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Dear Conference Participant,

A very warm welcome to Lisbon, the Calouste Gulbenkian Foundation, and our Conference on Evolutionary Patterns, Horizontal and Vertical Transmission and Micro- and Macroevolutionary Patterns of Biological and Sociocultural Evolution!

The EvolPat Conference is organized by AppEEL, the Applied Evolutionary Epistemology Lab of the Centre for Philosophy of Science of the University of Lisbon, in collaboration with the Calouste Gulbenkian Foundation, and with the support of the John Templeton Foundation.

This conference is one of the outputs of an international project we are running titled "Implementing the Extended Synthesis in Evolutionary Biology into the Sociocultural Sciences". The project is financially supported by the John Templeton Foundation. Our big questions are: What are the candidates of an Extended Synthesis in Evolutionary Biology? How do the biological sciences currently define horizontal and vertical evolution as well as micro- and macroevolution? And how can these evolutionary theories be implemented into the study of the Sociocultural domain?

These questions also define the agenda of our conference. With our plenary and invited speakers, as well as in our selection of presenters, we systematically searched for kindred minds who also investigate the means by which current advances in evolutionary biology are pressing for an extension of the Modern Synthesis on the one hand, and how such research can help advance a fuller understanding of sociocultural evolution on the other.

In the name of the scientific and organizing committee, I want to sincerely thank the plenary and invited speakers for participating in our event. Your enthusiastic acceptance to talk at our conference proves the willingness there exists to cross disciplinary boundaries. We also want to kindly thank the scholars who responded to our call for abstracts. All of you enable us to provide this rich and diverse program, where microbiologists can meet with anthropologists, paleontologists with linguists, and philosophers of science with bioinformaticians.

We also want to extend our gratitude to our sponsors, and we want to particularly thank the Calouste Gulbenkian Foundation for providing our conference with a home in such beautiful surroundings.

Finally, as chair of the conference, I want to acknowledge the work and effort put in by the members of the Scientific and Organizing Committee. Your advice, support, and the long working hours are tremendously appreciated.

We wish you stimulating conversations and network opportunities that will last well beyond the duration of the conference!

Warm regards,

Nathalie Gontier
(Conference Chair)

INTRODUCTION TO THE CONFERENCE THEME

The 3-day **International Conference on Evolutionary Patterns: Horizontal and Vertical Transmission and Micro- and Macroevolutionary Patterns of Biological and Sociocultural Evolution** aims to provide an interdisciplinary platform where evolutionary scholars from the exact, technological, life, human and sociocultural sciences can exchange ideas and techniques on how to conceptualize, model, and quantify biological and sociocultural evolution.

The conference is centered around the following four themes:

1. Conceptualizing, Quantifying and Modeling Horizontal and Vertical Evolution in Biological and Sociocultural Sciences

In recent years, bioinformatic approaches have greatly advanced the means by which biologists are able to conceptualize, quantify and model horizontal (Symbiogenesis, Lateral Gene Transfer, Hybridization, Virolution) and vertical evolution (Natural Selection, Punctuated Equilibria Theory and Drift). These techniques can and are currently applied to model horizontal and vertical sociocultural evolutionary processes. During the conference, emphasis will lie on tree and network models that allow the formalization and visualization of ancestral-descent relationships, horizontal and vertical transmission and exchange of biological and sociocultural traits, and inter-individual interactions.

2. Conceptualizing, Quantifying and Modeling Micro- and Macroevolution in Biological and Sociocultural Sciences

The Modern Synthesis argues that microevolutionary events (genetic mutations and chromosomal recombinations) suffice to explain macroevolutionary events (the origin and evolution of species). The existence of horizontal evolutionary mechanisms makes it necessary to redefine the means by which microevolution can occur and cause macroevolution. And Drift and Punctuated Equilibria Theory or the Red Queen Hypothesis demonstrate that macroevolution, in biology as well as in culture, is caused by physical and ecological mechanisms, in addition to microevolutionary mechanisms. During the conference, we will focus on shared bioinformatic methodologies that depict patterns, processes and modes of micro- and macroevolution of life and culture.

3. Hierarchy Theory and the Units, Levels and Mechanisms of Evolution

Theories on horizontal transmission and rapid or slow vertical evolution challenge our classic notions of "trait", "organism", "group", "species", "speciation", and "evolutionary mechanism." These theories shed new light on what can be units of evolution, where and at which level(s) evolution occurs, and how evolution occurs - how different evolutionary mechanisms interact to cause evolutionary change through time. In other words, there is currently an ontological and epistemological demand to recognize the multiplicity of units, levels and mechanisms of both biological as well as sociocultural evolution, and thus, to extend the Evolutionary Synthesis. This demand also necessitates a scientific investigation into how different biological and sociocultural units, levels and mechanisms alternate and interact hierarchically, and together bring forth the phenomenon of evolution. During the conference, we will investigate how various biological evolutionary mechanisms can be universalized to model and conceptualize sociocultural evolution.

4. Unification of the Biological and Sociocultural Sciences into an Extended Synthesis

Bioinformatics, phylogenetics, network and agent modeling, hierarchy theory, and debating the units and levels of evolution provide new means to unify biological and sociocultural sciences into an Extended



Synthesis. During the conference, emphasis will lie on how these unifying approaches delineate a shared research program and how this program differs from other unification approaches.

We welcome evolutionary scholars active in all academic fields who either develop theoretical models, methodologies and theories on biological and sociocultural evolution; or create concrete software, imaging and modeling techniques that capture aspects of biological and sociocultural evolution.

PLENARY & INVITED SPEAKERS

Plenary Speakers

Michael Benton is Professor of Paleobiology, leader of the Paleobiology and Biodiversity Research Group and Program Director for the MSc and undergraduate programs in Paleobiology, all housed in the School of Earth Sciences of the University of Bristol, UK. He is President of the International Paleontological Association from 2012-2014. His research includes the diversification of life through time, quality of the fossil record, shapes of phylogenies, mass extinctions, Triassic ecosystem evolution, dating the tree of life, and the use of phylogenetic means to assess the quality of the rock and fossil records.

Tal Dagan is Professor of Genomic Microbiology at the Christian Albrechts University of Kiel, Germany. She researches microbial genome evolution by Lateral Gene Transfer, and is pioneering in the development of phylogenomic networks. She currently runs an interdisciplinary program where she implements network thinking to study the evolution of genomes and languages.

