CUNY, USA

It is widely agreed that there is no unified species concept that that can be used to both describe and categorize the entire diversity of life. There has been extensive debate about whether the concept *species* accurately captures a real feature of the natural world (de Queiroz, Dupré, Ereshefsky, Hey, Mishler). I try to move beyond the existing debate by arguing that the most important task for delimiting species is to understand the processes that generate diversity. A focus on identifying the processes crucial to creating differences in lineages is important because the causal processes underlying species integrity (or lack thereof) do not act uniformly act across the diversity of life (Hart; Padial and de la Riva; Sobel). This necessitates us to be species pluralists because different kinds of species kinds are produced by the differential interaction of causal processes. I further suggest that this kinds-of-kinds pluralism does not require one to be an antirealist about species, and that the species category is united by being the collection of entities that are produced by the lineage-splitting processes that act on populations.

The Problem of Species B (submitted papers)

Is the Ontology of Homologous Traits a Matter of Pragmatics?

Pearson Christopher, Southern Illinois University Edwardsville, USA

Homologous traits are analogous to species in philosophically interesting ways. Homologous traits and species are units of evolution, for example. Not surprisingly, metaphysical questions that are well known for species can also be seen as salient for homologies. Species are classically viewed as classes wherein individual organisms are members of a class. But ever since Ghiselin (1974) and Hull (1978), many theoreticians have defended the view that species are individuals, whereby organisms stand in a part-whole relation to species. In the case of homologous traits, it now common to see defended the position that homologies are homeostatic property cluster (HPC) kinds (Wagner 2001, Rieppel and Kearney 2007). Alternatively, and as one might expect, the evolutionary change/anti-essentialist rationale underlying the species as individuals view would appear to apply no less to homologies.

Between the kind and individualist views, there is also a third way, one that contends that the ontology of species, and homologies as well, is not metaphysically determined (Brigand 2009). This third way maintains that the recognition of species and homologies as either classes or individuals is a matter of pragmatics. The present paper is an attempt to further advance this pragmatic approach to thinking about the ontological character of homologous traits. In particular, the paper aims to articulate the comparative practical advantages of the respective kinds and individualist view of homologous traits. For the kinds perspective, I point to developmentally derived inductive inferences about homologies, and for the individualist perspective I cite the practice of circumscribing clades via what I term associative identification.

Models of species metaphysics
Ventura Rafael, Duke University, USA

Debates about the ontological status of species have traditionally been divided into two camps: advocates of Hull's individuality thesis, and its critics. In this talk, I avoid the dualism of opinions by defending a form of pluralism. According to this view, all of the following statements are true: (1) some species are individuals but not kinds; (2) some species are kinds but not individuals; and (3) some species are both individuals and kinds.
To argue for these theses, I delineate three models of speciation. Model 1 is the familiar case in which there is a strong positive correlation between resemblance and relatedness. Since related organisms are similar, organisms belonging to a single lineage also form a robust kind. Species-individuals are therefore species-kinds and both ontological forms coincide.
In Model 2, resemblance is negatively correlated with relatedness. Organisms of the same kind resemble one another but do not constitute a single individual because they are the scattered parts of distinct lineages. If any species were to approximate this scenario, ontological categories would drift apart and individuals and kinds would *not* coincide.
In Model 3, there is no correlation between resemblance and relatedness. Some organisms form kinds, but members of such kinds are not the parts of an individual lineage. As a consequence, species-kinds and species-individuals do not coincide and ontological categories again become dissociated. Some details about microbes support the relevance of this model.
My conclusion is that the ways in which species happened to evolve explain their ontological status.

Informationally-Connected Property Clusters and Polymorphism
Martinez Manolo, CUNY, USA

I present and defend a novel version of the homeostatic property cluster [hpc] account of natural kinds. The core of the proposal is a development of the notion of co-occurrence, central to the hpc account, along information-theoretic lines. The resulting theory retains all the appealing features of the original formulation, while increasing its explanatory power, and formal perspicuity. I showcase the theory by applying it to the (hitherto unsatisfactorily resolved) problem of polymorphic species.

Psychological Altruism from a Biological Point of View A

Altruism, Egoism, or Neither? The Evolution of Psychological Capacities for Helping Behaviour
Schulz Armin, London School of Economics and Political Science, UK

In this paper, I assess the role that evolutionary theory can play in the debate about the plausibility of psychological altruism. In particular, I try to resolve a specific kind of argumentative impasse that has been reached in evolutionary theorising concerning psychological altruism: the fact that egoistic architectures can evolve so as to be behaviourally indistinguishable from altruistic ones. This indistinguishability stems from the fact that any behaviour that could result from an ultimate desire for the well being of others - what 'altruism' is typically taken to mean - could just as reliably result from an egoistic ultimate desire (say, for the maximisation of one's own pleasures) that is coupled with a suitably 'sticky' belief (say, that helping others is the best way to maximise one's own pleasure). Given this, I then present a new evolutionary argument suggesting that the latter kind of egoistic helping behaviour is evolutionary unstable. This instability derives from more general facts about when it is adaptive for an organism to rely on representational mental states (like beliefs and desires) when deciding what to do. Specifically, the adaptive benefits of representational cognition vis-à-vis reflexes lie in its ability to streamline complex decision problems in a specific way. In turn, this suggests that, evolutionarily, the reliance on 'sticky states' in the determination of helping behaviour will be merely a temporary stepping stone on the way either to full blown altruism or to reflex-determined helping behaviour that is neither altruistic nor egoistic.

Two Types of Psychological Hedonism
Garson Justin, CUNY, USA

I develop a distinction, suggested by LaFollette's 1988 paper, "The Truth in Psychological Egoism," between two types of psychological hedonism. *Inferential* hedonism (or " I-hedonism") holds that each person only has ultimate desires regarding his or her own hedonic states (pleasure and pain). *Reinforcement* hedonism (or "R-hedonism") holds that each person's ultimate desires, whatever their contents may be, are differentially reinforced in one's cognitive system only by virtue of their being associated with pleasure. In short, I-hedonism is a theory about the content of ultimate desires; R-hedonism is a theory about theirfunction. I'll argue that accepting R-hedonism and rejecting I-hedonism coheres well with the neuroscientist Anthony Dickinson's theory about the evolutionary function of hedonic states, the 'hedonic interface theory'. In his view, pleasure and pain regulate one's hierarchy of desires *not* by being part of the representational content of one's ultimate desires, but by serving as a kind of reinforcement mechanism that grounds the "belief-desire psychology" in the biological needs of the organism. Finally, I'll defend R-hedonism from a potential objection. In *Unto Others*, Sober and Wilson develop a fairly compelling argument that psychological altruism (as a view about the content of one's ultimate desires) is more likely to have evolved by natural selection than I-hedonism. I'll suggest that their argument against I-hedonism cannot be converted in any straightforward way into an argument against R-hedonism, because, unlike I-hedonism, we have noa prior basis for comparing R-hedonism and its alternatives with respect to their energetic efficiency (or metabolic cost).

Why there might not be an evolutionary explanation for psychological altruism
Stich Stephen, Rutgers University, USA

Following Batson and Sober & Wilson, I will use "psychological altruism" for the claim that people have ultimate (or non-instrumental) desires for the well-being of others. Behavior is psychologically altruistic if it is motivated, at least in part, by such an altruistic desire. The first claim I will defend is that it may be premature to seek evolutionary explanations of psychological altruism, since it is far from clear that psychological altruism *exists*. Batson and colleagues have set out what is perhaps the best case for the existence of psychological altruism. However, their work has focused almost entirely on a cultural group - WEIRD American college students - who are known to be outliers in many psychological tasks. If psychological altruism is a culturally local phenomenon, then it is far from clear that we should expect an evolutionary explanation. The second claim I will defend is that almost all of the psychological work on altruism is compatible with the hypothesis that the ultimate desire motivating putatively altruistic behavior is actually a desire to comply with norms. The third claim I will defend is that the work of Boyd, Henrich and others has provided a compelling account of the evolution of norm psychology which suggests that non-self-interested, group-beneficial norms should be widespread, though the details should differ from culture to culture. This is *not* an account of the evolution of psychological altruism, but it does provide an evolutionary explanation of the behavior that may have been mistakenly taken to be altruistic.

Psychological Altruism from a Biological Point of View B

Preference altruism: a conceptual link between economics and evolutionary biology

Clavien Christine, Université de Lausanne, Switzerland

An increasing number of researchers in economics argue that humans behave more altruistically than classical economic theories allow for. The most common form of altruism discussed in this literature is labelled "strong reciprocity" (SR), which is the combination of a predisposition to reward others for norm-abiding behaviours, and a propensity to impose sanctions on others for norm violations (Fehr & Fischbacher 2003). Evolutionary explanations (usually cast in terms of group selection theory) are proposed to account for the emergence and maintenance of this behaviour. First, I'll argue that conceptual clarification of "strong reciprocity " is needed in order to overstep its unsatisfactory level of generality. Second, I'll propose the notion of "preference altruism" as a candidate link between economics and biology, and explore its epistemic virtues for developing connections between neo-classical economics theory and evolutionary biology.

In the literature, SR carries two related but distinct meanings. At times, it refers to "behavioural altruism", which involves bearing some cost in the interest of others. At other times, SR denotes " preference altruism", which refers to other-regarding preferences contained in humans' utility functions (Clavien & Chapuisat 2013). These two meanings are close but not equivalent to the psychological and the biological versions of altruism (Sober & Wilson 1998).

At first glance, one might think that "behavioural altruism" (similar to the biological use) is the most promising link-concept between economics and biology. After analysis however, " preference altruism" (closer to psychological altruism) proves more helpful. I'll show examples of population genetics models, based on kin selection theory, that investigate altruistic preferences.

Psychological Altruism from a Biological Point of View - Some Recent Perspectives

Chandra Sripada, University of Michigan, USA

I challenge psychological hedonism and psychological egoism, the theses that apparently altruistic actions are instead always motivated by desires for pleasure or other self-interested goals as ultimate ends. My challenge is based on a model of human motivational architecture that has received substantial quantities of support in the recent cognitive neuroscience literature. The model divides motivational architecture into two distinct systems. The function of the reward/ instrumental system is learning; it is responsible for identifying which states of affairs predict, on the condition that certain action sequences are undertaken, the receipt of rewarding outcomes. The function of the hedonic system is representational. Pleasure functions to signal that rewarding states of affairs are in fact being realized.

If this model is correct, then this has ramifications for psychological hedonism and egoism. First, psychological hedonism is unlikely to be true because it contradicts the distinct functional roles assigned to pleasure and reward; the model says pleasure has a representational function, while psychological hedonism says it has a reward function. Psychological egoism is unlikely to be true because this theory makes predictions about neural activation patterns in the brain structures that implement the model's two systems. These predictions are not supported by the neuroscientific evidence.

Public/scientist partnerships in the production of biomedical knowledge: the gamers, the advocates and the enablers

Public/scientist partnerships in the production of biomedical knowledge: the gamers

Magnus David, Stanford Center for Biomedical Ethics, USA

Foldit, an online game developed by researchers at the University of Washington made headlines in 2011 when its gamers were able to solve for the crystal structure of the Mason-Pfizer monkey virus retroviral protease. Their efforts highlighted the new ways that "citizen scientists" are helping researchers produce knowledge. These efforts share three features. They utilize crowdsourcing, soliciting help from a large (on-line) international community rather than from researchers or employees at a particular institution. They incentivize participation through gamification, transforming the key work activities involved in research into public games. Finally, the gamers are primarily not scientific researchers, but members of the public. This approach to research sometimes involves breaking down complex tasks into simpler ones that can be mastered fairly easily or more complicated games (EteRNA players design RNA's that result in real world experiments) where success seems to hinge on the emergence of a small cadre of expert gamers or teams of gamers for breakthroughs.

These new approaches to carrying out science raise several significant ethical, legal and social issues. As the researchers explore ways of improving both recruitment and productivity from players, are the players research subjects (and hence subject to regulatory oversight)? If not, are they researchers (and hence owed credit in authorship and potentially a stake in intellectual property)? In general, there are unresolved tensions between the different roles of these participants (gamer, researcher, subject)-with each role carrying different and sometimes conflicting norms.

Public/scientist partnerships in the production of biomedical knowledge: the enablers

Milner Lauren, Stanford Center for Biomedical Ethics, USA

A new kind of public-private partnership is being initiated to advance biomedical research by enabling widespread data-sharing and diverse collaborations between groups within and outside of the scientific community. Although the specific compositions and goals of these partnerships vary, they share a number of important features: all solicit data from diverse groups (i.e., industry, academia, government, disease advocacy organizations and private citizens), all limit intellectual property and patenting rights to facilitate free access to data, all focus on developing common methodological and analytical tools to support a highly distributed network of data usage, all promote the active involvement of project participants at multiple stages of research (from proposing research questions to data analysis and interpretation) and all state that the overarching mission of their partnership is to accelerate the pace and enhance the quality of research with direct benefit to human health. These groups aim to shift biomedical research from an isolated and expert-dependent process to one which relies on expansive networks of individuals from both expert and non-expert communities.

These partnerships raise a number of legal, ethical and social issues regarding research participation and researcher conduct. How can informed consent be obtained and privacy protected for projects with a indeterminate number of researchers and research goals? How can expectations and standards of researcher conduct be communicated and enforced? The blurring of traditional research roles in these partnerships requires the reevaluation of traditional approaches to research ethics.

Public/scientist partnerships in the production of biomedical knowledge: the advocates

Cho Mildred, Stanford Center for Biomedical Ethics, USA

Arguably one of the most significant changes to the conduct of biomedical research in the last century has been the rise of patient advocacy groups throughout the entire spectrum of research activities. Patient advocates, often representing specific diseases, now play a major role in funding, recruiting scientists to conduct research projects, obtaining biological samples and research subjects, collecting data, publishing results, and holding patents on inventions from the research.

This shift has begun to influence the infrastructure of science. For example, the Combating Autism Act of 2006 not only appropriated nearly $1 billion for autism research, it established a novel agency to coordinate autism-related activities across all US agencies, and a grant peer review system that is composed equally of lay members (representing various lay communities and patient advocates) and scientists.

This new paradigm raises a number of ethical issues, largely because the traditional framework of research ethics was built under the assumption of a power imbalance between researchers and the subjects of research. However, this imbalance may be turned upside-down in patient-driven research. The new arrangements potentially create situations in which the patient advocate's interest in the integrity of the research may be in conflict with other interests such as desire for a treatment for their disease, financial interests, or strong prejudice against certain scientific ideas or methods. On the other hand, patients' interests may also be legitimate, even if they are at odds with traditional scientific process.

Public Health Issues A (submitted papers)

Bridging the Social-Biomedical Divide: Uncovering Explanatory Conflicts in the Public Health Literature

Salami Eniola, Hendrikse Jesse, University of Calgary, Canada

Purpose and Research Objective: Monism is the view that there is a single salient explanation for any given phenomenon in the natural world. Philosophers Helen Longino and C. Kenneth Waters have examined how monistic positions lead research programs to discredit other scientific approaches. This phenomenon presents a barrier to interdisciplinary research. To date, no study has sought to systematically characterize monistic conflicts in public health research. The present study seeks to fill this gap in the literature by uncovering instances of monism-derived conflict between the social and biomedical approaches in the public health literature on childhood obesity.

Methods: The project is a narrative literature review of review articles on childhood obesity in North America. Articles are collected from online health science databases and are examined using qualitative content analysis.

Expected Results: Completion of the literature search has revealed that the majority of articles concerning childhood obesity in North America emphasize biomedical approaches. Content analysis of these articles is expected to uncover monistic attitudes or connotations within the articles, using superlative, exclusive and pejorative language as empirical measures for instances of monism-derived conflict.

Implications: Monistic approaches to investigation are barriers to interdisciplinary research. Explanatory conflicts between research programs should be of interest to the field of public health given the discipline's focus on multifaceted health solutions. Understanding of the nature and extent of monism in public health can serve as a first step to eliminating such barriers.

Fetal Risk, Federal Response: Alcohol Warning Labels and Fetal Alcohol Syndrome

O'neil Erica, Arizona State University, USA

In the late 1960s and early 70s, physicians in the United States and France published the first medical observations linking alcohol consumption during pregnancy with adverse birth outcomes. Coined Fetal Alcohol Syndrome (FAS) in 1973, the syndrome's etiology was difficult to arrive at due to complications presented by dosage, exposure, timing during pregnancy, and a host of maternal factors. Despite the ambiguities surrounding FAS, within three years US government agencies were discussing the idea of requiring warning labels to alert the public to the risk of FAS. However, the first legislative subcommittee hearing devoted to FAS occurred in 1978, and it was a full fifteen years after FAS's initial definition that Congress passed the Alcohol Beverage Labeling Act mandating warning labels.

This paper examines the medical emergence of FAS and early legislative discussions of the risk of alcohol consumption during pregnancy. I will introduce two preceding historical case studies of substances that impacted fetal development, thalidomide and cigarettes, and examine the federal regulatory response to the risks posed by each. By discussing comparative antecedents, my goal is to situate FAS within the historical legislative framework for how emergent fetal risks were interpreted as public health concerns. I will then outline the substantial differences surrounding the public health response to FAS, differences that have much to do with the politicized history of alcohol in the US. Further, as FAS occurs disproportionately in marginalized socioeconomic groups, dimensions of social justice at the science-policy interface are also critical to this public health history.

Sorting out patients and diseases in early XIXth century Paris. An historical account of how medicine met its subject

Ermakoff Antoine, Université Paris VII Paris-Diderot, France

This paper focuses on the study of the Conseil Général des Hospices Civils de Paris in the early nineteenth century, the biggest hospital institution in western Europe of the time, ruling all Parisian relief systems precisely when French medicine was experiencing the rise of the "Paris school of medicine" (E.H. Ackerknecht (1967), Medicine at the Paris Hospital, 1798-1848; M. Foucault (1963), Naissance de la clinique). Through it, it aims to show that the sorting out of hospital patients, and decisions about who was to benefit from various treatments, belong not only to physicians on medical grounds. The distinction between hospital and hospice, the creation of specialized hospitals for venereal and skin diseases or sick children, all crucial to the constitution of clinical medicine and its subsequent specialization had more compounded rationales. The outcome, highly propitious to physicians, can actually be seen as a mix of public health, economic and moral motives enforced by political authorities and administrators, as well as by physicians themselves. Supporting the same measures to sort out patients, but for diverging ends, doctors and administrators shaped hospital medicine.