John Jungck is Director of Interdisciplinary Science and Professor of Biology at the University of Delaware. He holds joint appointments in the Department of Mathematics and the Bioinformatics Program. He is a leader in Biology Education Reform, a Mathematical Molecular Evolutionary Biologist, and a Computer Software Developer of biological simulations, tools, and databases. His research interests are in Mathematical and Theoretical Biology (Bioinformatics, the origins of genetic codes, image analysis and simulation of patterns in nature, and evolutionary analysis of complex data sets), History and Philosophy of Biology, and Interdisciplinary Education. He is the Editor of *Biology International*. He is the former Editor of *Bioscene: Journal of College Biology Teaching* and the *American Biology Teacher*. He has Chaired the Education Committee of the International Society for the History, Philosophy, and Social Studies of Biology.

Carl Knappett is Professor at the University of Toronto where he holds the Walter Graham and Homer Thompson Chair in Aegean Prehistory in the Department of Art. He sits on the International Scientific Committee of the renowned Fyssen Foundation (based in Paris) that supports research in Archaeology, Anthropology, Ethology, Psychology and Neurobiology. He is one of the leading and pioneering archeologists applying network models to depict the diffusion of material culture as well as regional, sociocultural and political interactions amongst prehistoric populations. He runs an Aegean Material Culture Laboratory, that focuses on the modeling of maritime interaction in the Bronze Age east Mediterranean. He will give a plenary on the use of network models in archaeology.

Daniel McShea is Professor of Evolutionary Biology and a member of the Centre for Philosophy of Biology at Duke University, North Carolina. His research lies in the field of Paleobiology, with a focus on macroevolutionary trends in the history of life, Philosophy of Biology, with emphasis on evolutionary epistemological debates on the origin of complexity and biological hierarchies and hierarchical causation (upward and downward causation); and animal behavior, especially the evolution of emotions. Together with the philosopher Robert Brandon, he developed the Zero-Force Evolutionary Law that explains how complexity can evolve in the absence of selection or constraint at various ranks of life.

Alex Mesoudi is Reader in Anthropology and is a member of the Centre for the Coevolution of Biology and Culture at Durham University, UK. He currently functions as the Principal Investigator of a Leverhulme Trust funded Research Project entitled "Human Cultural Transmission: From Psychology Lab to the



Artefactual Record". He is developing innovative mathematical/agent-based models of cultural evolution that enable the formalization of cultural transmission at the micro-evolutionary level. He uses these models to develop a Darwinian theory of cultural evolution.

Mark Pagel is Professor in the School of Biological Sciences and head of the Evolution Laboratory at the University of Reading, UK. He builds statistical models to examine the evolutionary processes imprinted in human behavior, from genomics to the emergence of complex systems to culture. His latest work examines the parallels between linguistic and biological evolution by applying methods of phylogenetics, or the study of evolutionary relatedness among groups, essentially viewing language as a culturally transmitted replicator with many of the same properties we find in genes. He is looking for patterns in the rates of evolution of language elements, and hoping to find the social factors that influence trends of language evolution. He has also used statistical methods to reconstruct features of dinosaur genomes, and to infer ancestral features of genes and proteins.

Tyler Volk is Professor of Biology as well as Science Director of the Environmental Studies Program at New York University, New York. One of his academic duties includes the teaching of a seminar on "Transdisciplinary Investigations across Multiple Evolutionary Scales". He is the author of books that explore patterns at multiple levels, in "Metapatterns Across Space, Time, and Mind," "Gaia's Body: Toward a Physiology of Earth," "CO2 Rising: The World's Greatest Environmental Challenge," and "Death and Sex" (with D. Sagan). His research has focused on metapatterns (such as borders, binaries, centers, cycles) as functional principles in various levels of systems, roles of life in the earth system, biogeochemical aspects of global change, entropy, energy, and advanced space life support (for NASA). His overarching concerns are for the present and future of humans in a global environment and for a harmonious personal and social evolution of consciousness.

Richard Watson is Senior Lecturer in the Natural Systems research group at the University of Southampton's School of Electronics and Computer Science, UK. His research uses computational models and theoretical computer science frameworks to investigate and characterize the algorithmic principles of biological evolution. This includes works on Symbiogenesis, the Baldwin effect, Co-Evolution, Niche-Construction, Epigenetics, sexual recombination, developmental modularity, group selection and the major evolutionary transitions. In particular, his current research uses adaptive networks models to characterize the two-way interaction between social evolution and the co-construction of social structures that provide the context for social evolution. He is the author of *Compositional Evolution: The impact of Sex, Symbiosis and Modularity on the Gradualist Framework of Evolution*, <http://eprints.soton.ac.uk/260415/>, MIT Press (Vienna series in Theoretical Biology), and vice president of the International Society for Artificial Life.

Invited Speakers

Quentin Atkinson is a Senior Lecturer in the School of Psychology at the University of Auckland, New Zealand. Previously, he spent 3 years at the University of Oxford as a Research Fellow in the Institute of Cognitive and Evolutionary Anthropology. He has also done post-doctoral work in the school for the Study of Religion at the University of Aarhus, Denmark and with Professor Mark Pagel in the Zoology Department at the University of Reading, UK. His research interests covers a range of areas, centered on human evolution and cooperation. This includes the evolution of language, religion, large-scale cooperation and common pool resources, and the human expansion from Africa. He is also a keen environmentalist and in 2008 published an edited volume with Dr Niki Harré on how New Zealanders can tackle climate change.

Alberto Bisin obtained a Ph.D. in Economics from the University of Chicago in 1993. He then was visiting professor at Delta, Ecole Normale Supérieure and assistant professor at MIT. In 1996 he moved to New York University, where he is Full Professor in the department of Economics. He is fellow of several research institutes, including the NBER, CESS, CIREQ, IZA, IGER. He consulted for the Federal Reserve Bank and is on the Advisory Board of the Institut d'Etudes Avancées of the Université Cergy-Pontoise. He is Associate Editor for *Journal of Economic Theory* and *Economic Theory*. Bisin's publications range from mathematical economics to applied and empirical work, from finance to social economics. His work has appeared in, e.g., the *Journal of Political Economy*, the *Quarterly Journal of Economics*, *Econometrica*, the *Journal of Economic Theory*. His research has been supported by various private as well as governmental foundations.

Andreas Bohn holds a PhD in Physics from the Darmstadt University of Technology, Germany (2003). Since 2008 he is Head of the Systems Biodynamics Group of the Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa, Portugal. His research is rooted in computational and theoretical studies of complex light-driven biosystems, such as circadian clocks or phototrophic microbial biofilms, and is characterized by numerous interdisciplinary collaborations with experimental biologists from various fields of research. To meet the challenge of obtaining systems-level understanding of the studied organisms, in the last years he became increasingly involved in brokering the knowledge of diverse specialists using different scientific tools and languages, and the role of integrative computational tools, e.g. from the semantic web, in coping with the social context of life science research.

Folmer Bokma is Professor in the Department of Ecology and Environmental Sciences at Umeå University, Sweden. As a senior researcher, he runs a lab that investigates the premises of punctuated equilibria theory in a neontological context. He is one of the pioneering researchers that uses computation-intensive analyses of molecular phylogenetic data to draw conclusions on macroevolutionary events. He estimates rates of morphological and genetic evolution: speciation rates, extinction rates, and rates of gradual and speciation change of morphology, gene expression, co-expression, gene family size and sequence divergence. His course will focus on macroevolution in general and punctuated equilibria in particular, in a variety of extant species.

Michael Bradie is Professor in Philosophy of Science at Bowling Green State University, Ohio, where he teaches courses on Philosophy of Science, (Evolutionary) Epistemology, and Logic. He is a leading expert in the field of Evolutionary Epistemology, and famous for distinguishing between the EET – The Evolutionary Epistemology of Theories and EEM program – The Evolution of Epistemological Mechanisms in 1986. He is currently working on a project exploring the implications of evolutionary theory, cognitive neuroscience and cognitive ethology for our understanding of the nature of morality.

Maurizio Casiraghi is Researcher in Zoology at University of Milano-Bicocca, Department Biotechnologies and Biosciences. There he also teaches Biological and Molecular Evolution courses. Maurizio Casiraghi began his scientific activity studying behavioral ecology and population genetic of social Hymenoptera. Then Maurizio Casiraghi focused his interests on symbiosis and, in particular on the relationships between animals and intracellular bacteria; in this contest he studied the model filarial nematodes - *Wolbachia pipientis* (a Gram-negative bacteria). Nowadays the research area of Maurizio Casiraghi concerns: Biological and molecular evolution; DNA barcoding (both for base researcher in biological systematics and tool for diagnostic and food traceability); phylogeny reconstruction.

Jorge Carneiro is a Principle Investigator at the Oeiras Associate Laboratory and the Leader of the Theoretical Immunology Group at the Gulbenkian Institute of Science, Portugal. This group uses



mathematical modeling to understand the development of the immune system and its regulation, as well as lymphocyte signaling, differentiation and commitment. He has an interdisciplinary background, and performs laboratory work as well as research in biomathematics. He was a Ph.D. student at Institut Pasteur of Paris (France) where he prepared his thesis on mathematical modeling of the immune system, under the supervision of John Stewart. He was the Vice-President of the Portuguese Society of Immunology from 2004 to 2006. He is the Deputy-Director of the PhD Program in Computational Biology and also of the FLAD Computational Biology Collaboratorium.

Claudine Chaouiya is professor of Computer Science, in secondment from the Aix-Marseille University (France) to the Gulbenkian Science Institute (IGC), Oeiras, Portugal. Her research interest was initially related to the modeling and validation of 'man-made' systems such as manufacturing systems or communication networks. Since 2001, she has been developing methods to model and analyze biological networks, focusing on dynamical properties of these complex systems. In July 2008, she joined the IGC, where she has set up the Network Modeling group to define feasible computational solutions for efficient handling of large regulatory networks.

Alex de Voogt is Assistant Curator of African Ethnology at the American Museum of Natural History, New York, USA. His research interests are diverse but concentrate on the dispersal of board games and the development of expertise in master players, as well as on the development and history of scripts.

Frank Kressing studied Cultural Anthropology, Comparative Linguistics and European Ethnology at Eberhard Karls University, Tübingen. He is a Research Scientist at the Institute of the History, Philosophy, and Ethics of Medicine at Ulm University, Germany. Kressing's present research interests are centered around the topics of Evolutionary Epistemology and Global Health. His areas of fieldwork cover South America (specifically: the Bolivian Kallawayaya region), South and Central Asia (Ladakh/India), and the Balkans (Albania). Previously, he held a Research Fellow position in the Department of Cultural Anthropology at Ulm University; he was a Lecturer in the Department of European Ethnology at the University of Augsburg.

Matthis Krischel is a Research Scientist of History Theory and Ethics of Medicine at RWTH University of Aachen, Germany. He was trained at the Technische Universität Berlin; and the University of Oklahoma. His research interests include History of Biology (Evolution and Classification in the life and human sciences), History of Eugenics, Medicine in Nazi Germany, and History of Urology (Urology in Nazi Germany).

André Levy is Post-Doctoral Researcher at the Eco-Ethology Research Unit at ISPA – University Institute, The Higher Institute for Applied Psychology, Lisbon. His main research interest lies in community genetics, i.e. the genetics of biotic interactions and their ecological and evolutionary consequences, in particular that of interactions between plants and their insect and microbial enemies. Are geographical ranges of plants influenced by their enemies, and vice-versa.

Margarida Matos is Assistant Professor at the Department of Animal Biology of the Faculty of Sciences of the University of Lisbon since 1997 and Researcher at the Centre for Environmental Biology since 1992. She has taught many courses in Evolution and supervised several master and PhD theses. Her research field is Evolutionary Ecology, using Experimental Evolution as tool. Her main focus is the study of the evolutionary patterns and processes during adaptation, by characterizing real time evolution of repeated colonizations of *Drosophila subobscura* to a novel, laboratorial environment. Ongoing projects include the analysis of the evolution of populations founded from contrasting latitudes, to understand the role of

History and Selection during Adaptation. She is also analyzing how genetic drift interacts with natural selection, by comparing the evolutionary fate of populations of contrasting size. She has authored several scientific publications in books and journals of recognized merit in Evolutionary Biology.

Telmo Pievani is Associate Professor of Philosophy of Biological Sciences for the Department of Biology at the Italian University of Padua. He is the Secretary of the Scientific Board of the Genoa Science Festival; editor in chief of Pikaia, www.pikaia.eu, an Italian web portal on Evolution; and with Niles Eldredge and Ian Tattersall, he curated the International "Darwin 1809-2009". His research interests lie in Philosophy of Biology, The Structure of Evolutionary Theory, and Darwinian Heritage.

Luis Mateus Rocha is Professor at the School of Informatics & Computing at Indiana University, Bloomington, Complex Systems Program Director, member of the Center for Complex Networks and Systems and core faculty of the Cognitive Science Program. He is also the director of the FLAD Computational Biology Collaboratorium at the Instituto Gulbenkian da Ciencia, Portugal. From 1998 to 2004 he was a permanent staff scientist at the Los Alamos National Laboratory, where he founded and led a Complex Systems Modeling Team during 1998-2002, and was part of the Santa Fe Institute research community. His research is on complex systems and networks, computational biology, artificial life, embodied cognition and bio-inspired computing. He is interested in the informational and control properties of natural and artificial systems which enable them to evolve. This means both understanding how information and control is fundamental for the evolutionary capabilities of natural systems, as well as abstracting principles from natural systems to produce adaptive information technology.