Public Health Issues B (submitted papers)

Bacteriophage and the American Pharmaceutical Industry

Farnsworth Carolyn, University of South Carolina, USA

The growing number of antibiotic-resistant microbial infections poses a serious threat to the future efficacy of antibiotic treatments. Around the world, news media and scientific articles alike warn their audiences of this potentially disastrous situation, and call for the speedy development of antibiotic alternatives. One such alternative, phage therapy, has received considerable attention in recent years. Largely developed and extensively practiced in the former Soviet Union (notably at the Eliava Institute in the Republic of Georgia), phage therapy is widely presented as archetypical of a long-overlooked Eastern European approach to science and therefore as a novelty to Western biomedicine. However, phage therapy is neither a recently revolutionary concept nor a treatment historically unknown to Western nations. Prior to the 1940s antibiotic revolution, several prominent American pharmaceutical companies produced and marketed phage products. These products gradually disappeared from the American pharmacopeia, an observation that cursory analyses dismiss as the inevitable consequence of inadequate research and premature production on the part of phage manufacturers. On the contrary, this paper presents a more complex story of the short-lived American phage industry, analyzing the pharmaceutical publications of Eli Lilly & Co. and E.R. Squibb & Sons- and considering in turn contemporaneous scientific articles, as well as archival documents from the Eliava Institute. As scientists, medical practitioners, and drug manufacturers today endeavor to fortify our antimicrobial armament, examining the history of pharmaceutical endeavors will allow for a more informed approach to the development and implementation of strategies to combat infectious disease.

Nathan Shock and the "Biomedicalization of Aging"

Park Hyung Wook, Nanyang Technological University, Singapore

Nathan Shock, the leader of the NIH's gerontology program from 1941 to 1976, played a pivotal role in creating the science of aging as a research field in America. By illustrating his works, I explore the complexity surrounding the term, the "biomedicalization of aging," a subject studied recently by several scholars including Tiago Moreira and Paolo Palladino. Indeed, "biomedicalization" is understood in many different ways. Whereas it was often equated to molecular reductionism, Peter Keating, Albert Cambrosio, Adele Clarke, and Ilana Löwy have shown that biomedicalization involves a set of more complex changes in laboratories, clinics, and patients' social worlds with a deep cultural repercussion. According to them, modern biomedicine, while stressing the detailed identification of diseases in the laboratory, has complex relations with patients' activism, the blurring boundary between laboratories and clinics, and the neoliberal commercial interest. Focusing on aging and gerontology as the subject, my paper shows the complexity and inconsistency related to biomedicalization. I first will discuss how Shock tried to find the physiological and biochemical mechanism of aging using model organisms, biomolecules, and senior patients in the Baltimore City Hospitals. Then I illuminate how this work was placed in a broader social context associated with the elderly's continued social participation, job security, and health management. This explains, I claim, his unique choice of publishable results, his refusal to cooperate with the American Geriatrics Society, and psychologist James Birren's creation of a separate section of gerontology in the NIH after being disillusioned by Shock's "heavy biomedical orientation".

Socially and morally responsible cognitive neuroimaging: Mental rotation case study

Bentley Vanessa, University of Cincinnati, USA

The neuroimaging of sex/gender differences is problematic because it appears to present a biological explanation for differences between men and women that can be used to justify stereotypes, prescribe certain social structures, and limit resources for individuals interested in pursuing non-gender-normative pursuits. Focusing on the specific question of sex/gender differences in mental rotation I attend to the details of the studies to identify problematic practices and suggest modifications to avoid socially and morally harmful science. I find that most fMRI studies of sex/gender differences fail to elicit the supposed male performance advantage and there is little overlap (and no consensus) on different sex/gender-linked areas or networks underlying mental rotation processing.

I identify a number of problems with these studies and conclude that current practice in the neuroimaging of sex differences is sexist, ignores relevant evidence from other scientific fields, and inaccurately presents its results as stemming from "natural" sex differences rather than investigating the possibility that sex differences arise from different gendered rearing environments. Using feminist standpoint theory, I suggest modifications to current practice to begin to address these problems. As a start, these modifications involve: 1) analyzing data blind to gender; 2) assessing the influence of spatial activities, science classes, and the effect of practice on activation; 3) dividing groups based on performance rather than sex/gender; 4) broadening diversity of participants; 5) investigating the effect of strategy use on activation; 6) separating questions of proximate and ultimate causation; and 7) being reflexive in reporting results.

The Question of Levels (submitted papers)

What is reductionism?

Delehanty Megan, University of Calgary, Canada

What exactly is meant by reductionism in the context of the philosophy of biology? As with many such terms, it is hard to come up with a brief, but adequate characterization that doesn't exclude certain proponents - or opponents - of the view. In this paper, I will argue that reductionism must involve an explanatory asymmetry: the reductionist claims that lower level explanations are always as good or better than higher level explanations (setting aside the purely pragmatic sense of "good" as cognitive accessibility). Importantly, the reductionist should allow that, in some cases, higher level explanations are equally good as lower level explanations. I will argue that this position is justified both on purely philosophical grounds as well as being justified by reference to experimental practice (i.e. the sorts of experimental systems that are characterized as "reductionist").

The problem of ontic levels in mechanistic explanation

Alvarado Ramon, University of Texas at El Paso, USA

Accounts of mechanistic explanation have what I term the *problem of ontic levels*. The problem arises from two core but conflicting commitments of the mechanistic view: that mechanistic explanations are ontic, or that they are structures in the world, as opposed to mere representations or descriptions; and that mechanistic explanations are multilevel, that is to say that the entities at one level can be explained by merely revealing the realizing mechanisms at the level below it (Craver, 2007). Evidently, there is a tension. Either the ontic commitment is a commitment to the existence of entities at the lowest explanatory level and entities at the higher levels are mere heuristic stops (Gillet/Bickle), or we must explain how higher level entities earn their ontological status. In this paper I suggest an alternative view of the ontic commitment that may ease its compatibility with multilevel explanations. To do so I rely on the view that certain irreducible relational features, such as those elucidated by computer simulations of network interplay, redeem the status of levels as ontologically viable (Symons 2008). Using implications of Symons' approach, I walk through examples from the biological sciences that are considered both complex and mechanistic. I suggest that the irreducible relational features found in these examples are evidence that mechanistic explanations can be both multilevel and ontic. Further, I conclude that if this is the case then the ontic commitment is better off interpreted as a claim of structural realism.

Levels, Hierarchy, and Scale

Von Stein Alex, University of Arizona, University of Arizona, USA

Biologists often rely on the assumption that nature is hierarchically organized into levels. In its simplest form, the assumption is that each entity at level n is a part of strictly one entity at level n+1. When analyzing competition between populations, for example, we would like it to be the case that each individual is a member of only one population. This assumption is intuitive, but probably not correct. If we delimit genuine populations as bound together by certain sorts of interactions between individuals, then because these interactions often fail to be transitive, individuals may be members of several populations - contradicting strict nesting. Other problematic cases abound. Ecosystems, for example, are not composed solely of communities of organisms. The transfer and distribution of molecules such as nitrogen are also constitutive of ecosystems.

There are several important implications to be drawn from the problems with strict nesting. First, levels are not "sealed off". Entities interact across levels, even levels that are compositionally "distant". Second, the failure of strict nesting raises problems for the claim made by many ecologists that associated with each change in level there is an associated change in spatiotemporal scale. Finally, while much attention has been paid to compositional levels, I argue that this focus has blinded us to issues of scale, in particular to issues about the scale-dependence of empirical patterns and epistemic issues of cross-scale inference.

Reasoning with Diagrams in Biology

Novice and Expert Understandings of Space in Scientific Diagrams

Sheredos Ben, University of California, USA

Professional biologists are skilled graphic designers. In creating diagrams, they harness spaceon- the-page to aid their own reasoning, and to communicate rich (but not error-free) theoretical conceptions of their domain of inquiry. I examine uses of diagrammatic space in portrayals of the mechanisms of circadian rhythmicity in various living systems (from humans to algae) to articulate aspects of what DiSessa labels the "meta-representational competence" that experts exhibit in their reasoning with these diagrams.

Meta-representational competence must be acquired. Novices can, as shown by cognitive scientists like Tversky and Hegarty, complete various tasks of diagram comprehension best if the distribution of ink on the page has a "natural mapping" to the semantic structure of a theoretical domain. It is thus often suggested that educators and working scientists alike would do well to design graphics so as to exploit any "natural mappings" which are available. I aim to add nuance to this view, by pointing out that in the course of coming to emulate expert practice, aspiring scientists must carefully learn to temper their reliance upon "natural mappings." Distinct subregions of space-on-the-page within a single diagram often require distinct mappings to a variety of theoretical domains. A great source of diagrams' utility in biology consists in enabling researchers to *coordinate* these theoretical domains, but this requires a bifurcation of the total space-on-the-page into *multiple* spaces which each support an independent mapping. As I show by example, there is frequently no sensible way to perform a "global" mapping from total spaceon- the-page to theoretical domains.

Diagrams and the production of visual evidence

Laura Perini, Pomona College, USA

Basic research in the life sciences often yields visual data, but that is only a first step in the production of an image that can serve as evidence in scientific reasoning. Historical, social science, and philosophical studies have shown that often data images must be subjected to intensive practices of interpretation before they can be used as representations. That interpretive practice is often supplemented by altering the original image, by combining multiple parts of data images and by superimposing diagrammatic forms on visual data. In this talk I will clarify how diagrams contribute to the meaning and evidential relevance of data images.

Between Phenomenon and Mechanism: Diagrams as Vehicles of Intermediate Explanatory Reasoning

Burnston Daniel, University of California, USA

Philosophers of science in the new-mechanistic tradition have characterized mechanistic research as progressing by first delineating a phenomenon, then explaining it by discovering the parts and operations of the responsible mechanism. I argue, drawing on diagrammatic representations in mammalian chronobiology, that this bifurcated account of practice misses a key process that mediates between the two recognized stages. In *intermediate explanatory reasoning* (IER), researchers seek to uncoverspatio-temporal dependencies-precise, quantitative relationships involving known elements of a complex system. The method involves generating data regarding how temporal and spatial patterns in the properties of system elements (e.g., oscillatory patterns of gene transcripts or protein quantities in distinct cells or organs) covary, with the goal of uncovering the aspects of system organization that are vital to produce the phenomenon. While spatio-temporal dependencies are important in developing mechanistic explanations, they do not themselves posit specific operations that causally link parts of the system. Thus, IER is a qualitatively distinct aspect of explanatory reasoning, not yet addressed by mechanists.

A variety of *graphical practices* play vital roles in elucidating spatio-temporal dependencies in the system by conveying the results of key manipulations or recordings. For example, line graphs often are used to show how certain gene knockouts/knockdowns affect the behavior of the system or some of its parts; raster plots convey detailed information about circadian periodicity from individual cells. I show how analysis of these types of diagrams can yield important insights into practice.

Reconceptions: Life at the Frontiers of Health and Disease (*Interdisciplinary session*)

Reconceptualizing viruses against the shifting sands of opposing thought styles in cancer etiology and bacteriology

Sankaran Neeraja, Yonsei University, South Korea

The discovery that certain types of cancers might be caused by viruses occurred in the early twentieth century, a time when the very concept of viruses as we understand it today, was in a considerable state of flux. For a long time, in fact, viruses were defined rather by what they were not and what they could not do, rather than any known properties that set them apart from other microbes. Consequently when Peyton Rous suggested in 1912 that the causative agent of a transmissible sarcoma of chickens was a virus, the medical research community was reluctant to accept his assessment on the grounds that cancer was not infectious and was caused rather by a physiological change within the cells. This difference in the bacteriological and physiological styles of thinking appears to have been prevalent in the medical research community at large as evidenced by the fact that when Felix d'Herelle in 1917 suggested that the causative agent of a transmissible lysis in bacteria, was caused by a virus, his ideas too, met with a similar reaction, with opponents arguing against a exogeneous infective explanation for causation in favor of a physiological explanation involving some factor intrinsic to the host bacteria. This paper examines the ways in which the concept of virus needed to be rethought and stabilized and the exogenous and endogenous explanations for cancer etiology and bacteriophage reconceived in common terms, before consensus was achieved and these phenomena understood properly.

Life in harmony: The balancing role of the immune system

Swiatczak Bartlomiej, University of Science and Technology of China, China

Throughout the history of immunology there have been two distinct ways of understanding the immune system function. One originating from Darwinian natural selection according to which, the immune system is a guardian of the organism's autonomy ready to recognize and fight any foreign invader and the other one, rooted in Lamarkian ideas, according to which the immune system is a peace-maker, a mediator striving for harmony and cooperation. The first view paved the way for the current paradigm of self/nonself discrimination in immunology. The second view, inspired by Lamarck, helped to shape the idea of immune balance, which despite its presence in immunology since its inception has never become a part of the mainstream model. This paper will examine the development of the idea of immune balance and the related concepts of immune harmony and equilibrium to evalute their potential to inform a future paradigm able to address the shortcomings of the classical self/nonself discrimination model. I will suggest that in the face of the current self/nonself paradigm crisis, immunologists should turn to the idea of the immune system as primarily engaged in counterbalancing the effects of the fluctuations in the microbial, chemical and self-induced environment to promote adaptation and well-being of the genetically defined organism.

Pathogens as Evolving Entities: Taking the “Microbe’s View of Infection” Seriously
Méthot Pierre-Olivier, University of Geneva, Switzerland

Biological associations between living organisms typically fall into three broad (continuous) categories: mutualism, commensalism, and parasitism. While the first two usually result in the organism maintaining a delicate balance, the last one induces changes in the host and often leads to detrimental effects on health. Unsurprisingly, instances of parasitism resulting in host damage have been one of the most researched areas of the medical sciences. And as a consequence, pathogens are often defined from a strictly medical point of view, namely as organisms capable to cause disease in hosts. The frontier between health and disease states in biological associations is fluid, however, and both mutualistic and commensal organisms, long assumed to be harmless, can produce disease phenotypes under specific ecological circumstances. Furthermore, a number of pathogens cause disease only in immunocompromised hosts, not in otherwise healthy individuals – a finding that prompted some to distinguish ‘primary’ and ‘opportunist’ pathogens. Finally, it emerges that not only host properties determine, to some extent, whether some microorganisms are pathogenic, but in some cases levels of virulence result from the immune system's over-response itself. So what is the distinguishing feature of pathogens and commensal species? Going beyond the restricted medical concept of a pathogen, this paper takes the ‘microbe’s view of infection’ seriously and argues that looking at pathogens as evolving biological entities could lead to a more interactionist perspective of virulence and pathogenicity and furthermore, to a better understanding of the selective pressures favouring the transition from harmless commensals to infectious agents.

Reductionism, Emergence, and Complexity (submitted papers)

Complex systems: A causal approach to biological species
Martinez-Bautista Elizabeth, Insituto de Investigaciones Filosóficas, Mexico

The issue of biological species has been treated in the philosophy of biology either under a semantic (Kripke 1971), or an essentialist (Boyd 1999, Slater 2011) position. In my view, these approaches do not capture the evolving capacities of species, nor the complexity of the causal processes which leads to emergent properties displaying sufficient stability for inductive practices and scientific explanations.

Along with other authors (Depew & Weber 1996, DeLanda 2011) I support "emergence" and "complexity" as central concepts to understanding the behavior of living systems. For this reason, I propose a philosophical approach to the issue of species from the perspective of complex causality.

The concept "complex causality" refers to the fact that, in a dynamic system such as the species, different causes may lead to the same effect. The multiplicity of causes is a mechanism that integrates qualitative and quantitative aspects of processes that maintain stability and lead to

the appearance of emergent structures that are responsible for evolution. Both, causes and effects can only be established statistically (DeLanda 2002).
The idea of complex causality has important epistemic consequences. For example, the treatment of the species from a holistic perspective helps to avoid epistemic reductionism which has led to discussions on characterization. Furthermore, it allows a redefinition of the concept of "natural kind" which departs from philosophical approaches relying either on essences or on linear causality such as HPC (Boyd 1999, 2010). Finally, it becomes a philosophical account consistent with current scientific research.

Approaches based on complexity darken rather than solve the mind-body problem

Blanco Carlos, Universidad de Navarra, Espagne

This paper aims to offer a broad criticism of the underpinnings of the so-called "complexity theories " in their approach to a problem that has puzzled philosophers and scientists for centuries: the relationship between mind and body. We will pay special attention to the ideas of Alicia Juarrero, a distinguished exponent of this explanatory model, whose epistemological implications will be outlined.

The Bilaterian Body Plan and the Evolution of Intrinsic Intentionality

Levine Alex, University of South Florida, USA

Attempts to naturalize intentionality- to explain the presence and emergence within the natural world of intentional relations, or "aboutness"-have taken various evolutionary turns.
Ruth Millikan's argument (1984, 2001) that intentionality can evolve as a biological proper function has garnered support among philosophers of mind and language, but it is grounded in suspect evolutionary theory. In consequence, it can be charged both with Panglossianism, and with epiphenomenalism. Dennett (1996) avoids these charges by denying that organisms have intrinsic intentional properties. More recently, Fitch (2008) has defended the biological reality of intrinsic intentionality by recourse to the inherent goal-directedness of eukaryotic cells.
I follow Fitch in arguing for the biological reality of intrinsic intentionality. But whereas Fitch extends his account of cellular intentionality to metazoa by considering nervous systems as structures of eukaryotic cells, I focus instead on the metazoan body plans within which such nervous systems arise. Almost all metazoa with nervous systems have two features in common: they exhibit Weismannian segregation; and they are motile. Both characteristics imply some degree of intrinsic goal-directedness or intentionality. But there is a further, fundamental difference between, say, cnidaria, with their blind-guts, and bilaterians. Drawing on Merleau-Ponty's (2012) account of the embodied character of intentionality, I argue that bilaterians, with their through-guts and localized sensory organs, exhibitintrinsic direction. Bilaterians don't just move; they aregoing somewhere. All higher-order intrinsic intentionality presupposes intrinsic direction.