Sven Steinmo is Professor of Public Policy and Political Economy at the Department of Political and Social Sciences at the European University Institute in Florence, Italy; and an Honorary Professor in Comparative Politics at the University of Southern Denmark, Odense. His teaching and research interests include the fields of comparative politics, public policy, institutional theory and most recently experimental social science methodology. He has been awarded multiple international honors over his career including the Riker Prize for the best book in Political Economy (APSA), the Gabriel Almond Prize for the best dissertation in Comparative Politics (APSA) as well as the German Marshall Fellowship, the Abe Fellowship and the STINT Advanced Researcher Grant. Steinmo's most recent book, *The Evolution of the Modern State: Sweden, Japan and the United States* was awarded the Gunnar Myrdal Prize (2011), by the European Association for Evolutionary Political Economy. In 2012 he was awarded a European Research Council "Advanced Researcher" Grant in support of his project "Willing to Pay? Testing Historical Arguments with Experiments."

Thierry Verdier is an Associate Chair and Chief Engineer at the French Ecole des Ponts – ParisTech. His main research interest lie in International Trade, Growth and Development, Political Economy and Income Distribution, Economic Sociology and Macro-economical dynamics.



GENERAL PROGRAM

Monday, May 27th

8:30-9:15	Registration
9:15-9:30	Welcome
9:30-11:00	Plenary Sessions Morning Auditorium 2
11:00-11:30	<i>Break</i>
11:30-13:30	Invited Speakers Session Auditorium 2
13:30-15:00	<i>Lunch</i>
15:00-15:45	Plenary Session Afternoon Auditorium 2
15:45-16:00	<i>Break</i>
16:00-18:00	Parallel sessions Session 1 - Room 1 Session 2 - Room 2 Symposium 1 - Auditorium 3
19:00	Conference Dinner

Wednesday, May 29th

9:30-11:00	Plenary Sessions Morning Auditorium 2
11:00-11:30	<i>Break</i>
11:30-13:30	Invited Speakers Session Auditorium 2
13:30-15:00	<i>Lunch</i>
15:00-15:45	Plenary Session Afternoon Auditorium 2
15:45-16:00	<i>Break</i>
16:00-17:40	Parallel sessions Session 4 - Auditorium 3 Session 5 - Room 1 Session 6 - Room 2

Tuesday, May 28th

9:30-11:00	Plenary Sessions Morning Auditorium 2
11:00-11:30	<i>Break</i>
11:30-13:30	Invited Speakers Session Auditorium 2
13:30-15:00	<i>Lunch</i>
15:00-15:45	Plenary Session Afternoon Auditorium 2
15:45-16:00	<i>Break</i>
16:00-18:00	Parallel sessions Symposium 2 - Room 2 Session 3 - Room 3 Poster session - Hall

DAY-BY-DAY PROGRAM & ABSTRACTS

Monday, May 27th

9:15-9:30 Welcome

António Carlos de Sá Fonseca - Vice-President, Faculty of Science of the University of Lisbon

Nathalie Gontier - Director AppEEL

9:30-11:00 Plenary Sessions Morning, Chaired by Nathalie Gontier

9:30-10:15 **Mark Pagel** - The Cultural Survival Vehicle

There is agreement that there is something important to explain about human social behavior. We are distinguished among all animals for living in groups that have forms of cooperation that, on the face of it, pose a challenge to conventional Darwinian accounts of evolution. We routinely help others, we share our knowledge and skills, we give up seats on trains, pay taxes, hold doors for people, give money to charities, and even sometimes risk our health and well-being to fight wars. This remarkable social organization manages to combine the altruism, inventiveness and cohesion of multicellular organisms and the great eusocial insects, even when there is no possibility of our help being reciprocated, and the people we help are not related to us. I call this social structure the *cultural survival vehicle* and suggest that understanding its origins provides the starting point for a theoretical and empirical investigation of our psychology and morality, social behaviors, our language and our vast range of individual differences within society.

10:15-11:00 **Alex Mesoudi** - The Experimental Study of Cultural Evolution

In biology, one of the key benefits of Darwin's theory of evolution was that 'macroevolutionary' patterns and trends, such as temporal patterns observed in the fossil record or spatial patterns observed biogeographically, could be explained in terms of 'microevolutionary' processes such as selection, drift, mutation or migration. The same benefit can be gained by viewing human cultural change as a Darwinian evolutionary process. Here, 'macroevolutionary' patterns and trends, such as temporal patterns observed in the archaeological record or spatial patterns observed in the ethnographic record, can similarly be explained in terms of 'microevolutionary' processes, sometimes borrowing the same concepts as in biology (e.g. cultural selection or cultural drift) but sometimes introducing novel cultural microevolutionary processes that have no parallel in genetic evolution (e.g. non-random 'guided variation'). As in biology, lab experiments can be used to explicate this macro-micro link, by simulating different microevolutionary processes and comparing the resulting data to real-life macroevolutionary patterns. I will describe a series of experiments that have aimed to do this. These studies have simulated patterns of projectile point variation in the prehistoric Great Basin region of the United States, linking different levels of regional variation to different cultural transmission biases, and exploring the conditions under which we would expect to see the observed patterns of cultural variation. This interplay of experimental methods and real-world data, pursued within an explicit evolutionary framework, promises to significantly enhance our understanding of human cultural change.

11:30-13:30 Invited Speakers Session, Chaired by Nathalie Gontier

11:30-11:50 **Alberto Bisin & Thierry Verdier** - Multi-disciplinary Perspectives on Cultural Transmission

Preferences, beliefs, and norms that govern human behavior are partly formed as the result of heritable genetic traits, and are partly transmitted through generations and acquired by learning and other forms of social interaction. Cultural transmission arguably plays an important role in the determination of many



fundamental preference traits, like discounting, risk aversion and altruism. It certainly plays a central role in the formation of cultural traits, social norms, and ideological tenets, like e.g., attitudes towards family and fertility practices, and attitudes in the job market. Relatedly, distinct cultural traits determine how individuals interpret and react to common (e.g., strategic) choice environment. We conceptualize cultural transmission as the result of interactions between purposeful socialization decisions inside the family and other socialization processes. We study the determinants of the persistence of cultural traits and more generally the population dynamics of cultural traits. We discuss the links between the economic and other approaches to cultural evolution in the social sciences as well as in evolutionary biology.