Reductionism, eliminativism, and the concept of life in Descartes' biology

Hutchins Barnaby, Ghent University, Belgium

Descartes is quite probably the archetypal reductionist of early-modern natural philosophy, and reductionism seems, at first glance, to be especially evident in his biology. He clearly *is* a reductionist about the operations of the body (where muscular movement, vision, the heartbeat, etc. are all reduced to corpuscular mechanics). He may even be a reductionist about the vegetative soul, whose functions he translates almost wholesale into his material account of the body. When it comes to life itself, however, I argue that Descartes is not a reductionist but a certain kind of eliminativist. That is, he does away with any conception of life, and the category is not to be found reflected in his material physiology. There is, though, a strand of secondary literature that looks for just such a reflection, and then attempts to reconstitute a Cartesian concept of life from it (in terms of cardiac heat (Aucante, Bitbol-Hespériès, Hall), necessary and sufficient life functions (Mackenzie), a special kind of organisation (Ablondi), etc.). I show that this is an illegitimate move by arguing that it comes from taking Descartes to be a reductionist about life. When he describes the functions of living bodies purely in terms of the micromechanics of material particles, this is not the same as reducing life itself to those particles; instead, he accounts for each of the functions associated with living bodies on a local level, while allowing any general notion of life to dissolve away.

The Resistance of the Modern Synthesis (submitted papers)

The adaptive landscape as a unificatory tool

Petkov Stefan, Bulgarian Academy of Science, Bulgary

The adaptive landscape, as pioneered by Sewell Wright, forms a conceptual framework consisting of three elements: *a diagram, a formal mathematical model and a metaphoric dictionary*. The latter relates the formal model to the graphic, which is thus interpreted in terms of adaptive peaks, peak shifts and changes in the relief.

The adaptive landscape played a key role during the 20th century evolutionary synthesis documented in the writings of Wright, Dobzhansky and Simpson. The uses of the metaphor, however, are viewed today as methodologically problematic. The critics have pointed to some inconsistencies in the construction of the diagrams and to the vagueness of the metaphoric vocabulary, concluding that the metaphor and the graphical representations could be abandoned completely in favor of rigid mathematical models. The defenders of the integrity of the adaptive landscape conceptual framework usually refer to its numerous applications in evolutionary research and insist that it is an important heuristic tool.

In my paper I provide additional support for the claim that the integrity of the adaptive landscape conceptual framework should be preserved. It builds on analyses of recent research revealing that the adaptive landscape is still used as a basis for theoretical, empirical and explanatory unification. The flexibility of the graphics and the metaphoric dictionary is not a sign of inherited inaccuracy, it rather makes the conceptual framework suited to encompass a wide range of evolutionary studies, facilitating thus the goal of reaching a more unified view of evolution.

Niche Construction and the Insides and Outsides of the Modern Synthesis

Chiu Lynn, University of Missouri, USA

Does niche construction challenge or extend the Modern Synthesis? The major assumption of the Modern Synthesis is that the internal mechanisms that govern mutation are random with respect to the external factors that govern environmental change (Lewontin 1983, 1985, 2000, 2001). Inspired by Richard Lewontin, scientists (Odling-Smee, Laland, Feldman, Day, O'Brien, etc.) and philosophers (Godfrey-Smith, Sterelny, etc.) argue that niche construction constitutes a significant challenge because it undermines this internalist/externalist presupposition. However, these scholars adopt a causal reading of niche construction that merely denies that the two mechanisms are causally autonomous. I argue that it does not follow that the two mechanisms are thus not random with respect to each other. Therefore, the current development of niche construction theories do not challenge but merely extend the Modern Synthesis. In this paper, I will show that Lewontin's account is fundamentally different from these later developments and, based on his views, I develop a model of niche construction that genuinely challenges the Modern Synthesis. Niche construction demonstrates that the selective environment of a population constitutively depends on the variation between each member's ability to interpret and alter the environment. If so, changes in the external selective environment are not random with respect to changes in the variation between individuals, rejecting the Modern Synthesis presupposition. As the impact of niche construction relies on the way individuals passively interpret and/or actively alter the environment, this implies that the special features of living systems are essential to evolutionary theories in biology.

At the boundary of sexual selection: examining the evolutionary explanations for the absence of the human baculum

Siu Edwin, Florida State University, USA

An argument often used to support a sexual selection hypothesis, is that a trait otherwise lacks a positive adaptive function, and therefore, natural selection is unable to explain its presence. But how would we recognize sexual selection in a mixed case, where a trait may be under simultaneous positive natural selection? The attempt to produce a sexual selection explanation for the absent human baculum can help answer this question. In most mammals, a baculum (or penis bone) is found in male individuals and plays a functional role in successful reproduction. Human males, however, are unusual in that they lack a baculum. Richard Dawkins has suggested a sexual selection explanation, stating "that females could glean all sorts of clues about a male's health, and robustness of his ability to cope with stress, from the tone and bearing of his penis." However, this hypothesis is not a clear case of sexual selection because the signal itself could contribute to fitness (it is easy to imagine how erectile dysfunction might reduce a male individual's reproductive success). Other evolutionary explanations for this absence have tended to focus on the duration and frequency of copulation in humans which has reduced the need for the baculum compared to other species. Is it possible to identify sexual selection in such a mixed case and would this support the general claim that sexual selection is an independent mechanism?

Roles of viruses in Ecology, Evolution and Origins of life

Viruses: Essential Agents of Life

Villarreal Luis, University of California

For the last 15 years, I have focused my study on the general role of virus evolution on Life. In the last decade metagenomic assessments have led us to realize that viruses are the dominate biological entities of the biosphere and are the most numerous, diverse and dynamic genetic agents on Earth. Although viruses have long been dismissed from the Tree of Life a simply destructive and selfish extra-genomic genetic parasites, comparative genomics now makes it clear that viral colonization distinguishes all domains of life. I have been pursuing how and why some viruses (and their defective relatives, transposons) are able to stably persist in their host and sometimes become a colonizer of the host genome. The ability of a virus to persist is a transforming event for host population survival and requires specific mechanisms and strategies. These viral derived mechanisms, however, provide new mechanisms of immunity and identity for the host. I am now tracing how viruses have contributed to host group survival from bacteria to human social evolution.

What roles for viruses in origin of life scenarios?

Kostyrka Gladys, IHPST & Université Paris 1 Panthéon-Sorbonne, France

Until the 1960s, viruses were often central in origin-of-life-theorizing. In the debate opposing metabolic and genetic approaches on the origin of life question, viruses were used by the proponents of the last approach in three different ways (Podolsky, 1996). First, the virus, taken as a metaphor of life, let open the possibility that life appeared under the form of pure genes, in a non-metabolic fashion. Second, the virus could be seen as an "operational model": understanding how the virus operates may help understanding, by analogy, how life could have emerged. Third, viruses as a phylogenetic lineage could be seen as "living fossils", descendants of the first life form.

Today, viruses are not central in origin-of-life scenarios anymore [Lopez-Garcia & Moreira 2012]. And yet they are still part of the debates, and may play some important roles, according to different scenarios [Forterre 2005, 2009; Koonin 2006]. After a brief description of the present structure of origin-of-life-research and the different types of explanation used in this field [Malaterre 2010], I describe how viruses are integrated - or not - in this structure, depending on the meaning scientists give to the words "origin" and "viruses." I then analyze why and how the roles played by viruses in origin-of-life scenarios evolved from the 1960s until now. I particularly focus on two questions: how far do some specific definitions of viruses influence the way scientists formulate hypotheses about their roles in origin-of-life-scenarios? Do viruses still play a role in the maintenance of the dichotomy between the metabolic and genetic approaches?

Selection at the level of the community and ecosystem (*Interdisciplinary session*)

How to define the selective environments in which symbiotic communities evolve?

Prévot Karine, Université de Paris X – Nanterre, France
Bouchard Frédéric, Université de Montréal & CIRST, Canada

Symbiotic associations force us to examine the relationship between the adaptive success of a community and the adaptive success of the constituting individual organisms. The emergent symbiotic individual qua integrated functional unit appears to have a distinct adaptive success from that of its parts. This allows for the possibility of selection acting on this higher level of organisation with resulting emergent adaptations. Symbiosis in insects, more specifically symbioses involving *Wolbachia* is helpful to think about the selection process at the community level. Mechanisms such as apoptosis or immunological tolerance that make it possible for the host to tolerate its new partner provide new and distinct adaptations that are absent from symbiont-free insects.

Many have discussed the idea that communities could emerge as new units of selection, arguing that there is fitness transfer between levels of organisation that make it possible for new units of adaptations to emerge. What has not been sufficiently discussed is that the transiency of many symbiotic associations makes such fitness transfers difficult to identify and track through time.

In this presentation, using the example of *Wolbachia*, we focus on how ecological conditions at the community level affect how we can define and construe selective environments for communities in general and symbiotic communities in particular. In traditional evolutionary accounts, the individual and the species are relatively stable and the environments properties fluctuate. In the case of communities, the stability premium belongs to the environment while the unit of selection is less stable. We will explain how this asymmetry should inform our understanding of community evolution.

Evolution in metacommunities: The role of population structure

Goodnight Charles, University of Vermont, USA

A metacommunity can be defined as a set of communities that are linked by migration and extinction and recolonization. In metacommunities evolution can occur both by process that occur within communities such as drift and individual selection, but also by among community processes such as divergent selection due to random among communities differences in species composition, and group and community level selection. The effect of these among community level processes depends on the pattern of migration among communities. Migrating units may be individuals (migrant pool model), groups of individuals (single-species propagule pool model), or multi-species associations (multi-species propagule pool model). The most interesting case is the multi-species propagule pool model. Although this pattern of migration may a priori seem rare, it becomes more plausible in small well-defined "communities" such as symbiotic associations between two or a few species. Theoretical models and experimental studies show that community selection is potentially an effective evolutionary force. Such evolution can occur either through genetic changes within species or through changes in the species composition of the communities.

Artificial selection of ecological interactions in microbial communities

Blouin Manuel, Karimi Battle & Lerch Thomas, Université Paris-Est Créteil Val de Marne, France

Artificial selection of communities in laboratory conditions generally consists in selection procedures on two-species communities of macro-organisms. Alternatively, artificial selection has been applied on multi-species microbial communities, but they lack to provide clear evidence for selection occuring at the level of ecological interactions. We set up an original protocol for microbial community selection at low cost, in a minimal time and space. The selected trait was the CO2 emission. For twenty one generations, we selected three communities among thirty in each one of the six lines for random (control) or low CO2 emission. In the low emission lines, we observed a decrease in CO2 emission as compared with the control treatment, which means that artificial selection was efficient. At the end of the selection experiment, the genetic structure of the community was analyzed with a fingerprint method, which provides an indicator of the number of species through the number of DNA fragments of different lengths. We found that diversity was lower in the selected lines as compared with the control lines. We evaluated ecological interactions between "species" on the basis of the correlation coefficient. We observed an effect of the artificial selection treatment on the structure of the interaction network. The same species could be involved in positive interactions in the control, but in negative interactions in the low CO2 emission treatment. Agregation also differed between the two treatments. These results indicate that artificial selection can be efficient in selecting ecological interactions emerging at the community level.

Simulation vs. Experiment in Evolutionary Biology

Why aren't all cells in neoplasms cancer stem cells? An evolutionary explanation for cancer non-stem cells

Sprouffske Kathleen, University of Zurich, Switzerland

Cancer is an evolutionary system in which tumor cells outcompete normal, somatic cells. Conventional views assume all cells in a neoplasm can propagate the tumor. Alternatively, the cancer stem cell hypothesis posits that only a fraction of the cells (the cancer stem cells) can act as tumor-propagating cells, and most of the tumor is composed of cells with limited replication potential. Here, we offer an evolutionary approach to this controversy. We used several evolutionary, computational models to investigate cancer cell dynamics and conditions consistent with the stem cell hypothesis. Our models predict that if selection acts at the cell level, neoplasms should be primarily comprised of cancer stem cells. In contrast, experimental data indicates that neoplasms contain large fractions of cancer non-stem cells. We explore several solutions explaining the paradoxical existence of cancer non-stem cells in neoplasms, including the possibility that selection acts at the level of multicellular proliferative units.

What's the Difference Between Experiment and Simulation?

Parke Emily, University of Pennsylvania, USA

Experiments in biology are often considered to be epistemically superior to simulations. While some have suggested that computer simulations are a kind of experiment (e.g., Peck 2004, Parker 2008), others have argued that there are significant methodological and epistemic differences between the two (e.g., Winsberg 2008, Morgan 2003, Guala 2005). A common theme in accounts of these differences is the idea that experiments *replicate* (aspects of) their targets in the world, while simulations *represent* or *mimic* them.

I argue that these category distinctions focus us on the wrong issues. The relationship between one's direct object of study and ultimate target of inquiry matters. But this relationship does not characterize a clear distinction between experimenting and simulating, either in kind or in epistemic implications. To develop this point, I focus on recent examples of studies of speciation, using both computer simulations and experimental evolution of microbial populations. This case lends support to a general conclusion: Whether we are better off studying a phenomenon in the world by interacting with experimental systems or computer simulations depends on a complex of factors-including the kind of question we are asking and what we are asking it about-and not on some absolute assessment of the primacy of one kind of scientific inquiry over another.

Social microbes

Multispecies individuals as units of selection
Dupre John, University of Exeter, UK

Microbes, especially but not exclusively bacteria, frequently exist in closely integrated consortia including multiple types of cell. Indeed multispecies communities are the dominant living systems on Earth, and it is such systems that are typically exposed to natural selection as an integrated unit. This implies, contrary to very widespread assumptions about evolution, that entities that compose lineages are distinct form the entities that are exposed to selection. This paper will explore some of the consequences of this situation for our understanding of evolution, especially the evolution of cooperation.

Gene mobility and the concept of relatedness
Birch Jonathan, University of Cambridge, UK

“Genetic relatedness” is often understood as an intuitive measure of genealogical kinship. In formal work on social evolution, however, relatedness is more commonly conceptualized as a generalized statistical measure of genetic similarity. These “intuitive”' and “generalized” measures come apart when genetic similarity is caused by a mechanism that does not rely on shared ancestry. In microbial populations, we know of at least one such mechanism: horizontal gene transfer (HGT). We might conclude from this that the “generalized” measure of relatedness triumphs over the “intuitive” measure in microbial contexts, but I argue that there is a further twist in the tale. For I contend that HGT demands a yet more radical revision of our intuitive concept of relatedness, because it implies that we cannot even talk of an organism's genotype simpliciter-only of its genotype at a particular time. This introduces a temporal aspect to relatedness, and leads us to ask: at which stage in the life-cycle should relatedness be evaluated? In particular, is it genetic similarity at the time of action that matters to the evolution of cooperation, or genetic similarity at the time of reproduction? I argue that, when HGT is at work, neither of these suggestions is correct: the sort of genetic similarity that really matters to the evolution of cooperation is diachronic similarity between actors at the time of action and recipients at the time of reproduction.

A genotypic view of social interactions in multispecies microbial communities
Mitri Sara, Foster Kevin, Oxford University, UK

Microbes live in dense communities composed of different strains and species, whose members can have positive or negative fitness effects on other cells. Disentangling social interactions between strains and species is central to understanding microbial communities and how they respond to perturbations. In particular, we are interested in how ecological factors, such as the spatiogenetic organization of a community or the availability of resources affect selection for cooperative or competitive interactions, and how selection shapes communities accordingly. Based on ecological and evolutionary theory, we propose a general null model which we call the genotypic view. This states that cooperation will occur when cells are surrounded by identical genotypes at the loci that drive interactions, where identity comes from recent clonal growth or horizontal gene transfer. Different genotypes will typically compete. We show how empirical data from the literature offers support for this view with relatively few examples of cooperation between genotypes.

Bacterial individuality
Clarke Ellen, University of Oxford, UK

Many claims have recently been made about how research into bacterial sociality and cooperation motivate new ways of thinking about individuality in microbes. In particular, it has been suggested, in light of evidence concerning quorum sensing and other emergent behaviours, that the bacterial communities known as 'biofilms' might be conceptualised as constituting a form of higher-level organismality. Furthermore, it has been suggested that some of the properties of these communities should be thought of as community-level adaptations. I evaluate these claims and try to spell out exactly what, if anything, turns on them.

Some Problematic Concepts in Evolutionary Biology (submitted papers)

Plasticity cannot explains itself
Nicoglou Antonine, IHPST & Université Paris 1 Panthéon-Sorbonne, France

The assumption that plasticity is nothing more than a property of the genotype and that it is specific to particular traits within a given range of environments is based on the idea that the precise scientific - genetic - notion of "phenotypic plasticity" and a more general - sometimes metaphorical - notion of "plasticity" used across different disciplines of biology (in evolution, behavioral ecology or in cellular biology) can be assimilated. By focusing on the theoretical analysis of phenotypic plasticity, biologists have mainly addressed the issue of what its mechanistic bases are (Schlichting & Smith 2002) and they have tried to reach a general consensus assuming that phenotypic plasticity should be considered as an *explanandum* – its *explanans* being the process of natural selection to which is added the assumption of a genetic basis for plasticity. However, theoreticians of the Extended Synthesis - whose aim is to offer an extended view of evolutionary theory based on recent data - have assumed that the same phenomenon of phenotypic plasticity is not only an *explanandum* of evolution but that it is also anexplanansof evolution (Pigliucci 2010). This assumption has led to a certain confusion concerning the explanatory status of phenotypic plasticity.

In this presentation, I will show how a general notion of plasticity (distinguished from the specific notion of "phenotypic plasticity") might either be considered as an *explanans* of variation or as an *explanandum* of natural selection. I will argue that a distinction between "phenotypic plasticity" and a more general notion of "plasticity" is important in order to offer a clarification on the explanatory status of plasticity. I will argue that this clarification sheds light on the reasons for a recurrent use of a general notion of plasticity in all disciplines of biology alongside the existence of the genetic notion of phenotypic plasticity.

Gradualism: Complications and Implications
Sansom Roger, Texas A&M University, USA

Claims that evolution is gradual play various important roles in evolutionary theory - from defending the plausibility of evolutionary theory's explanations of biological phenomena to bestowing "creativity" to natural selection (Gould, *The Structure of Evolutionary Theory*). Darwin was a great gradualist and gradualism remains central to Darwinism, but I shall argue that the concept is more imperiled than it is generally assumed to be. I distinguish relative gradualism from absolute gradualism and show how each notion carries out different roles in evolutionary theory. Relative gradualism faces the problems of what a trait is and how trait value change should be measured. Absolute gradualism also requires determining how much trait value change in one event disqualifies a period of evolution from being gradual. Finding no objective direct answer to this problem, I propose, instead, an objective notion of transition length and ask: what is the maximum proportion of change within that transition that could happen in one event while that transition remains gradual? I shall use these notions to investigate the logical relations of gradualism between parts and wholes. Finally, I shall suggest what systems are prime candidates for gradual evolution and what are not.

Hannibal (The Cannibal) Lecter and (Un)natural Selection
White Michael, School of Life Sciences, Arizona State University, USA

Hannibal (“The Cannibal”) Lecter 'selects for' ('selects against'?) certain humans. Since having a heart and having kidneys are coextensive traits, the fact that we find deceased humans for which he has selected does not reveal which coextensive phenotypical trait he is selecting for. Suppose that Hannibal is silent about this matter? The truth of one but not of the other following counterfactual conditional would answer the question. (A) If there were humans with hearts but no kidneys, Hannibal would select for them. (B) If there were humans with kidneys but no hearts, Hannibal would select for them. In the absence of appeal to Hannibal's intentions, Fodor and Piattelli-Palmarini would be skeptical about the existence of any nomologically necessary principles for distinguishing the two conditionals. That is, if we substitute for 'Hannibal' something like 'a set of exogenous environmental variables', they are skeptical about whether there exists a fact of the matter concerning which trait is being selected for.

The forensic scientist, however, will not regard the humans selected for as merely 'black boxes'- i.e., simply human corpses. If the scientist finds, at the crime scenes, corpses selected for with intact hearts and chafing dishes with the remains of deviled kidneys, the question might well be regarded as answered. In this presentation, I follow up on this unlikely analogy: I suggest that F & P-I's critique of natural selection may best be interpreted as an argument in support of Evo- Devo. I additionally argue that there is no incompatibility between certain theories' being *science* and their being *natural history*.

The Plant and the Pollinator Tale: how to take Teleology seriously in Biology and yet avoid being a Lamarkian?
Ongay De Felipe Iñigo, American School of Bilbao- Fundación Gustavo Bueno, Spain

The topic this paper shall address is the connections between teleology, behavior and selection within the context of Evolutionary Theory. I start off by considering how Darwin´s initial account of Evolution by Natural Selection did not take teleology and Evolution to be so disjointed from each other as later architects of the Synthetic Theory have pictured them to be. Secondly, I shall raise a philosophical question concerning the role of teleology and behavior in current interpretations of Evolution and Natural Selection. I shall contend that if any sort of teleology is excluded from Biology the concept of Selection would cease to make sense in explaining evolutionary processes. Much debate has recently arisen in Philosophy of Biology over the status of selection as a natural force with various philosophers and biologists alike affirming that Natural Selection is not to be interpreted as a real cause directing the evolutionary change of populations. I contend that in the absence of teleology they are actually right. In turn, i defend, if there is a place for teleology in our undersanding of Evolution by means of considering the ethological operations of animal organisms in the wild as the real agents guiding the process of organic change, the concept of Selection would be epistemologically safe. Finally, I will discuss specific cases of pairwise coevolution in which different individuals actively select one another thus guiding evolution by way of their behavior.

The space of explanations in evolutionary biology A

Statistically autonomous explanations
Ariew Andre, University of Missouri, USA

Ian Hacking (The Taming of Chance, 1990) calls Francis Galton's account of the "reversion to mediocrity" phenomena found in the distribution of hereditary genius an early instance of a "statistically autonomous explanation". To Hacking, "autonomous" is opposed to "causal". Galton's explanation does not cite possible underlying causal features of a population. Rather, it involves demonstrating that regression is a mathematical consequence of the Normal Law. In my talk, I will present Galton's early demonstration of reversion through his use of a quincunx, a shot-dropping machine. The aim is to strengthen and elucidate Hacking's view that statistically autonomous explanations are an important form of explanation in the history of science. I will show that the key features of statistically autonomous explanations in Galton's reversion are found in early 20th century population genetical accounts of evolution by natural selection.

Consequently, population genetical accounts of natural selection are also instances of statistically autonomous explanation. One key feature is found in the explanandum: the phenomena to be explained is an instance of a large-scale regularity that would not be explained by reference to individual level effects. The other key feature is found in the explanans. The aim of a statistically autonomous explanation is to demonstrate that the large scale regularity would happen if such-and- such were the case even if such-and-such could never actually happen in real world populations (Gibbard and Varian, "Economic Models", 1978). Finally, I regard statistically autonomous explanations as an alternative to Michael Strevens' fully causal "kairetic account" of explanation (Strevens, "The Causal and Unification Approaches to Explanation Unified- Causally", 2004).

Multilevel Mechanisms of Evolutionary Change
Darden Lindley, University of Maryland, USA

Theodosius Dobzhansky in his 1937 *Genetics and the Origin of Species* claimed that "the mechanisms of evolution as seen by a geneticist" consist of mechanisms at three levels. This multilevel analysis still captures the key mechanisms of evolutionary change. First, mechanisms produce the variations that are the raw material for change, including mutation mechanisms of imperfect copying of DNA (including repair mechanisms), as well as larger scale chromosomal changes and recombination. The second level includes mechanisms that change populations, genotypically and phenotypically. The most important is the mechanism of natural selection, which is the only known mechanism for producing adaptations. In the natural selection mechanism, the crucial joint activities of variant organisms and a critical environmental factor produce populational changes in subsequent generations. Finally, isolating mechanisms give rise to new species that are reproductively isolated from previous conspecifics. This paper argues that natural selection is, indeed, a mechanism (despite recent claims to the contrary) and places the natural selection mechanism into the context of the multilevel mechanisms of evolutionary change.

Articulating mechanisms and topologies as mutually required in explanatory strategies.
Huneman Philippe, IHPST & Université Paris 1 Panthéon-Sorbonne, France

Evolutionary biology displays topological explanations, namely explanations which, instead of considering underlying mechanisms, explain by pinpointing topological properties of abstract spaces (such as food-webs) associated to the system, which entail the explananda (Huneman 2010). This is often used to explain the stability of an ecological community (e.g. Montoya, Solé 2002). I will investigate how mechanistic and topological explanations are connected in evolutionary theory.
Prima facie they are answering different questions: mechanisms are used to investigate the production of these topological structures (e.g. scale-free food webs) which possess the properties used as explanantia in topological explanations (e.g., specific mechanisms of predation may yield food webs of a given topological nature). Here, mechanistic explanations explain what makes topological explanations possible.
However, I here consider two reverse relations, less self-evident. 1. The mechanisms of allele frequency changes in populations are modeled by population genetics; yet such modeling has to make assumptions, about especially the possibility of bracketing development, and about considering the dynamics of a few loci as capable of representing the whole dynamics in the genomes population. Such assumptions will be characterized in terms of topological properties of genotype/phenotype maps, because what is required is the mappings to be conservative of some kinds of neighborhoods. 2. Modeling selection over fitness landscapes may involve mechanisms of trait optimization, but only under some conditions of local invariance of the landscape, which are topological conditions.
Hence a two-ways relation: topological (resp. mechanistic) explanations can provide conditions of validity for mechanistic (resp. topological) explanations.

The space of explanations in evolutionary biology B

Asymptotic Idealization in Evolutionary Explanation
Strevens Michael, New York University, USA

Batterman and others have argued that many explanations have an asymptotic form: they explain a state of affairs or behavior by showing that it emerges "in the limit". Explanatory models of this sort have two properties that, on the DN account, explanations are supposed to lack: (a) the "premises" of the model do not entail the explanandum, and (b) the model is idealized in certain ways having to do with the infinitude introduced by the use of limits, and so false of the real world. My talk will present a simple example of asymptotic explanation in evolutionary biology; it will show how to understand the limiting aspect of the relevant model, and in particular to relate it to the conventional wisdom among biologists as to what the model is doing; and it will attempt to fit the model into a modern theory of scientific explanation.

Varieties of Invariance
Walsh Denis, IHPST, University of Toronto, Canada

An explanation serves two functions: metaphysical and cognitive. Its metaphysical function involves identifying a feature of the world, the explanans, that relates in the appropriate way to the explanandum. Its cognitive function involves describing the relation in such a way as to provide understanding. One of the principal virtues of Modern Mechanism, I argue, is that it offers a generalizable model for the structure, or anatomy, of an explanation. Mechanistic explanations are bipartite. They cite a mechanism -an entity undergoing an activity- and an elucidating description. The hallmark of the relation between a mechanism and the effect it explains is invariance. Invariance is a robust counterfactual relation. The relation between a mechanism and its effect is one such invariance relation, but I argue that there are others as well, and these may form the basis of alternative modes of explanation. I claim that statistical and teleological explanations conform to the same bipartite structure. Each identifies a property of a system that bears a robust invariance relation to a particular kind of event to be explained. Each, in turn, provides a distinctively elucidating description of that relation. Some phenomena are susceptible of complete explanation in mode than one mode. Explanations of the same phenomena in different modes (say, causal and teleological) neither supersede nor exclude one another: they are ‘miscible’. I use examples from evolutionary biology to illustrate this relation of ‘miscibility’.

Maximum Entropy Explanations in Biology
Aidan Lyon, University of Maryland, USA

There are many robust and simple patterns in biology that arise out of the aggregation of a myriad of chaotic, and complex processes. A phenotypic trait such as height is the outcome of a huge complex array of interactions between genes and the environment. However, as Galton (1889) and many others have noticed, such traits often exhibit a very simple pattern: they are often normally distributed. Similarly simple patterns occur all throughout nature: the log-normal, power law, and exponential distributions-just to name a few.

Recent work, particularly by Frank (2009), has shown that these distributions can, in some sense, be explained by their maximum entropy properties. Frank argues that by maximising the entropy of a probability subject to a few informational constraints, one obtains a framework that neatly unites and explains many of the robust and simple patterns that we observe in biology. However, it's not at all clear how entropy and its maximisation can explain anything in nature. Entropy, in this context, is usually understood in terms of information, or the lack of information, that some ideal epistemic agent has (e.g., Frank 2009, Jaynes 2003). But how can the information that some agent has explain why, for example, heights are normally distributed? Intuitively, it can't. In this paper, I survey a number of interpretations of the entropy of a probability distribution and examine how they can be embedded in a theory of explanation so that we can make sense of such maximum entropy explanations in biology.

The Status and Prospect of Genetic Explanations of Behavior

The gene of
Roubertoux Pierre, Aix-Marseille Université, France

During several years we believed it would be possible to draw up a list of diseases, morphological characteristics and behavioral traits linked to each gene. The publication of the genome sequences (Caenorhabditis elegans, Man, Mouse, Dog etc...) kindled the expectation. The post genome area demonstrated that the attempt was not vain. Links between genes and phenotypes, including behavioral phenotypes, do exist but they are more complex than previously thought. The relationships between genotype and brain and between brain and behavior are not linear and consequently, genomic, brain and behavioral levels of organization are not isomorphic. Passing from the DNA that is the most elementary level of the biological organization, to the amino-acids level, to the neuronal level and then to the behavioral level increases the quantity of information but it reduces concurrently the capability to predict the upper level from a lower level. Pleiotropy, epistasis, alternative splicing, interactions between genes and the environments or neuronal integration contribute to the dilution of the genetic causality.

Explanatory Virtues and Genetic Causation
Kronfeldner Maria, Bielefeld University, Germany

Cognitive, behavioral or medical characteristics of human beings (e.g. traits such as language or diseases such as schizophrenia) are often said to be causally complex. Causal complexity comprises that (1) an effect has *many* causes and that (2) a cause has *many* effects. We can thus react to it in two ways: (1) by selectively focusing on particular causes and relegating other causally relevant factors to the status of mere conditions (causal selection), and (2) by dividing the phenomenon into parts that are more tractable (reconstituting phenomena). These strategies conquer complexity by dividing either the explanans or the explanandum, or both. As a result, we get a more simplified picture: effects that 'have a cause of their own' and causes that 'have an effect of their own'. The focus in this talk will be on reconstituting phenomena. When we use this strategy, we are guided by heuristic norms that relate to what I call explanatory virtues, criteria that (if fulfilled) make an explanation a good one. The focus will be on stability, specificity, and proximity. The paper describes how these explanatury virtues are related, how they can conflict, and in which sense they are instrumental for further epistemic values (such as parsimony, generality, predictive fruitfulness, etc). It will also explicate how levels of analysis and disciplinary boundary politics enter the picture. Examples are from norm of reaction studies and talk about endophenotypes in discussions about genetic causation.

Can Genes Explain Human Personality? Doubtful!
Schaffner Kenneth, University of Pittsburgh, USA

The five factor model of personality (FFM) is a widely accepted model in psychology. But in spite of the claimed strength of the FFM, genetic approaches to personality applying the model have regressed to their "infancy". The story behind this regression is of even more general interest, since it is a corollary of what has developed in the past six years in behavioral and psychiatric genetics. These changes were required by what has amounted to a major revolution occasioned by the development of the genome-wide association studies (GWAS) methods. The application of GWAS methods has also generated the controversial problem of "missing heritability," in which GWAS results only account for a very small portion of the variance of traits of interest. But more importantly, GWAS has led to the clearer realization that genes typically will have tiny effects, and there will be a huge number of them-probably thousands of genes affecting relatively simple traits. The bottom line currently is two major investigators in the area, South and Krueger, state "that molecular personality genetics is in its infancy as a field", and that GWAS findings suggest that there are likely thousands of genes of small effect size that influence personality, and that at present these results "tell us little about the biological pathways involved in personality and psychopathology".
This presentation will review these issues, and point the way that pathway analyses may be offering some future solutions.

Gene-Environment Interaction in the 21st Century: Its Rise, Its Fall, Its Rise?
Tabery James, University of Utah, USA

At the turn of the 21st, Terrie Moffitt and Avshalom Caspi published a series of papers on gene-environment interaction. These articles were published in premier scientific journals, and the results were hailed in the media. One paper in particular, on the relationship between the serotonin transporter gene and exposure to stress in the development of depression, has been replicated dozens of times and cited over 4000's times. A 2009 meta-analysis of those replications, however, was negative, suggesting that the original result may have just been due to chance. But then a 2011 meta-analysis came back positive, suggesting a confirmation of the original result. A commentary in *Archives of General Psychiatry* (which published the 2011 meta-analysis), worried, “The reader is therefore entitled to ask, ‘What should I believe? Which explanation is true?’”. I will situate this most recent debate over gene-environment interaction in the longer history of research on the phenomenon. That history reveals that there have been two quite distinct ways to understand interaction in terms of how to conceptualize it, how to investigate it, and how to weigh evidence for it. My thesis for this talk is that these competing understandings are playing out yet again in this 21st century debate over gene-environment interaction.

Systems Biology A (submitted papers)

Hierarchical approach at the core of organicist and systemic views in biology

Umerez Jon, University of the Basque Country, Spain

There are, at least, three wide conceptual elements that characterize, quite obviously, the philosophical significance of, at least, the "developmentally oriented" strand of early twentieth century organicism: centrality of the organism, systemic perspective, and hierarchical thinking in terms of levels of organization.

The hypothesis I want to explore in this work would hold that one of the aspects that deserves scrutiny, from an epistemological point of view, as a signal of the persistence of early 20th century organicist views in later decades is, precisely, hierarchical thinking.

I hold that it happens that both its presence and oblivion are coincident with a more general attitude (positive or negative) towards organicist like views in the life sciences. Even in some cases, this hierarchical view may be the only apparent trace of a more encompassing view.

As a specific and practical illustration I will offer the long trajectory of experimental and theoretical research of Paul A. Weiss. The concepts of 'system' or 'levels of organization' were key elements in the theories of organicists such as Bertalanffy, Needham and others. Among them, the work of Weiss in particular embodies rather nicely the continuity of hierarchical thinking in biology from the 20s to the 70s and the analysis of his scientific and intellectual career corroborates these claims.

As a complementary claim, I maintain that the absence of a genuine hierarchical approach in some current proposals as, for instance, within the emerging area of Systems Biology might indicate a different source and ambition of these proposals.

Institutional and Epistemic Practices in Systems Biology

Rajagopalan Ramya, Fujimura Joan, University of Wisconsin-Madison, USA

Within academic research universities in the US, there is a growing trend to build infrastructures that facilitate interdisciplinary and collaborative modes of doing science. At the same time, molecular researchers in the life sciences are building frameworks for viewing organisms as complex systems embedded within larger ecosystems, in what some call high-throughput, dataintensive, post-genomic science. One goal of these efforts is to accelerate an understanding of the complexities of biological systems that investigates interactions beyond just genome sequences and DNA. We have been studying systems biologists as they have moved from an independent academic laboratory to a newly built research institute which seeks to be a " transdisciplinary, hyper-collaborative" space for addressing complex problems of relevance to health and society. Our findings analyze how this institutional environment affects the questions that systems biologists in this institute are pursuing. We examine how they bring together perspectives from engineering and the life sciences, to develop tools for studying, quantifying, visualizing, and modeling processes in simple systems, such as viruses. Their goal is to be able to predict virus interactions with and within cells, tissues, and whole organisms. In the process, they are devising new understandings of what constitutes heterogeneity, variation and even the " environment" in biological systems, while grappling with how to develop generalizable models for predicting the outcomes of basic molecular processes. We use our "before and after" ethnographic data to explicitly link changes in institutional organization with both the content of scientific knowledge produced and the practices of its production.

Mechanisms in Systems Biology: do they explain enough?
Mekios Constantinos, Stonehill College, USA

Models play a prominent explanatory role in top-down and bottom-up systems biology. As demonstrated in the present study, these models generally meet the most recently stipulated theoretical constraints that define what counts as mechanism. In light of these observations, I argue that a purely mechanism-based framework that complies with the constraints of the new mechanistic philosophy can be regarded as explanatorily adequate to the extent that it allows for the reliable manipulation and control of biological processes in the context of systems approaches. Nevertheless, such framework remains limited in its capacity to carry out the comprehensive explanatory integration demanded for the holistic understanding of complex biological systems, whose attainment constitutes systems biology's most ambitious objective. In addition, in their current formulation the models endorsed by the new mechanists are not sufficient for capturing the rich explanatory pluralism that characterizes the practice of systems biology. The contention that this pluralistic character of systems biology is only revealed through a pragmatic view of its practice suggests that moving beyond theoretical considerations is required for gaining a better insight into the nature of explanation. I propose, however, that philosophers do not need to make a choice between adopting a theoretical or pragmatic attitude: the dilemma is spurious because both perspectives contribute in a mutually complementary way to constructive thinking about explanation in biology.