11:50-12:10 Frank Kressing & Matthis Krischel - Lateral and Vertical Transfer in Biology, Linguistics and Anthropology : An Account of Widely Neglected Ideas in the Formation of Evolutionary Theories

Models of biological and cultural evolution that developed from the 19th century onward are in their majority centered on the unilinear transmission of cultural and biological replicators as well as on phylogenetic images of descent – the tree of life and the tree of languages metaphors. But not all biologists, linguistics and anthropologists of the 19th century subscribed to the idea of human development in the sole form of unilinear evolution in successive stages, leading from inferior to superior states. Competing with the prevailing theories of evolutionism, the idea of diffusion in regard of words, grammatical features, cultural traits, and whole cellular organs played a considerable role in the realms of both linguistics and biology, and later cultural anthropology. The scope of this paper is to give an historical account regarding the idea of transmission by diffusion, of vertical transfer in biology, linguistics, and cultural/social anthropology. Historical and contemporary examples are the idea of Sprachbund (areal typology) and mixed languages (pidgins, creoles) in linguistics, endosymbiosis in biology, and diffusionism in cultural anthropology (Kulturkreise, culture areas).

12:10-12:30 Michael Bradie - Modeling Biocultural Evolution

There have been a number of attempts in recent years to integrate biological evolution and cultural change. Richard Dawkins introduced the 'meme' as a cultural analog to the gene and the 'science' of memetics was off and running. E. O. Wilson proposed that a biological approach to human social behavior and culture – sociobiology - would be fruitful because the 'genes hold culture on a leash.' In the aftermath of criticism of Wilson's original program sociobiology has morphed into the growing field of evolutionary psychology. Richerson and Boyd, in a number of papers and books, have promoted what they call a dual inheritance model of gene-culture coevolution. What exactly is the relationship between biology and culture? [1] Culture is one (albeit complex) product of biological evolution [the 'leash' option]; [2] Culture is grounded in biology but 'evolves' more or less independently of biological constraints [the 'cultural memes' option]; [3] Culture and cultural change interacts with and helps shape biological evolution (the 'dual inheritance' model); [4] Although culture would not exist if biological organisms did not exist evolutionary models of culture and cultural change are neither fruitful nor particularly insightful [the 'metaphor gone awry' option]. What, exactly, can we hope to expect from such efforts? Are the mechanisms underlying biological evolution and cultural change sufficiently similar to warrant thinking of cultural change as cultural evolution or is these, at best, a suggestive metaphor or analogy that connects the two processes? Dobzhansky once famously remarked 'Nothing in biology makes sense except in the light of evolution.' To what extent can it be truly said that 'Nothing in culture makes sense except in the light of biology?'

12:30-12:50 Quentin Atkinson - Tracing Human Cultural Ancestry in Time and Space

Recent work on cultural evolution has successfully applied phylogenetic methods from biology to comparative cultural and linguistic data to test hypotheses about cultural ancestry, chronology and sequences of change. However, relatively little attention has focused on explicitly modeling large-scale spatial processes of cultural change. Here I report results from a range of collaborative research projects that uses tools from population genetics and phylogeography to analyze spatial information derived from

comparative cultural data. This work identifies the legacy of phylogenetic and spatial processes in a range of cultural data.

12:50-13:10 **Alex de Voogt** - The Language Boundary in Cultural Transmission: Helicopters, Games and Script

In the dispersal of cultural traits, language differences are generally considered a boundary that impedes (horizontal) transmission. Although language differences are not necessarily impossible to overcome, it seems obvious that they do not facilitate transmission processes. Recent studies on the distribution and development of technology, ancient gaming and the adoption of writing systems shed new light on the role of language in facilitating and/or obstructing cultural transmission processes.

15:00-15:45 Plenary Session Afternoon, Chaired by Nathalie Gontier

15:00-15:45 **Tyler Volk** - Levels, Realms, and Metapatterns in Biological and Cultural Evolution

The universe seems to be arranged in levels of basic types of being, from elementary particles to atoms to cells, then organisms, and human states. Are there overarching patterns within and among the levels? Of interest is the fact that these levels can be arranged in a time sequence, in which former whole systems become parts within the next, higher level of system. We might term this process "syneosis" from "together" and "new." Given the conference focus on comparing the two great pattern-creating realms biological and cultural evolution, I will examine processes and structures for each level's origin, evolution, and emergence to the next level, for prokaryotic cells, eukaryotic cells, multicellular organisms, animal societies, human bands of conscious individuals in cultural fields, agricultural villages, and states. All these levels of syneosis potentially contain 3 scales of metapatterns: (1) within-level, (2) across-level and within realm, and (3) across-realm. Within-level metapatterns can derive from evolutionary convergences that achieve similar advantages from getting larger. Across-level metapatterns (but still within the realms biological or cultural evolution) can derive from fundamental dynamics that are used at the levels within a given realm. Finally, across-realm metapatterns can derive from commonalities generated by any evolution-type process that uses a logical skeleton of propagate-vary-select. In this talk I will lay out this general model of 3 scales of metapatterns for examining levels in the realms of biological and cultural evolution, with an eye to opportunities for future work.

16:00-18:00 Session 1, Chaired by Alberto Bisin

16:00-16:20 **Carl Henning Reschke** - Hierarchy and Modularity in Biology and Economics

This paper discusses the perspectives of a unification of concepts of systemic evolutionary biology and the economics of organization of information. Systemic evolutionary biology (e.g. Riedl 1978) puts emphasis on the notions of hierarchical organization and modular structures to systematize information, which is gained from tests of 'biological hypotheses' in the environment and the efficient organization of these empirical data into successively adapted organisms. Similar arguments on the aggregated processing and structuring of information have been made in economics of organizations and management esp. by Herbert Simon (1962) and Peter Drucker (1986). Related arguments in economics have been advanced by Friedrich Hayek (1932, 1945) and Joseph Schumpeter (1911). The paper discusses the similarities and differences in these approaches to derive a set of suggestions for modeling of information structuring and change in social organizations.

16:20-16:40 **Derk Venema** - Legal Darwinism Without Skyhooks

Human behavior seems to control the 'evolution' of the law. This makes it seem doubtful whether the development and changes of the law are Darwinian evolution: 1. Selection: Human behavior selects legal rules from different normative opinions, for example in parliament. 2. Variation: Human behavior



produces the variation of normative opinions that are input for law-creating processes in politics and in courts of law. 3. Replication: Human behavior replicates legal rules by repeated rule-following, rule-applying, rule-acknowledging. This behavior – from citizens following traffic rules, to judges applying statutes – does not produce perfect copies, but it yields variants, different interpretations that in turn compete for legal recognition. For practicing lawyers and legal scholars, it is essential to presuppose that this selecting, replicating and variation producing human behavior is the product of a more or less free will which implies responsibility. People deliberately ignore red lights, sign contracts and decide court cases because they want to attain certain goals. Consequently, people are rightly held accountable for those actions. A truly Darwinian explanation has no need for these skyhooks (intelligent design, goal-directedness), yet the law seems to depend on them. I offer a Darwinian interpretation of legal rules as units of information (cultural replicative units or memes), that are part of the human extended phenotype. The legally essential element of a free will be explained as a necessarily counterfactual condition for the law's evolutionary success as a system of norms for human behavior.