Systems Biology B (submitted papers)

Metabolic data and mathematical models
Donaghy Josephine, University of Exeter, UK

The availability of different types of metabolic data has had a significant influence on the construction of mathematical models of metabolism. In this paper I will examine distinctions between different metabolic data types in the 1970's and 1980's. Researchers commonly distinguish stoichiometric and kinetic data. Stoichiometric data pertains to the composition of metabolic systems and the structural relations between those components. These were widely assumed to be general and stable properties of the metabolic systems of particular species. By the early 1970's researchers considered this information to be almost complete. Kinetic data pertains to how the rate of individual reactions responds to changes in context such as substrate availability. In some cases these properties were assumed to be general and stable properties of reactions, in others these properties were assumed to be specific to the context of a reaction in a particular metabolic system. In both cases researchers considered there to be insufficient kinetic data available and devised modelling strategies which compensated for this. In the current situation of data intensive biology mathematical modelling plays an increasingly important part of biological research. It is important to understand how mathematical modelling is shaped by differences in the availability of data types and the different assumptions about the biological properties to which those data types pertain.

Systems biology and the limits of philosophical accounts of mechanistic explanation
Brigandt Ingo, University of Alberta, Canada

Mechanistic explanation has been developed as a philosophical alternative to traditional models of explanation as derivation from laws and equations, with Carl Craver having criticized several mathematical models as merely describing but not explaining. In contrast, I discuss systems biology as an area where explanation in terms of mechanisms and explanation by mathematical models is integrated. Against the vision of mechanistic explanation in terms of structural organization and qualitative interactions only, the paper lays out three cases from systems biology, focusing on questions about qualitative phenomena (rather than the explanation of quantitative details) where equations are still indispensable ingredients of the explanation. The development of mammalian teeth is modeled by nonlinear differential equations, so that the outcome to be explained is sensitive to quantitative parameters. The modeling of apoptosis illustrates the general phenomenon of bistability, i.e., a system being in either of two qualitatively different states (alive state and apoptosis state of a cell), to be quantitatively explained by a threshold behavior. The development of vertebrate segments is based on the presence of regular oscillations of gene activities inside individuals cells, and its synchronization between cells, which are qualitative explananda necessitating a mathematical model. Apart from the relevance of equations in mechanistic explanations, systems biology shows that a broader philosophical conception of mechanisms is needed, which takes into account quantitative changes and functional-dynamical aspects, transient entities and the generation of novel entities, complex interaction networks with feedback loops, and system-wide functional properties such as distributed functionality and robustness.

Bridging the gap between system and molecular biology. The case of melanoma
Boniolo Giovanni, University of Milano, European Institute of Oncology, Italy

Since the seminal papers by A. Barabasi and colleagues, network biology has increased its relevance in the scientific community. This way of connecting data has had supporters and critics. Surely it offers the enormous advantage to link, also with an immediate and intuitive visual rendering, information before disconnected. Nevertheless, it implies a lost of detailed molecular information. This is not an unexpected consequence, indeed. Systems biology (network biology in particular) allows a way of considering molecular entities and processes which is, *ab initio*, different from that one offered by molecular biology. Working with the former means missing details, working with the latter means missing the overall view. Is there a manner of connecting them?

I want to address this point and, after discussing the epistemological differences between the two approaches, I present a formal bridge between them that should permit to move from the information typical of network biology to the information typical of molecular biology. This bridge could spur philosophers to rethink in term of epistemological pluralism the scientific approaches. Many times we - philosophers - are too strictly tied to a given particular epistemological perspective to successfully cope with a science, such as contemporary biology, which follows its own paths and almost every day shows us different aspects.

I will exemplify the usefulness of a pluralistic perspective by discussing the melanoma network and the molecular level of the disease. In this way I will illustrate how we could have a real integration between the information pertaining to the systemic level and to the molecular level.

What is a ‘hypothesis’ in contemporary biology?
Roberts Eve, Dalhousie University, Canada

Indistinct conceptions of 'hypothesis' account for much confusion about the epistemology of contemporary biological research. Systems biology -particularly the omics disciplines (genomics, proteomics, metabolomics and the like)- challenges the received notion that all science is hypothesis-driven. Closer examination reveals multiple levels at which hypotheses or alternate-drivers can operate. Elsewhere I have suggested that contemporary biological research can be broadly categorized as either hypothesis-driven or non-hypothesis-driven. The latter is comprised of at least two subcategories, system-driven and data-driven. In system-driven research the complexity of a biological system is addressed directly; in data-driven research a collection of data already assembled is interrogated to find new information 'hidden' there. Omics research is system-driven research, ostensibly without a hypothesis.

Yet, when asked, the omics researcher will contend that s/he has a hypothesis. Typically it is something like "there are numerous unidentified proteins in this system" or "multiple genes contribute to this cellular process". I propose that biological research involves a hierarchy of 'hypotheses'. First, as Kuhnian normal research, the research enterprise has a hypothesis locating it within its research paradigm. Secondly, it features what I call a *hunch* hypothesis: a broad motivation of the research project. Finally, there is an operational level immediately proximate to experimental design. For hypothesis-driven research, a detailed hypothesis governs experimental design. For system-driven research, the system being investigated directly informs experimental design. The character of 'hypothesis' in biology has been elusive because multiple layers of hypothesis are at work; however, what really counts is what governs experimental design.

Taxonomy and Phylogeny (submitted papers)

How Should Phylogeny Guide Biodiversity Conservation?

Maclaurin James, University of Otago, New Zealand

Much of biological conservation focuses on ecologically, culturally and economically valuable species and the ecosystems that support them. However, many species cannot claim such credentials. They are not valued by humanity for social or economic reasons and they do not serve important and unique ecological roles. How should conservation biologists prioritise the conservation of such unremarkable species? In this paper, I explore solutions to this problem based on phylogenetic interpretations of biodiversity.

Phylogenetic ancestors

Zaragüeta Bagils René, Université Paris VI & Muséum National d'Histoire Naturelle, France

The concept of ancestors in modern phylogenetics is particularly obscure. However, the interpretation of phylogenetic trees requires evolutionary concepts such as ancestry. The relationships that exist between cladistic analyses and phylogenetic information conveyed by cladograms (phylogenetic trees resulting from the application of cladistic theory) may be interpreted as follows:

- Cladistic analysis defines monophyletic entities, i.e. taxa and homologues that the theory of evolution must explain.
- The theory of evolution entirely justifies cladistic theory.

In both cases, the concept of evolutionary ancestor is critical. It is difficult to consider a historical account on taxic diversification without taking into account ancestor-descendant relationships. However, systematists have been elusive about the issue of ancestry. The problem of defining and understanding what an ancestor is is simply evacuated by considering it "hypothetical"; ancestors are assumed in historical narratives, but the ancestor is declared as unidentifiable in the fossil record, and either absent or implicit in phylogenetic trees. The concept of phylogenetic ancestor thus needs to be clarified.

Here I analyse the inconsistencies found in some of the best manuals of phylogenetics concerning the idea of ancestors. I provide a solution for eliminating these inconsistencies and clarifying the notion of phylogenetic ancestry. I give some of the consequences that a consistent idea of ancestor has on our representation of the taxic diversification process, on the information conveyed by phylogenetic trees, and on our own ancestry as humans. Finally, I show that the concept of ancestor is reducible to the concept of taxon.

Hierarchies and orders in systematics and phylogenetics

Prin Stéphane, Muséum National d'Histoire Naturelle of Paris, France

Following a general conception of hierarchies in systematics and phylogenetics (e.g. Mayr, 1982), these are of two kinds, i.e. division and grouping. Within this framework, some authors (Williams, 1992; Knox, 1998) have criticized Hennig for conflating the phylogenetic tree (a hierarchy of division) with the phylogenetic system (a hierarchy of grouping). As a result, it is impossible to deduce the phylogenetic tree from the phylogenetic system while the converse is possible (Dayrat, 2005).

However, these criticisms lead to several problems. First, there are not two but at least three kinds of hierarchies in systematics and phylogenetics: (1) the tree-like genealogy of species, (2) the cladistic hierarchy and (3) the Linnaean hierarchy. Second, the distinction between the ontological (the species/non-species distinction), epistemological and formal aspects are not discussed by the critics.

I argue that, from a formal point of view, there is a particular concept of order which subsumes all the systematic and phylogenetic hierarchies of taxa. Within it, there is a more restricted concept which formalizes both the tree-like genealogy of species and the cladistic hierarchy, i.e. both are isomorphic. However, these two kinds of hierarchies are not biologically equivalent.

I conclude that either evolution is a matter of succession of transitory species and cladistics is instrumentalist, or cladistics represents correctly the result of (the process of) evolution (in terms of kinship) and evolution is a matter of differentiation of new clades inside old and persistent clades (i.e. all clades evolves, not only the species).

Teaching Biology A (submitted papers)

The Ghost in the Classroom. Evolution, Ernst Haeckel and German biology didactics (1859-1933)

Sommerey Constance, Maastricht University, Netherlands

When Darwin's *On the Origin of Species* (1859) entered Germany, it rapidly spawned controversies over evolution's place in the class room. It was especially Germany's leading proponent of evolution Ernst Haeckel (1834-1919) who questioned the monopoly of religion on the teaching of the meaning of life. Evolution, for him, was a worthwhile substitute for dualistic accounts of creation. This belief was articulated in his monist philosophy which postulates that matter and spirit are united in the organic substance. Churches and conservatives were appalled by Haeckel's heretic idea to replace religion by evolution in school curricula and to possibly convert Christian students into materialist atheists. In 1882, the Prussian ministry of education reacted and banned biology as a whole from secondary education.

In 1925, over 40 years later, the Weimar ministry of education eventually declared biology and evolution integral parts of the curriculum. School book authors were now confronted with the choice of how to rhetorically present this socially and politically sensitive topic. Should evolution be presented as a hypothesis or an established scientific world view? I argue that the enduring juxtaposition of evolution and religion in Germany had culminated in their incommensurability.

If a school book author wanted to portray evolution as *the* valid theory of organic development, his presentation concurrently had to surrogate the biblical version of creation. This paper presents a rhetorical analysis of Weimar school books to illustrate how authors appropriated Haeckel's rhetoric of a *scientific* Genesis in their attempts to persuade adolescent students into embracing evolution.

H.G. Wells: Biology Crammer

Elwick James, York University, Canada

Why does someone study biology? Our most familiar reason is because someone is curious, or because they can acquire valuable skills and knowledge. This perspective is known today as 'human capital theory'. While useful, it may not sufficiently explain individual *student* intentions, such as those of H.G. Wells (1866-1946). Most studied by historians of biology for his time in T.H. Huxley's teaching laboratory, it is less-well known that he got there only by doing well on Huxley's exams. For although Wells was curious, another central motivation for learning biology was to earn *certificates* and thereby advance himself. This paper therefore introduces credentialing theory to discuss H.G. Wells's early exam-taking, and then his exam-tutoring as a coach for the feared zoology exams of the University of London. By focusing not so much on knowledge as on its *signs*, credentialing theory reveals a tension between outer display and inner possession; plays up the importance of exams over curricular issues such as textbooks or labwork; and shows how people like Wells were keenly aware of the relative values of different certificates. The credentialing perspective gives us new insight into a world of "payment by results" in which it was assumed that teaching effectiveness was indicated by one's students' exam successes, and reveals a world of competitive exam coaches far less prestigious than the Cambridge Maths Tripos tutors written about by Andrew Warwick. Above all, we see how a relentless scepticism about whether signs of knowledge denoted its authentic possession led to repeated public outbursts about the dangers of 'cramming'.

Concepts of dominance in 20th century genetics pedagogy
Jamieson Annie, University of Leeds, UK

Various writers have raised concerns about the concept of dominance in current high school and undergraduate genetics teaching. The emphasis, in foundational teaching, on the traditional Mendelian dominant/recessive dichotomy can instil in students an overly deterministic view of genetics that is at odds with the much more interactionist conception we see in 21st century genetics and genomics research. Recent textbooks largely continue to promote Mendel's peas as the type-specimen of genetic action, with all else being amendments or exceptions to Mendel's laws. Moreover, the simple patterns of inheritance shown in Mendel's peas -smooth vs. wrinkled, yellow vs. green, for example- encourage the linear view that one gene controls one trait. But this was not always the case; many early 20th century authors presented a much more flexible and nuanced view both of dominance and of the nature and range of action of the gene. So, when and why did this hard-line, reductionist view begin to appear and how did it become the received view in textbooks? This paper will explore representations of dominance in a range of textbooks and monographs from the first half of the 20th century (prior to the discovery of the structure of DNA) and explain how intellectual and conceptual developments, like the New Synthesis, the rise of 'environmental eugenics', or the bio-social programme of, for example, Lancelot Hogben and Julian Huxley, affected these representations.

Teaching Biology B (submitted papers)

Research Integrity and Everyday Practice of Science
Grinnell Frederick, UT Southwestern Medical Center, Canada

Science traditionally is taught as a linear process based on logic and carried out by objective researchers following the scientific method. Practice of science is a far more nuanced enterprise, one in which intuition and passion become just as important as objectivity and logic. Whether the activity is committing to study a particular research problem, drawing conclusions about a hypothesis under investigation, choosing whether to count results as data or experimental noise, or deciding what experimental findings to present in a research paper and in what order to present them, ethical challenges inevitably will arise because of the ambiguities inherent in practice. Sir Peter Medawar criticized scientific papers because one could not learn the "adventures of the mind" that led researchers to make their discoveries. These adventures and the ambiguities that they reveal should become a component of research integrity education by introducing scientific memoirs into the curriculum. For instance, by reading Watson's *The Double Helix* students will learn that the path to discovery is anything but linear and that the researchers involved are anything but disinterested. Unless the ambiguities of practice are acknowledged and their sources understood explicitly, research integrity education will not adequately prepare the individuals receiving the training for the kinds of decisions essential to responsible conduct that they will have to make as scientists. Also, research integrity education should begin early, perhaps in conjunction with science fair, to help avoid misimpressions on the part of students (and their teachers) about the nature and practice of science.

Object Lessons in the Life Sciences
Dyer Ruthann, York University, Canada

The use of material objects in the teaching of biology has a long history with live organisms, specimens and models being used in the classroom. This presentation will examine how everyday objects have been used to generate interdisciplinary enquiry into concepts within the life sciences.
The history and social science within which an object is/was produced and used will be linked to the associated biological science and technologies using principles of material culture research.

A qualitative and quantitative analysis of contents concerning of pluralism of processes and evo-devo in higher education textbooks of evolution and vertebrate zoology
Santos Wellington, Universidade Federal da Bahia, Brazil

This article reports the results of a comparative content analysis of three evolutionary biology textbooks and three vertebrate zoology textbooks, significantly adopted in the biology higher education syllabuses in several universities of Latin and Anglo-Saxon countries. Through a documental quali-quantitative analysis of the textbooks, performed by using content analysis methodology, we undertook an investigation of the approach and recontextualization of contents related to evolutionary developmental biology (evo-devo) and process pluralism in the selected books. Based on this investigation, we sought to answer the following question: to what extent and in what manner those contents, related to important advances that took place in evolutionary biology in the last two decades, are recontextualized in evolution textbooks and in the discussions on evolution present in vertebrate zoology textbooks? The findings of this study show that evolution textbooks are still at an initial phase of recontextualization of the contents related to process pluralism and, thus, to what has been called the extended synthesis in the field of evolutionary biology. However, they are in a more advanced stage of recontextualization than the analyzed vertebrate zoology textbooks, in which a substantially smaller diversity of evolutionary mechanisms was observed, with a large emphasis only on natural selection. These findings are not surprising, since the idea of an extended synthesis is not well established yet in evolutionary biology itself. With regard to the evo-devo contents, a more significant level of recontextualization was observed in the textbooks of both fields, showing that at least part of the content of the so-called extended synthesis already reached biology higher education.

Teaching Biology C (submitted papers)

The teaching of evolution in Mexico
Torrens Erica, Facultad de Ciencias, Mexico

One of the most interesting aspects of the current studies on the history of evolution is the growing attention in exploring its role and scope in non-scientific fields, for example, in education. Some scholars have explored how the theory of evolution was introduced to the classroom and when the efforts to include the topic in textbooks began.

In the Mexican scene, the teaching of evolution has undergone many changes in the last few decades. Starting by posing the question: why evolution was introduced in the curriculum of primary schools until 1974? Our study is focused on a comparative analysis of the content of evolution in primary and secondary Mexican biology textbooks since 1974, from a HPS perspective but it also explores the social tensions behind the introduction of one of biology's most fundamental ideas into basic education.

Interestingly enough, in Mexico since 1954 textbooks for basic education are free and universal. This means that every Mexican child from 6 to 15 years old receive the same educational material (2.7 million copies of every subject are published every year), making textbooks a truly influential element in Mexican education.

Our results will shed light into: 1) the content of evolution in biology textbooks since 1974, 2) the dominant values and ideology of the era in which each different textbooks was written, 3) how certain social, political and scientific dynamics occurring in the Mexican scene from late Eighteenth century have had a direct impact in basic school biology.

Advisability of training course 'The history of bacterial phytopathology' in higher education institutions

Gamaliia Vira, Borys Grinchenko Kiev University, Ukraine
Zabuga Oksana, D.F. Chebotarev State Institute of Gerontology NAMS of Ukraine, Ukraine

During the beginning of XXI century some new directions in the history of science, including the history of bacterial plant pathology were developed. However, for the understanding of the place of bacterial plant pathology as a separate discipline in the biological sciences, its content, objectives and methods should be defined clearly.

Bacterial phytopathology is the science of plant diseases, resulted by bacteria. The mission of this branch is the detection of such diseases, the development of their prevention and control, isolation and study of pathogens. The modern bacteriological phytopathology uses heritage disciplines of biological, medical, agronomical and several other fields (morphology and plant anatomy, biochemistry, biophysics, genetics, breeding, microbiology, immunology, climatology, meteorology, etc.). Solving its own tasks, bacterial phytopathology is related to an improving of human wellness and ecological situation, besides it is involved into a reconstruction of the evolution of biosphere.

Like all new ideas, the bacterial phytopathology has passed a complex path of its development.

It should be noted that a significant role in its establishment and institutionalization have played Ukrainian scientists.

The teaching of the bacterial plant pathology will be useful not only for future farmers and microbiologists. This discipline can become the one of the components of a general course of the history of science directed to the formation of outlook and a true understanding of a place and role of human in the system of nature.