16:40-16:17:00 **Daniel Garcia-Rivero** - Interdemic Selection, Social Hierarchy, and the Cascade Effect in Cultural Evolution: An Approach from Prehistoric Archaeology

The modern theoretical discussion of the key points of evolutionary theory in archaeology has a historiography of at least four decades. Attention has been placed on, for example, the similarities between organic and cultural systems, modes and tempos of cultural evolution, levels of selection operating on cultural traits and systems, the role of adaptive fitness of the material culture to human carriers, etc. In recent years an effort has been made to apply these concepts and theoretical models to specific archaeological phenomena, which is particularly important not only to test and validate these theoretical models but also to explain and understand the empirical world, past and present, around us. This paper deals with the question of the units and levels at which selection operates more or less simultaneously and of the rhythms and tempos of cultural evolution. Our approach is applied to a temporal and geographical scale that allows special emphasis to be made on the analysis of the main active mechanisms involved in a process that weaves together the evolutionary events of both interdemic and intrademic levels. The empirical study enables a diachronic analysis, piecing together these microevolutionary stories, of the populations of the fourth and third millennia BC in the Southwest of the Iberian Peninsula. The archaeological record considered for this purpose includes the relative frequencies and spatial patterns of settlement and other cultural traits, such as Bell Beaker pottery and other singular objects of prestige, warfare technology, etc. which allow us to sequence, test and explain the macroevolutionary history of these human groups.

17:00-17:20 **Ruggero Rangoni & Mara Menegon** - The Evolution of Property: An Agent-Based Model

It is usually that property is respected if possession is never or rarely contested and, when it is contested, the contest usually ends with the owner maintaining her possession. We can adopt this definition of property for both animals and human beings, since the property-respect behavior is widespread both among human societies and animal species, from butterflies (Davies, 1978) to horses (Stevens, 1988). As Sugden (2004) has suggested, the respect of property has evolved biologically among animals and culturally among humans. Gintis (2007) has proposed a game-theoretical model to exemplify fights for a contested good, which resembles the hawk-dove game and the war of attrition, first conceived by Maynard Smith (1974), and which can be adopted to analyze both biological and cultural evolution. He claims that, given some intuitive conditions, the evolutionary process would lead the population to settle on a property equilibrium, i.e. the widespread respect of property. However, given the appropriate environmental variations, the population would settle on a conflict equilibrium, in which fights for possession are the norm. We have developed an agent-based model derived from Gintis' equation-based model. Agent-based modeling allows us to explore all the possible scenarios and to verify Gintis' hypothesis. We aim at demonstrating that the property equilibrium proposed by Gintis, which is characterized by the absence of fight, isn't the only possible outcome to be labeled as a norm of property.

The conflict equilibrium, in fact, could be characterized by relatively harmless fights in which the owners are always the winners.

17:20-17:40 **Pietro Battiston & Luca Stanca** - The In's and Out's of Influence in Social Networks: Does Indegree Matter?

This paper presents an experimental investigation of social influence in communication networks. We propose an experimental design aimed at disentangling the roles of indegree and outdegree in determining social influence. We find that, after repeated communication within a social network, social influence depends not only on being listened to by many others (higher outdegree), as predicted by the persuasion bias hypothesis, but also by listening to many others (higher indegree). The results are consistent with the hypothesis that, in a social network, agents receive weights that are proportional to their indegree.

17:40-18:00 **Laura Desirée Di Paolo & Flavia Fabris** - Mechanisms of Heredity: Microbiome Inheritance in a Niche Construction Perspective

As Niche Construction Theory [NCT] points out, individuals and species react toward selective pressures, modifying them, and triggering evolutionary consequences on other species as well. This approach, earlier applied on genetical transmission, now is profitably employed in Social Learning models, but seems missing in microbiome theories. As the Hologenome theory has previously demonstrated, the whole population of bacteria and the genome have a symbiotic relationship. Our aim is to use NCT in order to understand if bacterial activities, affecting host organisms, have also evolutionary implications on their hereditability. This can be useful to shed light on the inherited persistence of microbiome, focusing by means of which mechanisms this conservation happens. Therefore, the open question will be if and how these mechanisms can be analyzed into a complex, social environment, and how this perspective could enable a comprehensive, extended evolutionary synthesis.

16:00-18:00 Session 2, Chaired by Michael Bradie

16:00-16:20 **Matt Haber** - Evolution and the Levels of Lineage

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. My *Levels of Lineage Perspective* frames research on these patterns, and is a commitment to the following: -The biological world is hierarchically organized; -A level of the biological hierarchy is constituted by lineage-generating entities; -The parts of the biological hierarchy are, in part, constituted by and constitutive of other parts of the hierarchy; -Genealogical discordance is exhibited between levels; -No single level of lineage offers a privileged perspective of phylogeny. This perspective permits a robust response to recent challenges against the phylogenetic project. Recognition of the prevalence of lateral gene transfer (LGT) has some questioning the Tree of Life metaphor and even the phylogenetic project itself. I remain more optimistic, instead seeing a new challenge for the systematists: elucidation of the patterns of genealogical discordance. This acknowledges the genuine challenge LGT (and other genealogical discordances) present to phylogenetic thinking, yet recognizes the value of the patterns they produce. I set this new challenge in three parts: (1) determining the predicted patterns of discordance on competing accounts of evolution (e.g., multilevel selection, ZFEL, etc.); (2) identifying where divergent predictions, and how observed patterns of discordance act as tests of competing accounts of evolution; and (3) generating methods of inference and effective display/visualization of patterns of discordance. In short, I propose to systematize the study of genealogical discordance.

16:20-16:40 **Benjamin Jantzen** - Dynamics, Symmetry, and the Levels of Selection

Most attempts to answer the question of whether populations of groups can undergo natural selection focus on properties of the groups themselves rather than the dynamics of the population of groups. Those



approaches to group selection that do emphasize dynamics lack an account of the relevant notion of equivalent dynamics. I present a new framework for assessing dynamical equivalence that is based upon the notion of a dynamical symmetry, a transformation of a system that commutes with its dynamical evolution through time. In this framework, structured sets of dynamical symmetries are used to pick out equivalence classes of dynamics. Every member of such an equivalence class is dynamically independent of all other members, and in this sense constitutes a natural unit, belonging to a natural dynamical kind. By characterizing dynamical kinds via symmetry structures, the question of levels of selection becomes a precise question about which populations respect the dynamical symmetries of Darwinian evolution. To answer this version of the question, I argue that evolving Darwinian populations are characterized in part by a group of fitness-scaling symmetries. I then demonstrate conditions under which these symmetries may be satisfied by populations of individuals, populations of groups of individuals, or both simultaneously.