Retrospective survey of ethical conceptions' development in the system 'man-environment'

Duplenko Yurij, National University Kyiv Mohyla Academy, Ukraine
Ruda Svitlana, Institute of Art Modelling and Design

The aim of presented paper and proposed training course is consideration of ethics mutual problem in the system "man-environment" in retrospective terms and in modern conditions as a complex interdisciplinary scientific branch.

Important aspects of ecology are philosophical and ethic problems, among which are such as ecological crisis, formation and modern state of ecological ethics considered as a section of social ecology.

First of all the knowing on a powerful influence of interlink between Man and Nature is very important. Nature has no homeostatic mechanisms which would allow it to compensate the

effects of modern anthropogenic loads until human activity is beyond of control. One of the base philosophical problems is formation and modern state of ecological ethics. History of moral human conceptions regarding environment and influence of ethno-cultural features on this process is considered in course. There are cosmic ethics; examples of literature Utopia; D. Andreev's conception; analysis of ecological-economical activities by S. Podolinsky; noosphere conceptions вy V. Vernadsky and P. Teilhard de Chardin; eco-ethical A. Schweitzer's conception.
The presentation of conception "relationship with the environment" from ethical relations point of view and demonstration of ways of introduction of continuous environmental enlightenment and education are followed. It shows that study of the differences between moral and legal regulation of eco-ethical behaviour opens prospect to creating a modern ecological-educational model for working-out a qualitatively new level of thinking and public actions.

Creative Nonfiction, Excerpt and Methodology
Gormley Melinda, University of Notre Dame, USA

Some well-known books on scientific topics written in the style of creative nonfiction are Erik Larson's *The Devil in the White City*, Rebecca Skloot's *The Immortal Life of Henrietta Lacks*, and Deborah Blum's *The Poisoner's Handbook*. Trained as an historian of science, I have been cultivating my ability to write creative nonfiction as a fellow with the National Science Foundation-funded program *To Think, To Write, To Publish* based at Arizona State University's Consortium for Science Policy and Outcomes. This program has partnered me with freelance science writer Melissae Fellet to produce an article on a science policy topic in the style of creative nonfiction that is slated for *Creative Nonfiction*. Together Melissae and I have used the peace activism of Linus Pauling to write about responsible advocacy in science. I am also writing on geneticist L.C. Dunn's activism in this manner as well. My paper will first present an original work of creative nonfiction covering an historical topic involving biology and advocacy that will be followed with a short discussion on the methodological challenges an historian faces when writing creative nonfiction.

Testing the ZFEL in a Macro-evolutionary

Quantifying the Zero Force Evolutionary Law
Fleming Leonore, Duke University, USA

This paper presents the first mathematical representation of the Zero Force Evolution Law (ZFEL). Using the framework developed by Price (1970), I derive an expression for change in phenotypic variance over time and establish that the ZFEL is inherently true in this framework. In other words, I show, formally, that in a system with variation and heredity, if selection and constraints are absent, variance will increase. I use this formalization to investigate 1) the ZFEL as a background tendency in evolutionary systems, and 2) the ZFEL as a strongly driven trend over the history of life. I conclude by illustrating how this formal model can be applied to real data by comparing human nucleotide mutation rates in coding and noncoding regions of the genome.

Testing the ZFEL in a Macro-evolutionary Context
Brandon Robert, Duke University, USA

The history of life on Earth shows a dramatic, though not smooth, increase in diversity. We argue that such an increase is an expected feature of life and that natural selection does not explain it. Reviewing the best current explanations of macro-evolutionary diversity we show that all of these explanations share a common feature, namely they rely on what we term the Zero Force Evolutionary Law. Stating this law explicitly allows us see what unifies the best current explanations of macroevolutionary diversity and to see that it is the fact that lineages' trajectories tend to move randomly with respect to each other that actually explains diversity increases. Measuring and quantifying the default rate of change of lineages is possible and would allow for a quantitative test of the ZFEL in a macro-evolutionary context.

Theory of organisms

Propagative and Repulsive constraints in molecular and cellular biology

Miquel Paul-Antoine, Toulouse le Mirail – Toulouse II University, France

There is an open debate in philosophy of biology today, regarding the characterization of a living organism as an individual. In the neo-varelian approach, a biological individual is not simply defined by its genetic identity, or by its physiological integration. Organisms are autonomous agents constituted by a distinctive regime of causation realized by organisational closure. Closure is defined as a given set of constraints in which each constraint contributes to the maintenance of the others at different time scales. Thus, biological systems will not simply capture, but also produce their own constituents within their environmental niche. Furthermore, they will not only have a physical open structure, but they will also perform biological functions. Organisational closure is not self-maintenance, or self-organisation. A bacterium is not a flame, or a crystal or a simple dissipative structure.

Yet in *Investigations*, Stuart Kauffman proposes a very different definition of autonomy. Autonomous agents are related to specific open biological cycles, through which they are able to construct constraints to propagate organization. We will show two examples of *virtuous* and *vicious* cycles in molecular biology. The first one concerns "evolvability", and the way by which a bacterium under stress conditions is able to reprogram its genome. The second one concerns the degradation of connective tissues in the process of aging.

Thus, our paper challenges the classical neo-varelian approach opposing open thermodynamic flows and closed functional structures. The problem for us is not solved by the distinction between physical flows and biological constraints, since we need to understand how biological constraints disappear or propagate during development, aging and evolution.

Towards a theory of organisms

Soto Ana, Sonnenschein Carlos & Montevil Mael, Tufts University School of Medicine, USA
Longo Giuseppe, Ecole Normale Supérieure, France

The theory of evolution has provided an increasingly adequate explanation of phylogeny. However, biologists have yet to generate a theory of organisms that would encompass ontogeny and life cycles, and thus phenomena on the time-scale from conception to death.

We propose that theoretical extensions of physics are required in order to grasp the living state of matter that will help to describe the proper biological observables, i.e. the phenotypes. Biological entities must also follow the underlying principles that we use to understand the inert matter. However, these physical laws and principles may not suffice to make the biological dynamics intelligible at the phenotypic level. Like Galileo, who proposed a principle of inertia as default state in mechanics, we have proposed two aspects of the default state in biology, and a framing principle, namely: i) Default state: cell *proliferation* with variation as a constitutive property of the living. Variation is generated by the mere fact that cell division generates two overall similar, but not identical cells. ii) Default state: *motility*, which encompasses cell and organismic movements as well as movement within cells. iii) Framing principle: life phenomena are never identical iterations of a morphogenetic process. Organisms are the consequence of the inherent variability generated by proliferation, motility and auto-organization which operate within the framing principle. From these basic premises, we will elaborate on the generation of robustness, the structure of determination, and the identification of biological proper observables.

The Darwinian input into development and carcinogenesis. On the default state of cells
Sonnenschein Carlos & Soto Ana, Tufts University, USA & Centre Cavaillès, France

Experimental biologists have rendered lip service to the role that evolutionary theory plays in development and in carcinogenesis. Following results of our experimental approach in the context of evolutionary theory, we have concluded that *proliferation* and *motility* are the default state of *all* cells. Here, we will only address the subject of the nature of the default state of cells regarding *proliferation*. The prevalent adopted premise is that *quiescence* is the default state of cells in metazoa. From an evolutionary perspective, multicellular organisms necessarily evolved from unicellular ones. Since all cell cycle components characterized so far from yeast to humans have shown to be highly conserved it becomes counterintuitive to postulate that the default state of *proliferation* inherent to unicellular organisms would have switched to *quiescence* in multicellular ones. This basic misunderstanding has generated significant epistemological conflicts when interpreting data on development and carcinogenesis where the control of cell proliferation plays a prominent role. Finally, the controversies over this subject are due to the adoption, over a century ago, of mistaken premises by those working in the field of experimental biology, and more specifically, in tissue culture. Dobzhansky's 1973 aphorism "Nothing in biology makes sense except in the light of evolution" is yet to be fully acknowledged by biologists at large.

Three Historical Studies on the Place of Microscopic Images (submitted papers)

The soft entrance of photography into the serious world of science at the Naples Station
Groeben Christiane, Stazione Zoologica Anton Dohrn, Italy

The Naples Station was built as a laboratory for marine biology, open to the international scientific community. This facility had two inbuilt structures that needed a different kind of care and attention than the one requested by the laboratory. The first structure, though planned by Dohrn, was the public Aquarium which was supposed to make the money the scientists needed for their research. The second one, almost imposed on Dohrn, were the wall paintings in the room he had set apart for music. In order to attract visitors, the Aquarium needed publicity which was achieved through print media. The Fresco room, on the contrary, had to fight for its visibility because Dohrn hesitated to disturb the privacy of his guest investigators.

In this paper the use of images to achieve public recognition for the three facilities (research, fresco room, aquarium) will be investigated. Since the early 1880s, preference was given to coloured and black and white illustrations of the inhabitants of the aquarium, whereas photographs were used for artefacts and tameable nature, including people. As an outreach, Dohrn used photographs to document the scientific activity of the Naples Station, the buildings, the labs and the equipment. They were intended as diplomatic tools to document his achievements for his patrons in public and political life. At the same time, there also was an increasing input of pictures taken by professional photographers, scientists and collaborators that slowly added to the pictorial history of the Naples Station.

Usage of photography by the biologist Wilhelm Giesbrecht – scientific instrument or documentation Device?
Steiner Katharina, Universität Zürich, Switzerland

Arriving in Naples in 1881, the German zoologist Wilhelm Giesbrecht first worked as a guest researcher at the Stazione Zoologica before becoming a permanent assistant there. Until now Giesbrecht has been best known for his fundamental research on the taxonomy of copepods. Both in exploring methods of microscopy and inventing fishing devices, he demonstrated remarkable innovation; his scientific drawings remain of crucial importance in today's research. In addition to this scientific heritage, Giesbrecht has left us with six photographic albums. We might expect these to be mainly visualizing photos taken within the context of the Zoological Station. But examining this collection -consisting of 1800 visual documents- the biologist reveals as a portraitist of Neapolitan life rather than as a biologist using the camera as a research instrument. In light of both Giesbrecht's scientific work and the optical and photographic methods used by biologists at that time, the question emerges of why Giesbrecht did not use photography as an instrument in his research: what role, if any, did the Station's research environment play here, and were there ideological or empirical factors? Focusing on a group of photographs taken in the Station's context, I will argue that Giesbrecht's use of photography nevertheless involved documentation of specific steps in his research. My broader aim is thus to discuss, with the help of visual examples, the role and nature of scientific photography in contrast to scientific drawings, and to outline the main core of the discourse prevalent at the Stazione in this period.

Disposition and Morphology: Imagen and classification in 18th century.

Valverde Pérez Nuria, Universidad Autónoma Metropolitana, Mexico

At the half of the 18th century the microscopic world almost disappears from the scientific field.

The difficulties in attaining both clear images and higher magnifying power challenged most of the actual observations of the 17th microscopists. A lack of a theoretical frame were microorganims could be teleologically (and theologically) explained also quickened a disengagement from microscopic research, although it remained a main tool in botany and natural history. Even if social curiosity maintained it as entertainment, it was going to be hard to found any novelty in the microscopic image, and even new microscopic images (except one: the projection microscopical layouts). The microscope seems to have reached the top of its power.

Instead, new technologies as wax models emerged to replace pictures in the teaching of medical practice. What was stressed was the ability of putting apart the body by selecting functional blocks. Although the reconstruction of the body was still important, suppression of movement makes impossible to retain functional integrity. However, it was movement what had led the fragmentation process. From Galvani to Bichat, the connection between inner and outer spaces was relocated: the outside does not refer to the external appearance of the body but to environment. Specific inputs affect similar inner surfaces: there must be then an interface that could connect both. Bichat's answer to the question seems to us very familiar: *Dans la vie animale, le premier ordre s'établit de l'extérieur du corps vers le cerveau, et le second, de cet organe vers ceux de la locomotion et de la voix*. Differences in connections would be the basis in the distinction between organic and animal life, between passive growing and locomotion.

But Bichat also makes a difference between movement and time, and embedded the last in the former by using the balance as heuristic model. *La vie*, he says, *est l'ensemble des* fonctions qui résistent à la mort [...] *tout ce qui les entoure* [to the living beings] *tend à les détruire* (Reflexions physiologiques sur la vie et la mort, 1800).Growing and aging can be understood as a changing proportion of opposite forces, that is, as disequilibrium. [As Bichat well knows, there was not need for a microscopical approach (Lacaba)]

What is the model that arises from this picture? Bichat retains two typical features of the Enlightenment: equilibrium (hence, balances) as basis of physical and economic dynamics and affinity and sympathetic attraction. But at least one thing has changed in the way the information is supposed to be retrieved from the body: the need to interpret histological reaction as a measure of aggression displaced body integrity to the outside. A new target for social policies and communal definition was born: safe environment.

The aim of this paper is to explore what were the main traits of the notion of system and environment that arise from Bichat's notion of tissue; and how and why this notion was challenged by the explaining potential of images related to the cell theory. Our main hypothesis is that diagrams and visual approaches to complex systems found a more suitable and modular language in cell theory, and that this approach was also more akin to a moral individualistic approach in vogue. However, notions of time, size and range -as well as environment and emergence/ plasticity- were also key in developing an alternative view of tissular reaction and intersystemic connections.

Topics in the Philosophy of Behavioural Biology

Simple learning systems and evolvability: Why culture isn't all that matters

Brown Rachael, Austalian National University, Australia

Traditional accounts of the role of learning in evolution have concentrated upon its capacity as a source of fitness to individuals. Research supporting its role as a non-genetic inheritance stream and genetic accommodation challenges the narrowness of this account by suggesting that social learning is both a source of fitness to individuals and a source of evolvability to populations. Unfortunately, although the evidence offered for this broader account is persuasive, there is widespread skepticism of it within mainstream evolutionary biology. Here, I use a case study from invasive species biology -the role of conditioned taste aversion in mitigating the impact of cane toads on the native species of Northern Australia- to demonstrate that, even should this skepticism be ultimately vindicated, there is still good reason to think that learning (whether social or not) provides a source of evolvability to populations. In doing this, I provide a broader account of the role of learning in evolution that is more palatable to the mainstream evolutionary biologist.

The role of psychological vs. behavioral approaches to studying the evolution of cognition

Driscoll Catherine, North Carolina State University, USA

The promise of evolutionary psychology is its being a means to identify and explain the origins of the *computational features* of psychological mechanisms and not merely behavioral dispositions or strategies (as in behavioral ecology). However, independent psychological and behavioral approaches to the evolution of cognition work face difficulties, including that psychological mechanisms cannot be straightforwardly predicted from the EEA, and that behavioral dispositions/strategies need not be adaptations in their own right.

The solution I suggest is to start such work at the behavioral level, and use that work as the basis for discoveries at the psychological level. This requires scientists to identify those behavioral strategies which require traditional adaptationist, cultural evolutionary or individual learning approaches. For various reasons, this choice must be "bootstrapped" during the course of work on those strategies, starting by using some initial clues to make a best guess at the appropriate approach. Should genuine behavioral adaptations be discovered, these can suggest evolutionarily and developmentally independent "chunks" of the mind responsible for them, and partial *computational descriptions* for those "chunks", the first step in describing a psychological mechanism. The evolutionary history of the behavioral adaptation is also *part* of the evolutionary history of the responsible mechanism(s). Socially and individually learnt strategies can help scientists identify the processes (and hence learning mechanisms) that acquired them; the nature of those processes can then help determine how those mechanisms came to evolve. Some important work would still remain, however, to fully describe psychological mechanisms and their evolutionary history.

Can Altruism be Unified?

Ramsey Grant, University of Notre Dame, USA

There is clearly a plurality of altruism concepts. Classically, biological altruism is distinguished from psychological altruism. Recent discussions of altruism have attempted to distinguish even more concepts of altruism. The question I am concerned with here is what the connection is between these concepts. In particular, is it best to consider 'altruism' to be polysemic, and that one should merely treat the various meanings as different in kind and focus on avoiding conflation? Or is there a way to place all of the concepts into a common framework -an altruism space- that could lead to new questions about how this space can be filled?

Towards Epistemologies of Biological Practice

The Ethos of Organism-Based Communities

Leonelli Sabina, University of Exeter, UK
Ankeny Rachel, University of Adelaide, Australia

This paper explores the social dimensions of the epistemology of scientific practices, and particularly the norms and commitments that affect the choices and intellectual directions of researchers working with model organisms. Much of the historical, philosophical and sociological scholarship on model organisms has stressed the importance of social ties between members of specific 'model organism communities'. We go one step further by arguing that organism-based communities such as the ones centered around *Arabidopsis, C. elegans* and *Drosophila* have developed a unique ethos -an ensemble of norms and values that includes a strong emphasis on strategic collaboration and the sharing of resources. This ethos is expressed and enforced through specific institutional mechanisms (such as steering committees and infrastructures); and strongly affects both the research directions pursued by these communities and the types of results, materials and methods favoured by the scientists involved. We conclude that a study of the epistemology of research practices in experimental biology needs to include references to the ethos of organism- based communities, which continue to play an important role as reference points for cross-species analyses (particularly when involving genomic data).

Why and How Biological Practice Matters to a Philosophical Analysis of Epistemic Reduction

Kaiser Marie I., University of Geneva, Switzerland

In contemporary philosophy of biology most authors agree that a philosophical analysis of biology must take seriously actual biological practice. However, it remains unclear which *role* empirical information about biological practice should play in a philosophical analysis and which *kind* of empirical information should be considered as particularly relevant. In this talk I draw on the debate about epistemic reduction in biology to explore these methodological issues. I argue that, on the one hand, an analysis of the concept of epistemic reduction must be based on a careful study of actual cases of reductive explanations, of biology's reductive investigative practices, and of the discussions about the "limits of reductionism" that take place in biology itself (most notably, in cancer research and in systems biology). On the other hand, developing a philosophical account should amount to a *critical reconstruction* of biological practice, and thus should involve normative assumptions as well. I illustrate this claim by revealing three respects in which my own approach to analyzing epistemic reduction in biology transcends a mere description of biological practice: first, it is based on a choice of *paradigmatic and important examples* of reductive explanations; second, it *makes explicit* assumptions that are only implicitly present in biological practice; and finally, in order to establish *coherence* it rejects some of the conflicting claims of scientists as too vague or incorrect.

From Conceptual Analysis to the Analysis of Conceptual Practice

Waters C. Kenneth, University of Minnesota, USA

Traditional approaches in philosophy of biology focus attention on biological concepts and theories, evidential support, and inter-theoretical relations. Newer approaches shift attention from theories to theorizing, from concepts to conceptual practices, and from theoretical reduction to reductive retooling. They point towards broadening the scope of philosophical attention to investigation, and hence towards analyzing how the integration of practical know-how, concrete knowledge, investigative strategies and theoretical knowledge provide the basis for systematic investigation of the biological world. In this presentation, I will illustrate the shift from theoryfocused to practice-centered epistemology by presenting an analysis of conceptual practice in contemporary genetics. I will show that geneticists have a flexible concept of the gene that can partition a DNA molecule in a multiplicity of ways. Shifting philosophical attention to conceptual practice in genetics reveals how biologists succeed in identifying and manipulating causal strands within systems of bewildering complexity.

The interplay of model building and science policy: the case of lock-and-key in 20th century biochemistry

Mertens Rebecca, University of Bielefeld, Germany

My talk will examine the interplay of model building and science policy in order to capture the role of models in the institutionalization of political agendas within science. I will claim that understanding the processes of model building and usage is crucial for understanding how science policy affects knowledge generation processes and vice versa. This claim will be advanced by examining the history of the lock-and-key model in the mid 20th century. Biologists' use of the lock-and-key model offers a revealing case study for examining the relation of epistemic and social values. As I will show, application of the lock-and-key model was largely restricted to synthetic programs in biochemistry and was related to agendas that highlighted what chemical synthesis could do for biology, medicine and social welfare. The lock-and-key model reached its political potential in the 1940s and 50s due to the impact of the molecular biology program and its institutionalization by the major American philanthropic organizations (such as, e.g., the Rockefeller Foundation). I will conclude that we should start thinking about models, not just as instruments for investigation and explanation, but also as instruments for the implementation of political agendas within science.

Towards a motricity approach in cognitive science

Differences between identity and self-consciousness from a motricity approach

Gastelum Vargas Melina & Argüelles San Millán Juan Manuel, Universidad Nacional Autónoma de México, Mexico

With respect to brain evolution there exist theories that exalt metabolic solutions or cognitive capacities. The formers suggest that the brain size that made possible our cognition is bound to evolutive strategies that rescued synapsis effectivity and established the structural order of the nervous system by means of the settlement of adaptations that allow functional efficacy. On the other hand there are theories that establish a causal order in the size of the group and the increase of complexity in the nervous system; these last sustain that our species cognitive audacities underlie the growing complexity of the gregarious order and therefore they are linked to social efficacy movement. Both approaches are inserted in a paradigm that suggests that the brain evolved as a consciousness system that makes predictions as a univocal way to establish an efficient movement. They are theories that are subscribed in the idea that mind has evolved as an essentially motor organ.

The capacity of having identity is then framed in a cognitive approach that is supposed as an efficient movement necessity in a niche that has a gregarious growing complexity.

A standpoint that has had huge acceptance supposes that identity and self-consciousness are at the least similar; the argument rests in the idea that the conclusion of being an individual joined to the autobiography that is given to us by memory supposes the identity phenomenon. In this work we will sustain that identity is a capacity that is not necessarily conscious and that it comes from recognition that a group attributes to an individual, and that entity "knows" who he is without more necessity than to understand the here and now. In other words we will sustain that at least individuals classified in the *pongidae* group recognize their place in terms of social hierarchies in a group and that does not imply that they can project their social opportunities from their biography inserted in what their community does. Going a little further, they can recognize their influences, powers and limitations from other's behaviour with independence to the formation of a concept of themselves.

Autonomous movement: the beginning of mental life from an embodied and ecological approach.

González-Grandón Ximena & Vergara Ortega Jimena, National Autonomous University of Mexico, Mexico

There is a tough tendency in recent embodied proposals to rely on neural correlations, such as so-called mirror neuron when explaining social learning, theory of mind or the generation of consciousness through evolution. Unfortunately, such explanations are grounded in the bottom-up perspectives and do not address the need to see the motor interaction as a structured and structuring process. These explanations remain within the problem of (1) how a detached subject is trying to apprehend the other and (2) if it is shaped by motor coordination dynamics. So, they are just transferring their cause to a neural correlation and simply re-describing the problem. We want to make a proposal grounded in a historical explanation and an embodied and ecological approach, about the experience of self-movement ‘kinaesthesia’ as central to mental animate life. In humans and non-human primates, as autonomous organisms, kinaesthesia and tactility are the first sensorimotor systems to develop. So, in the beginning, movement is not a pre-given program of capacities, but something that they actively learn by moving themselves discovering the possibilities of action of their bodies and correlative spatio-temporal dynamics in every percepto-motor process, within their particular social community (Sheets-Johnstone, 2011). We will sustain that we can get a more coherent explanation of the origin of mental life, if we consider: (1) autonomous agents constantly learning how to move (to walk, to grasp), challenging a kinaesthetically felt coordination dynamics in present time and (2) making sense of their physical and social surroundings.

The unification of the mind: a hypothesis

Padua-Gabriel Jose, University of Mexico, Mexico

Traditionally, cognitive activity has been studied as an isolated entity: consciousness, perception, mental image, memory, representation or emotion; just to mention some, and they all seem as autonomous expressions, without considering that each one of them manifests and its experienced in different ways if a subject is awake or asleep, stressed or under the effect of meditation or hypnosis, all of these related to a particular motor state.

This work proposes the definition of mental states as specific contexts that allow studying the differences in cognitive activity under each one of them. Those states are compound by physical parameters that are correlated in a situation: if a person's cardiac rhythm descends by the effects of meditation, it will do so in a conjunctively with his/her metabolic and respiratory rhythm and their cerebral behaviour. This compound variation, situated in a precise circumstance will give place to a type of consciousness, perception, memory and other specific activity. In this way all the characteristics that are present in cognition are determined by a mental state.

This work also refers to consciousness states. Consciousness as a cognitive activity should not be confused with a consciousness state: the former can be defined as the awareness in a situation while a consciousness state is the possibility in type and form of itself.

Finally, we have the construction of psychological states. These are the form of experience, its quality and representation.

This triad; mental, consciousness and psychological states relate and feed back to each other giving rise to mental principles.

Transhumanism (submitted papers)

Reimagining the Guiding Forces of Synthetic Biology: The Ethical Preoccupation of Transhumanism

Adams Laura, Florida State University, USA

"Humanity stands to be profoundly affected by science and technology in the future. We envision the possibility of broadening human potential by overcoming aging, cognitive shortcomings, involuntary suffering, and our confinement to planet Earth."

So begins the 2009 "Transhumanist Declaration", a document outlining the values and goals of those who identify themselves as transhumanists. This paper evaluates transhumanism where it intersects with the idea that technological advancement is inextricably entwined with social structure. With advances in synthetic biology and biotechnology come looming ethical and security challenges. While the wave of transhumanist literature that has been emerging in recent years seeks to abate these concerns with ethical arguments for human modification, the influence of social, economic, and political systems on the propagation and dissemination of technology are treated largely in a prescriptive way. This paper argues that these kinds of discussions would be more fruitful if reframed to consider the constraints placed on technology by social systems rather than by ethical considerations. For example, it may be more productive to discuss how political systems and social structures create and perpetuate security risks such as open-source biotechnology and "DIY biology" rather than the ethical role of government in regulating these enterprises. This paper argues that we should stop looking so much at what ethics we can impose on biotechnology, and start looking at what role our social systems play in creating the ethical dilemmas in the first place.

Bioethical issues on genetic enhancement: between conservatism and transhumanism

Perbal Laurence, Université Libre de Bruxelles, Belgium

Genetic enhancement refers to the use of genetic engineering to modify a person's nonpathological human traits; mostly physical and mental abilities. France has addressed these ethical issues in 2010 with a preparatory report to the revision of the bioethics laws. It made two recommendations (No. 79 and No. 80): the development of a public debate and a monitoring mission. The social and metaphysical issues are important indeed: which society and which humanity do we want? These are questions we propose to analyze in the light of secular and postmetaphysical values. In a secular world, there is no more sacred human "nature" and human beings must choose their own values, references and limits. Should we adhere to conservatives' caution? Or refuse any limitation to technoscience and adhering to the transhumanist precepts? If not, what are the ethical principles - in accordance with secular and postmetaphysical values - that can guide us in a society more and more technoscientific? The challenge is big but its ethical urgency is undeniable.

Transnational Science During the Cold War A

Practices of circulation: radioisotopes and cytology in the atomic age

Santesmases María, Centro de Ciencias Humanas y Sociales, Spain

Invented and manufactured elsewhere – in the U.S. – radioisotopes travelled in the immediate post-WWII better as knowledge than as practice: it was easier to know about their physicalchemistry than to test their effects on living matter. The effect of radioactivity, that of the bombs dropped on Hiroshima and Nagasaki, was indeed well-known. In the early days of their circulation, from 1948 on, a long journey was needed to get a sample of one of them. The journey was physical and political; it concerned transportation of a sample and diplomacy. As a product obtained under military security measures during WWII, its travels were not permitted - not because of its radiance, but for security reasons, as Angela Creager has shown. Social and biological knowledge travelled attached to every parcel containing a radioisotope in a small and carefully packed bottle, whose genealogy in Spain was the powerful tool that experimental research had become for a culture of learning based on travel. In the parcel within travelled the culture of the atomic age that was putting the basis for medical, human genetics.

This presentation will put travel at the core of a reflection on the circulation of a set of knowledge and practices in biology and medicine during the atomic age in which Spanish research settings participated.

A New Look at Radioisotopes: Eisenhower's Atoms for Peace and Its Consequences for Science and Medicine

Creager Angela, Princeton University Department of History, USA
Krige John, Institute of Technology, Atlanta, USA

What does research with radioisotopes teach us about the relationship between science and the cold war? Did state patronage corrupt the freedom of scientific inquiry? Did security interests subvert the circulation of knowledge? Did 'big science' dominate research practices? Did USSoviet rivalry shape the context in which research was done and knowledge shared? Was the 'peaceful atom' nothing but a vehicle for American hegemony? This paper will chart the trajectory of the use of radioisotopes in medicine, agriculture and biology from the late 1940s to the Atoms for Peace conference in Geneva in August 1955. It will use radioisotopes to trace the practices of cold war science that were made possible by the production and circulation of a particular research tool in the first decade after WWII. Our longitudinal study of the broad distribution and disparate uses of radioisotopes complicates the usual picture that the cold war impacted science by simply militarizing it. We will use radioisotopes to argue for a more nuanced picture of the interplay of knowledge, technology, and international relations in the atomic era.

Transnational Science During the Cold War B

Alfonso León de Garay and the set up of the Genetics and Radiobiology Program in Mexico, 1960-1970.

Barahona Ana, National Autonomous University of Mexico, Mexico

After spending two years at Galton Laboratory in London under the supervision of Lionel Penrose, Alfonso León de Garay founded the Genetics and Radiobiology Program (GRP) in 1960 within the National Commission of Nuclear Energy (CNEN) which has been founded in 1956. The Program rapidly became a disciplinary program, for it embraced research, teaching, and training of academics and technicians in radiobiology and genetics. The Program with its laboratories started in 1960, located in an apartment building in México City. At the beginning it consisted of a small staff composed of six researchers, including de Garay as director, Rodolfo Félix Estrada as chief of the *Drosophila* section, and 4 investigators who had all obtained their B.A. degrees in Biology in 1960. There was also a technician, a secretary, and a service assistant. By 1960 de Garay obtained 22 *Drosophila* mutants that were used to know the mutational effects of radiation sources with tracing isotopes. To obtain these mutants, and as part of the personnel training, there were organized annual course works about radioisotopes and nuclear instrumentation. Those course works were compulsory for the personnel who work in the Program. By 1962 de Garay and collaborators obtained 57 *Drosophila* mutants that were used for research and educational purposes. In this paper I will talk about the creation of the CNEN and the institutional need of creating a program to study the effects of radiation in human populations in Mexico. De Garay's role in the development and establishment of radiobiology and human genetics in Mexico was fundamental.

Cold War Collaboration and the 'American Challenge': The European Society for Nuclear Methods in Agriculture

Zachmann Karin, Munich Center for the History of Science and Technology, Germany

In 1969, physicists, biologists, agricultural experts and engineers established a political crossblock European Society for Nuclear Methods in Agriculture (ESNA) that claimed to both improve the world food situation and to limit environmental pollution. In order to achieve this goal, a new transdisciplinary research field was to be created that was named "nuclear agriculture", by analogy to the highly prestigious nuclear medicine. Nuclear research in agriculture and food grew into an area of cross-bloc collaboration and interaction. Here scientists broke open the politically fortified boundaries of the Cold War world and contributed actively to an emerging policy of détente. Whereas Eisenhower's Atoms-for-Peace initiative emerged in the spirit of containment and promoted collaboration with an impetus of American control, the scientists who participated in ESNA strove for European integration in the area of science in order to mobilize more resources and to enhance their own positions in their particular national contexts. By envisioning ESNA as a means to improve European performance in science and technology, the society's initiators connected ESNA's founding to the on-going West European discourse on the growing technological gap between the US and Western Europe. Thus, ESNA was to become part of the European response to the American challenge in science and engineering. This paper sets out to explore, how did this society transform Eisenhower's vision of the peaceful atom and what position did ESNA acquire within the Cold War world.

Human population studies and the World Health Organization

De Chadarevian Soraya, University of California Los Angeles, USA

In the postwar era international organizations like the WHO and UNESCO embraced science and medicine as prime vehicles to foster international cooperation. The paper will analyze how scientists used the opportunities offered by the WHO, who profited and how. It will look at some of the projects that were promoted, the tools that were created and their long-time legacies, especially in the fields of radiation biology, human genetics and human population studies.

Understanding Disease (submitted papers)

Clarifying Health and Disease in Darwinian Medicine via Phenotypic Flexibility and Robustness

Sholl Jonathan, KU Leuven, Belgium

While the recent marriage of evolutionary theory and medicine has greatly helped to explain the problem of ‘why we get sick’, Darwinian medicine's stress on adaptationism and the EEA has hindered attempts to develop a coherent account of health and disease. While research into the developmental origins of diseases and mismatch theory provide more detailed accounts of disease etiology, Darwinian medicine still struggles to incorporate individual-level adaptations to changing environments, thereby reducing health to the mere absence of disease, and disease to a disadvantageous deviation from (past) species norms. This paper will suggest that the phenomena of within-individual phenotypic plasticity (phenotypic flexibility) and biological robustness could be harnessed to better define these concepts. Furthermore, some insights by the philosopher of biomedicine, Georges Canguilhem, regarding historical norms, individuality and the impossibility to clearly separate organism and environment when defining health and disease, will be used to problematize appeals to past environments to explain current pathological states. Taken together, these insights will contribute to defining health as an individual-level capacity to tolerate environmental perturbations (robustness) and the ability to establish new norms in the face of varying environmental demands (flexibility). Conversely, disease is not merely a deviation from (past) species norms, but the presence of a new norm entailing a constrained flexibility and weakened robustness within the current environment. While Darwinian medicine's appeal to past environments can help explaining species-level vulnerability, some epistemological obstacles can be overcome by incorporating individual-level adaptations to changing environments into the definitions of health and disease.

Biology, Health and Medical Practice

Krueger James, University of Redlands, USA

Theoretical accounts of disease generally attempt to ground the concept in the relevant underlying biological facts. Discussions of such accounts have largely focused on whether they successfully identify necessary and sufficient conditions for a state to count as pathological. Correctly accounting for examples of pathology, however, is not the only basis for evaluating an understanding of disease. Here, I argue that we should expect any understanding of health and disease to be consistent with important aspects of medical practice. Specifically, any such understanding should be consistent with the ways that we attempt to treat, cure, and prevent disease. What we do when we treat, for example, must be intelligible in terms of reducing or eliminating pathology and promoting health. If it is not, it is hard to understand what it is that an account of health and disease provides for us. Such an account runs the risk of become an empty abstraction of little relevance to what medicine is or does. In making this case, I argue that the theoretical account of health offered by Christopher Boorse should be rejected because of its failings in this regard. This conclusion highlights the need for a more nuanced understanding of the relationship between biology and the biomedical sciences than what is implied by such understandings of disease.

Biological normativity, clinical normalcy and the theoretical definitions of health and disease

Saborido Cristian, Universidad Nacional de Educación a Distancia, Spain
González-Moreno María, CEU, Spain
Hernández Juan, Universidad Autonoma de Madrid, Spain

We develop a systemic-organizational account of the notion of biological normativity and present the implications of this theoretical model for the medical practice. Sharing with authors as Canguilhem the rejection of the bio-statistical notion of clinical normalcy, we try to ground the theoretical notion of biological normativity considering it as an inherent feature of biological systems. In the first part, we present a critical survey of the understanding of this specific normative dimension from the main approaches in the contemporary philosophical debate on natural norms. In the second part, we develop a different account, based on the adaptive mechanisms of organisms, that avoids the limitations of the other stances and allows us to explain biological mal-functionality in terms of current organization. In our account, the organizational closure -i.e. the web of mutual constraining actions of the material structures on their boundary conditions that collectively self-maintain the whole organization of the system- provides a naturalized grounding of the concept of normative function from a systemic framework. Organizational closure constitutes the causal regime in which biological functions (or malfunctions) appear and can be identified. In the third part, we consider some significant medical examples showing how our approach is able to avoid the counterexamples and limitations of the predominant approaches in philosophy of medicine, such as Boorse's bio-statistical account. We claim that our approach provides the theoretical resources for a naturalization of the notion of biological normativity with relevant implications for a different naturalist conception of notions of health and disease.

Understanding variation beyond the Modern Synthesis

Mutational Lamarckism and the Modern Synthesis view of mutational randomness as conditional independence

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Vecchi Davide, Universidad de Santiago, Chili

Current evolutionary biology is based on the legacy of the modern evolutionary synthesis (Huxley 1942). Nevertheless, the Modern Synthesis enshrined natural selection as the director of adaptive evolution not by providing evidence that it did, or could, account for observed adaptations (Leigh 1999), but rather by eliminating competing explanations (Mayr 1993). One of the eliminated competitors was Lamarckism, particularly "mutational Lamarckism", a hypothesis according to which mutations may be directed towards producing phenotypes that improve the performance of the organism in a particular environment. Contrary to this hypothesis, the Modern Synthesis' view claims that mutations are "random" (Lenski and Mittler 1993, Merlin 2010). Possibly because Lamarckism had largely felt into disrepute several decades before the eventual success of the Modern Synthesis, the precise meaning of the term "random mutation" was never deeply analyzed. However, current evidence of possibly legitimate cases of Lamarckism (Jablonka and Lamb 2005, Koonin and Wolf 2009) has revitalized the interest for clarifying the meaning of the term "random" in this context (Sarkar 2007, Jablonka and Lamb 2005, Millstein 1997, Merlin 2010). In this contribution we aim to analyze previous definitions of random mutations based on the concepts of statistical independence and correlation (e.g., Millstein 1997, Sarkar 2005, Jablonka and Lamb, Merlin 2010) and to show that they are deficient. We argue that the term " random mutation" refers to a triadic rather than dyadic relationship, that neither correlation nor independence are good concepts to formalize the neo-Darwinian concept of genetic randomness, and that as a consequence neither of them is suitable to define mutational Lamarckism. Our alternative proposal is that the best probabilistic concept to define random mutations isconditional independence. In this contribution we will illustrate our alternative proposal, show a way to formalize the concept of mutational randomness and provide some examples of its application.