16:40-17:00 Natalie Gontier - Applied Evolutionary Epistemology

Applied Evolutionary Epistemology builds on the field of evolutionary epistemology as it was introduced by Donald T. Campbell in the 1950s. From within comparative psychological approaches, and before Lewontin and Brandon introduced the units and levels of selection debate in the 1970-1980s, Campbell asked how evolutionary theory can be implemented into the sociocultural sciences, and what conceptual changes to evolutionary theory are required, in order for scientists to be able to investigate the evolution of behavior by means of natural selection, a theory originally introduced to explain the evolution of species. Crucial to his approach was that he “universalized” natural selection theory into the formula he called “blind variation and selective retention”. This formula has heuristic potential for how we can conceive of evolution by means of natural selection to occur outside the realm of biology. Theories that are currently classified as part of an Extended Synthesis in Evolutionary Biology, can also be put to use to study aspects of sociocultural evolution. There is therefore a current scientific need to abstract heuristic universal formulas from these non-selectionist theories, in order to better conceptualize how sociocultural evolution can occur by mechanisms such as drift, symbiogenesis, lateral transfer, etc.

17:00-17:20 Davide Vecchi - From Slot Machines to Pangenomes: On the Role of Biological Metaphors in the Study of Culture

Metaphors and analogies play an important epistemological function in biological practice. Frequently metaphors and analogies developed in one particular domain are transferred to other domains of research. But sometimes such transfer is only partially justified. Two instances of problematic transfer will be considered: the application of the analogy of the lucky jackpot and the metaphor of the tree of life to the study of cultural evolution. The lucky jackpot analogy and the tree of life metaphor are at the core of the Darwinian blind-variation-and-selective-retention metaphor. In this talk the aim is to evaluate their theoretical role in studies of cultural evolution, particularly in the light of contemporary research in microbiology. Developments in microbiology challenge the neo-Darwinian view of evolution in at least two respects. First, processes of hyper-mutation and compositional evolution are common in the micro-world. Secondly, processes of lateral gene transfer and evolution by association make non-vertical genetic and phenotypic resource-flow profuse. Hence, in the biological micro-world phenotypic resources are not generated analogously to the ways jackpots are caused by slot machines, while genetic resources might be considered “public goods” making extensive “cross-lineage borrowing” possible. It will be argued that the theoretical limits of the trial and error metaphor when applied to biological evolution render its transfer to cultural evolution unsurprisingly controversial and that, preposterous as it may seem, microbiology provides a whole array of new metaphors potentially useful to conceptualize cultural evolutionary dynamics.

17:20-17:40 **Damian Ortiz-Rodríguez & Ricardo Noguera-Solano** - The Dominion of Gene interactions: A Self-Organized Level of Complexity and an Instance of Higher-Order Patterns

The emergence of phenotypic variation is mediated and constrained by all the agents involved in the processes of replication, transcription and translation, which can collectively be conceptualized as a code-transduction process, from a storage phase to a morpho-functional one. Such phase is the phenotype of an organism, which is the source of all our inferences on living beings and their change processes. Gene Regulatory Networks (GRNs) are the organization of the code-transduction dominion entangled with the regular function of the organism. They can be studied as a whole level of complexity, with its own logical rules, restrictions and influences.

In the present conceptual analysis, we stress the importance of GRNs in the emergence of phenotypic variation as an ever-acting level of organization. The common usage of terms such as ‘epistasis’ and ‘gene interactions’ in experimental settings acknowledges the influence of interactions only when the phenotypic outcome differs from expectations. We try to conciliate between this meaning and the more general context that is the dominion of GRNs. At the same time, we propose that Natural Selection and the logical rules in the realm of GRNs, which constrain the existence in nature of only a subset of all the conceptually possible phenotypes, are only different instances of a more general ‘Principle of Conservation of Stable Forms’ in nature, with distinct constraints and characteristics in the different levels of complexity of the universe.

17:40-18:00 **Mathieu Charbonneau** - Evolution with Non-local Inheritance

It is commonly held that reproduction among parts of a population (e.g. organisms) is a necessary condition for the population to evolve by selection. Reproduction conflates two processes taking place at the level of the population parts: it both insures a parent-offspring relationship among the parts of the population, where offspring are material products of their parents (multiplication), and the similarity of parents and offspring by the transmission of some property (inheritance). Otherwise put, reproduction insures that like begets like. However, reproduction is a specific biological process and thus has limited applicability if the Darwinian theory of evolution is to be extended to non-biological domains (e.g., cultural evolution). Cases of horizontal transmission both in biological and cultural populations show that our standard conception of reproduction should be broadened by decoupling the multiplication and the inheritance processes. In this paper, I argue that once multiplication and inheritance are decoupled, we can examine their role in evolving populations in a new light. I show that multiplication and inheritance processes need not form a strict parent-offspring lineage at the level of the population parts, that is, they need not be local processes. Rather, both processes are better understood at the level of the population, thus making it possible that there be evolution by selection without any local parent-offspring lineage. This opens the possibility of identifying new Darwinian systems, both biological and extra-biological, which would not be recognized as such if parent-offspring lineages were to be restricted at the level of the population parts.

16:00-18:00 Symposium 1, Chaired by Oliver Morin

Attraction and Transformation and in Cultural Transmission: The Epidemiological Approach

Organizer: Oliver Morin

This symposium presents the epidemiological approach to culture. Like many naturalistic approaches of culture, it treats cultures as populations of ideas, behaviors, and artifacts, best seen as statistical constructs. Unlike many others, it stresses the importance of transformation biases in cultural transmission. Sharing culture is a process that involves not just preservative but also constructive psychological processes at every step in transmission. These constructive processes often result in modifications of the transmitted content that cannot be treated as random mutation or random noise. Ecological and cognitive biases orient cultural evolution in ways that are not adequately described or



explained just in classical Darwinian terms of inheritance and selection. Most Darwinian models of culture focus on the import of selection processes in cultural evolution (the first component of evolutionary change as partitioned by the Price equation, as distinct from the transmission component). Transmission is often seen as a process of imitation that aims at replication while putting up with random changes. Even when the role of biases in transmission is recognized, it is attributed to relatively superficial social-psychological factors while deeper cognitive factors are ignored. The epidemiological approach on the other hand stresses the limits and low fidelity of imitation, the importance of communication distinguished from imitation, and the role of constructive processes in explaining both the relative stability and the evolution of cultural forms. The symposium will present the idea of cultural attraction, a central component of the epidemiological approach, and two cases studies, one concerning the spread of culture among chimpanzees, the other changes in the representation of human faces in Renaissance paintings.