Phenotypic variation in ecological setting: a challenge for evolutionary modeling beyond the Modern Synthesis

Emanuele Serrelli, University of Lisbon, Portugal & University of Milano Bicocca, Italy

Organisms are niche constructors: they impact the environment and modify selective pressures that direct their own evolution as well as that of their non-conspecific fellows in ecological systems at various scales. The theoretical acknowledgement of niche construction has inspired many reflections about the active role of organisms in evolution, often proclaiming a revolutionary theoretical change. But if we look at formal models the claim is not yet justified. Ecologists have specified population-scale models of niche construction, but these cannot be adopted as evolutionary models: they don't incorporate heritable variation nor allow for directional selection and cumulative change. As evolutionists point out, these models are mere phenotype dynamics or population fluctuations with different possible outcomes -extinction or sustainability. Evolutionary models of niche construction, on the other hand, are not so revolutionary in their foundations, often being just classical population genetics provided with feedback loops between loci and selective pressures acting on them. The idea that variation among organisms boils down to genetic differences captured by gene frequencies dates back to the heart of the Modern Synthesis. But niche construction points directly to the world of physical and chemical interactions. This is the world where resource-impacting phenotypes are built through developmental processes, in turn subject and sensitive to the surrounding environment and the resources left over by previous generations. The produced phenotypes and their effects are hardly summarized by gene frequencies, yet evolutionary models need some kind of heritable variation and selection. The future challenge of evolutionary modeling beyond the Modern Synthesis is thus ecological, plastic variation that allows for inheritance with varying degrees and not-always allelic mechanisms.

Variation in a world with multiple levels, mechanisms, and units of evolution: The Applied Evolutionary. Epistemology Approach

Gontier Nathalie, University of Lisbon, Portugal

Scholars working within the units and levels of selection debate have been developing more and more refined heuristics of how evolution by means of natural selection works. A motivation of such endeavor has been the question whether individual organisms are the only, or the most appropriate, units of natural selection, or whether groups, traits, a (set of) genes or behaviors, developmental systems, population, species can also be considered as units of selection. Heuristics based on natural selection have also been applied in order to assess whether evolution by natural selection can occur within phenomena that are traditionally understood to be extrabiological, such as cultural units, artifacts, neural maps, cognitive traits, altruistic rules etc. This abstraction and extension of natural selection to the sociocultural domain, provides a unified scientific methodology that enables scholars to study the evolution of life as well as the evolution of cognition, science, culture and any other phenomenon displayed by living organisms by means of natural selection theory. Today, with the several pleas there exist to extend the Modern Synthesis, evolutionary biologists are acknowledging the importance of mechanisms such as lateral gene transfer, symbiogenesis, drift, etc. Applied Evolutionary epistemology is a methodology that provides more open heuristics to assess how these mechanisms associated with an extended synthesis work, what their units and levels, and where they are active. Associated with this endavour is not only the recognition of multiple units, levels and mechanisms of evolution, but also to acknowledgement that there are different kinds of evolution (the evolution of the brain, of languages, of culture, of niches, etc). This talk takes the debate a step further, asking how important inter-unit, inter-level and inter-mechanism variation is for a general understanding of evolution.

What is a gene? The gene concept faced to recent advances in genetics, molecular and developmental biology

Chromosome structure as a component of gene definition

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Alongside gene regulation mechanisms at the sequence level, several sources of variations in chromatin and chromosome structure impact gene expression, and show some cell-to-cell heritability. Therefore these are termed “epigenetic” mechanisms. Among them, the tridimensional folding of chromatin in eukaryotic cells during interphase, organised in semistable 'chromosome territories' seems to fit both requirements.

First, the spatial relative positions of such territories can undergo selective pressures, being partially but significantly inherited from mother- to daughter-cells, and between generations in multicellular organisms: these relative positions, yet probabilistic, even show a species-specific component.

Second, the nuclear location of a gene modulates its expression level: caeteris paribus, genes on central or peripheral chromosome territories will have differential probabilities of expression, and so for genes at the center v/s the periphery of a given territory. This advocates for the fact that natural selection operates not only at the sequence 'text' level, but also on the global architectures of genomes (the 'syntax'), e.g. in differentiating gene-poor from gene-dense regions in relation with their location, and in taking advantage of the probabilistic distance between sequences in a 3D space. Furthermore, this reminds that DNA is not only information but first of all matter, also selected for its own trade-off between its physical properties and constraints.

This could pave the way for a renewed consideration of biophysical sciences in evolutionary studies. A modern definition of a gene as a functional and heritable unit should take these structural dimensions into account.

What is a gene? The present crisis of the molecular concept of the gene

Deutsch Jean, Université Pierre et Marie Curie, France

The molecular concept of the gene, defined during the 1960s as a continuous segment of coding DNA has been faced to several drawbacks: the discovery of introns and the use of alternative promoters, the amount of non-coding regulatory signals, small and large regulatory non-coding RNAs, and last but not least, cell- and generation-transmitted epigenetics. The transmitted genetic signal, i.e. the gene, can take several forms, digital coding and analogical non-coding, the form of DNA and of RNA, and of the chromatin structure as well. To be turned into genetic information, the gene has to be interpreted, which needs the whole cell machinery. In addition, the various genetic messages, under their various forms, so-called genes, have to be interpreted in a correct sequence in time and space in the living organism, that is a correct genomic syntax.

Hox genes’ colinearity during Limb Development

Galperin Charles, IHPST & Université Paris 1 Panthéon-Sorbonne, France

The vertebrate limb was for many years a model-system for the study of the developmental pattern. It was during the reign of experimental embryology (J.W. Saunders, 1948; L. Wolpert, J. Lewis, D. Summerbell, 1975). The genetic approach came some fifteen years later. The genes hox were "pattern formation genes". They included the homeobox, discovered in 1984, and were distributed in four clusters in the vertebrates, put in line with Antennapedia and bithorax complexes in Drosophila.

Ed. B. Lewis showed in1978 that the genes of the bithorax complex obeyed the rule of spatial colinearity. This rule states that "the hox genes were clustered along the chromosome colinear with their domain of action in the thorax and abdomen of the fly". In I989, TIME became the main parameter. The timing of expression of the hox genes depends on their position in the complex according to the following rule: 3' early; 5' late"(the directions of DNA).

What are the mechanisms underlying the temporal colinearity? A remarkable synthesis was proposed by Denis Duboule in 1994. But in 2003 the effect of a single "regulatory element over different genes spanning 250 Kb (250.000 bases of DNA)" was the first example of a regulatory domain. The concept of "regulatory landscape" was invented.

We propose to follow the main steps in the future of this concept, essentially in relation to the concept of gene.

The molecular gene concept in the post-genomic era
Théry Frédérique, IHPST & Université Paris 1 Panthéon-Sorbonne, France

Genome-wide analyses of transcriptomes have revealed that the vast majority of the eukaryotic genome is transcribed, mostly as non-coding RNAs. Besides, the extensive overlap of transcriptional units and regulatory elements reveals that genomic architecture is not linear, but highly interleaved. Altogether, the pervasive transcription and the complex genomic organization challenge the concept of the gene. Despite multiple attempts, biologists did not reach a consensus on a molecular definition of the gene. Neither did they clarify whether sequences transcribed in non-coding RNAs should be or not considered as genes. But, more importantly, post-genomic analyses urge to reconsider the status of the gene concept. If the gene concept is to survive the crisis it currently faces, it will have to depart from three historical commitments associated with the classical molecular gene. First, the post-genomic molecular gene concept will have to take into account the great structural diversity of functional genetic elements in eukaryotic genomes. Second, it will have to pay more attention to the long evolutionary history of these genomes, which has resulted in a highly complex genomic organization. Finally, the gene can no longer be the privileged level to characterize the relations between genotype and phenotype. Therefore, the post-genomic era prompts to reexamine the explanatory value of the gene concept. The gene may lose some of its theoretical power, but, instead, a richer and finer representation of the structural and functional properties of the genome will emerge.

What Is Genetic Information? (submitted papers)

Genetic information as a conceptual metaphor
Ishida Tomoko, Keio University, Japan

What is genetic information? Many biologists and philosophers have been trying to answer this question, presupposing at least tacitly that genetic "information" exists. However, is it plausible to use the term "information"? Isn't it just a metaphor without which we can also do quite well?
Many thought that the answer is obvious. For them, genetic information is a kind of genuine information, not a metaphor. Yet, the answer is not, in fact, obvious, because there are some differences between genetic information and everyday information. For example, information transmitted by newspaper has a sender, the publishing company. In contrast, it's quite unclear what is the sender of genetic information.
So, should we admit such incomplete information to be genuine information? It might seem that whether we permit to use the term "information" to describe DNA or not is just a matter of definition. If we adopt loose definition of "information", then genetic information is genuine information, if not, just a metaphor. However, it's not a productive way to discuss. So, I ask a different question, “what is the role of the concept of 'genetic information' in life science?”
In this paper, I'll suggest that the concept of "genetic information" functions as a conceptual metaphor. Then, I show that this idea will eliminate the problem "whether 'genetic information' is genuine information?"

Is Shannon's Information Theory Applicable to Genetic Data?
Tal Omri, London School of Economics, UK

Shannon famously remarked that a single concept of information could not satisfactorily account for the numerous possible applications of the general field of communication theory. I employ some basic principles from Shannon's work on information theory (Shannon 1948) to develop a measure of information for describing ‘population structure’ using genetic data. This sense of information is somewhat less abstract than *entropy* or *Kolmogorov Complexity* and is utility oriented. Specifically, given a collection of genotypes sampled from known multiple populations I would like to quantify the potential for correct classification of genotypes of unknown origin. Motivated by Shannon's axiomatic approach in deriving a unique information measure for communication, I first identify a set of intuitively justifiable criteria that any such quantitative information measure should satisfy. I will show that standard information-theoretic measures such as mutual information or relative entropy cannot satisfactorily account for this sense of information, necessitating a decision-theoretic approach. I will also review very recent empirical work of biologists to assess the 'population signal' from genetic samples.

Defending a mathematical sense of biological information

Lean Oliver, University of Bristol, UK

Teleosemantic accounts of biological information are often motivated by the belief that the mathematical account of information, developed by Claude Shannon, is inadequate for biological purposes. Typical reasons given include the theory's lack of reference to content or correctness, and the implied parity of informational status between all causal factors in a biological process. It is therefore concluded that a richer sense of information is required to make the kinds of distinctions often made by biologists when using informational language, such as assigning a privileged status to genes in development, or in explaining "incorrect" outcomes thereof. I argue that these assumptions are mistaken, and that Shannon information can and should be considered a biologically relevant property with explanatory value. The teleosemantic view seeks to explain biological information as a product of natural selection, and which therefore only exists given a certain selective history. However, in doing so they are really just describing a certain kind of informational *function*, not information itself. Once the distinction between "information" and " having an informational function" is recognized, it is seen that the property on which selection is acting to produce such functions is that of natural, correlational information. In short, a Shannon-based account of biological information can avoid parity, and preserve correctness, by reference to function rather than by incorporating function into the definition of information itself. This approach is more inclusive of legitimately informational processes in biology which nevertheless lack the requisite selective history for teleosemantic definitions.

The genome and the stored program concept

Planer Ronald, Rutgers University, USA

The extension of the concept of information to genes continues to generate controversy. A closely related debate in the philosophy of biology concerns the existence of a "genetic program". Among those who do embrace the idea that genes carry information, many would also say that the entire collection of an organism's genes can be properly described as containing a kind of program. More specifically, the idea is apparently that a genome realizes a program in something like the way a set of symbol strings in the memory of modern computer can realize a program.

In this paper, I argue that the program concept has a real, albeit partial, application to the structure of genomes, particularly those of higher organisms. My basic proposal is that, to the extent that an organisms' genome can be properly said to realize a program, it is in virtue of the fact that it contains two different types of information-carrying entities, namely, *instructions and data* symbols. The instructions are realized by genes coding for transcription factors recognized by regulatory regions of certain classes of genes. The data symbols are realized by genes that code for purely "structural" proteins (i.e., non-transcription factors).

In the remainder of the paper, I explore a deep and fascinating analogy between the stored program architecture of modern computers, and the functional architecture of genomes. I argue that this is likely an example of evolution and intelligent agents converging on the same optimal design.

Working in biology: how laboratory and field practices shape biological knowledge

The mouse multiple: Intersections of welfare practices and experimental practices in the animal neuroscience laboratory

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The regulation of animal work in the laboratory has undergone dramatic changes in the past fifty years. What impact, if any, has this growing ecology of animal welfare practices had on scientific work in the animal laboratory? Certainly, the regulation of animal research has placed limitations on the ways in which scientists can permissibly use animals in their laboratories, and has created a venue in which they must account for and justify their practices. But once inside the boundaries created by animal welfare regulations, the divisions of space, labor, and expertise between animal care workers and scientists makes it seem as though experimental work can proceed with relatively little friction. This paper draws on ethnographic research in animal behavioral neuroscience laboratories to challenge the implicit division between the "ethical" mouse enacted by welfare regulations and animal care workers, and the "experimental" mouse enacted by neuroscientists. I argue that increasing prominence of animal welfare concerns both supports and creates problems for how practitioners understand the relationship of animal behavioral models to the laboratory environment. Behavioral techniques for controlling animal stress or studying the effect of housing environments have been widely diffused in the scientific community by the welfare professionals as tools for ensuring general animal well-being, but the growing association of these spaces and practices with welfare makes it difficult for scientific practitioners to retain control over these concepts, their affective associations, and their meanings.

Creativity in the paleobiology laboratory: why fossil preparators compare themselves to Michelangelo

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Laboratory work is the foundation of most biological research. This is an interpretation rather than a fact, as many researchers -scientists and social scientists alike- might argue that the field “nature” is the basis of biology. However, even specimens collected in the field must pass through the lab before being analyzed and, eventually, becoming the evidence for knowledge claims. Fossil specimens, for example, undergo extensive preparation involving rock removal, damage repair, and reconstruction of missing parts. Technicians called preparators choose, apply, and sometimes invent these techniques in paleobiology laboratories. During interviews and participant observation, preparators regularly describe their work as artistic and creative. One preparator said, "[Preparation] is like the same thing that Michelangelo said when he sculpted David... that he's revealing it out of the rock". This portrayal perhaps serves to defy the common conception of technical work as protocol-based and predictable. Revealingly, preparators discourage creativity among volunteer preparators, who are expected to follow directions rather than choose or design preparation methods. Preparators and their work are typically absent from research publications, making them "invisible technicians" in Steven Shapin's sense. This invisibility can imply that their work is too simple -or too black-boxed- to require explanation or justification. I investigate why these "invisible" preparators claim art and creativity as necessary to their work, and thus how researchers, technicians, and volunteers construct scientific practice and social order in today's biology laboratories.

A Feel for the Numbers: the Data and Discourse of Mark/ Recapture Studies

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Since the nineteen-seventies, wildlife biologists and environmental activists have converged on the Delaware Bay, in the northeastern U.S., to study a migratory shorebird called the "red knot." Ecologically linked with the spawning cycle of the horseshoe crab, the population of this bird has declined precipitously in recent decades with the advent of a horseshoe crab fishery on the east coast. Attempts to halt this decline have hinged on the numerical and statistical data gleaned from tracking shorebirds, and the the red knot political controversy has helped to generate one of the largest "mark-recapture" wildlife studies in the world. This paper places Delaware Bay shorebird studies in the larger historical context of twentieth-century bird-banding as a scientific practice and a direct, sensorial relationship between human and nonhuman nature. Since the turn of the twentieth century, wildlife biologists in Britain and the U.S. have promoted " banding" (or "ringing") amongst professional and amateur ornithologists as an important source of data on the populations and movements of migratory birds. The practice of capturing, marking, recording, and releasing these animals has indeed generated volumes of data, but these quintessentially bureaucratic wildlife management practices have also instantiated relationships with nonhuman nature that go beyond the numbers to include sensory experience, phenomenological attachments, and ethical imaginaries. Touch, technologically mediated 'sight', and intuitive data manipulation have come to dominate the practices and epistemological commitments of wildlife biology, and this history provides a wealth of potentially productive metaphors and methods for environmental ethics and policy.

Pregnancy testing with toads: Sourcing strategies of competing laboratories in postwar Britain

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After World War II, laboratories around Britain began using two kinds of toads for human pregnancy diagnosis: the South African clawed toad *Xenopus laevis* and the ordinary British *Bufo bufo*. This talk examines the divergent sourcing strategies adopted by competing laboratories, and so moves beyond the dominant historical account of (a) pregnancy testing, which centres on a single large *Xenopus* laboratory in Edinburgh, and (b) the supply of laboratory animals, which posits a simple shift from a free market of small commercial dealers to centralized state control. While the Ministry of Health in Britain and the Department of Inland Fisheries in South Africa did regulate the postwar trade in *Xenopus*, alternative means of obtaining exotic and domestic toads also flourished. For instance, the Family Planning Association, a registered charity, sourced *Xenopus* from the private shipping and tourism company Thomas Cook and Son, and a few pathologists managed to breed their own stock on a small scale. Only a handful of large and specialized 'pregnancy diagnosis centres' including the one in Edinburgh could afford the elaborate and expensive equipment required to maintain a healthy *Xenopus* colony, so many small hospital laboratories in London and the South of England preferred the locally abundant *Bufo*, which they could obtain and discard indiscriminately and so did not have to domesticate at all. Specialised commercial breeders continued to supply research and teaching laboratories with *Xenopus* and many other amphibians well after immunological test kits decisively replaced bioassays in the 1960s.

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