16:00-16:30 Dan Sperber - Attraction and Selection in Cultural Evolution

The study of cultural evolution faces a puzzle: at a population level, cultural items are stable enough to be recognized as cultural. Yet the study of imitation and communication shows that these processes don't have the level of fidelity that would explain this stability. On the contrary faithful reproduction is the exception rather than the rule, not so much because of failures of transmission, but because of the role of constructive processes. One explanation of this puzzle is that transformations that occur in transmission tend to converge towards specific points in the space of possibilities or "attractors". Attractors can be specific to a given population at a given time or be more general or even universal among humans. The talk will introduce the idea of attractor with a simple formalism. It will show how selection can be viewed as a special case of attraction rather than as an alternative construct in the explanation of cultural evolution.

16:30-17:00 Nicolas Claidière - The Spread of Culture Among Merging Groups of Chimpanzees

In spring 2010 a group of 11 new adult chimpanzees was introduced into a zoo facility at Edinburgh already containing a resident group with the same number of individuals. This represented a unique opportunity to study the integration of the two groups and to carry out a social diffusion experiment. During the 16 months following the reintroduction, the two groups formed two very distinct clusters despite the fact that they were sharing the same enclosure and that they have progressively started to merge. The persistence of these two groups explains in turns the success of a social diffusion experiment. Using the same experimental design as in Whiten et al. 2005, we were able to show how different behaviors spread within sub-groups of the same population by following the lines drawn by the relationships between individuals.

17:00-17:30 Olivier Morin - How Portraits Turned Their Eyes Upon Us: Cognitive Attraction and Demographic Dynamics

Direct eye-gaze catches the attention of adults and newborns. This cognitive appeal has cultural consequences. Among XVIth century European portraits, direct eye-gaze paintings are more likely to be featured in today's art books. In Renaissance Europe, the proportion of paintings that stare at the viewer grows gradually, strongly, and irreversibly. A demographic analysis of the shift shows that it was due to the arrival of new generations of painters, who acquired the new style in the years of their apprenticeship. Whether a portrait shows direct gaze or not depends strictly on its painter's date of birth (as opposed to the time of its painting). This dependency of cultural change on generation change is striking, since other changes in portrait poses can be shown to be completely independent of generational turn-over. Interactions between demographic and cultural dynamics will be discussed.

17:30-18:00 Discussion

Tuesday, May 28th

9:30-11:00 Plenary Session Morning, Chaired by Emanuele Serrelli

9:30-10:15 **Michael Benton** - The Tree of Life and Origins of Biodiversity

A key question of interest to all evolutionary scientists is to account for modern biodiversity: why are some groups so much more successful than others? Why, for example, are there 25 species of crocodiles and 10,000 species of birds today, when both groups share an ancestor and a history. It is difficult to see how such a question could be answered using traditional approaches, but combining data from biology and paleobiology may provide some answers. Advances in methods in molecular phylogenomics and paleobiology, coupled with novel numerical techniques and massive computing power allow us to investigate such questions, which link development, paleobiology, species numbers, and the roots of adaptation. In this case, the framework is the tree of life, and analysts are producing ever-larger phylogenetic trees – even of all 10,000 species of birds – based on objective analytical protocols. Such trees can then be dated by tying the branching points to a number of confidently dated and located fossils, and then a battery of analytical tools, founded in comparative phylogenetic methods, can be used to explore the tree for unusually high (or low) rates of diversification, patterns of trait acquisition and evolution, and overall morphological variance (disparity) through time, between subclades, and across character sets. Further, feeding and locomotory function can be compared between living and extinct forms, and the timing of acquisition of certain putative ‘key adaptations’ explored.

10:15-11:00 **John Jungck** - Morphing in Morphospace: Mathematical and Philosophical Perspectives on Macroevolutionary Biological Patterns

Evolutionary diversity is filled with myriad forms. G. Evelyn Hutchinson's famous article: "Homage to Santa Rosalia, or Why are there so many kinds of animals?" was cited by Stephen Jay Gould as articulating a fundamental question in biology. However, an important counterpoint has been: why have possible biological forms that could be generated by similar developmental processes based upon related genetic programs never been found in extant or extinct species? Historically this question was framed by David Raup in his analysis of the theoretical morphospace of gastropods, bivalves, brachiopods, and cephalopods. While many readers of his work were impressed that the general morphologies of extant and extinct members of these taxa could be reproduced with just three equations based upon three measurements on specimens, Raup was intrigued more that his three-dimensional plot of these taxa's morphologies showed that most of the morphospace was empty. Were seashells outside of these existing morphospaces too fragile in waves, too susceptible to predation, too constraining on internal organization, etc.? Since then, numerous scientists in theoretical morphology, morphometrics, biomechanics, and bioinformatics as well as artists and architects impressed by the aesthetics of these forms have explored these questions. Recently, economic perspectives of Pareto optimization has been used along with principal component analysis to explore the impact of natural selection of archetypal patterns, hybridization, and intermediate forms. Genomics has been struggling with a similar notion of nullomers. I will illustrate the power of D'Arcy Thompson's bioorthogonal transformations and Sewall Wright's adaptive landscapes in addressing these conundrums.

11:30-13:30 Invited Speakers Session, Chaired by Emanuele Serrelli

11:30-11:50 **Telmo Pievani** - Hierarchy Theories: A Comparison

We propose a taxonomy of hierarchy theories, or multilevel approaches to evolution, ordered by theoretical impact: 1) hierarchy of "units of selection" as replicators and interactors at each level; 2) double hierarchy of levels of evolutionary change, respectively in terms of genetic transmission



(genealogical hierarchy) and in terms of exchanges of matter and energy (ecological or economic hierarchy); 3) hierarchy of evolutionary systems over the long time of natural history and its major transitions. We try to figure out analogies and differences, and the efficacy of these different multilevel approaches in two fields: the unification of micro and macro-evolution (continuity between levels, autonomy and interdependence, reduction); the outcomes as predictive models to be applied in the parallels between biological and cultural evolution. We argue that the extension and revision of the Neo-Darwinian research program, labeled "Extended Synthesis", would take advantage of a double-hierarchy frame because it encompasses the plurality of causes and patterns (with their relative frequencies) that explain evolutionary phenomena today. The recent misleading controversy among kin selection vs. group selection theorists is a good case-study to test the efficacy of an integrated, multilevel, genealogical and ecological approach to evolution.

11:50-12:10 Folmer Bokma - Tempo and Mode in Evolution of Complex Organisms

Most evolutionary biologists appear to believe that populations and species are well adapted to their environment, as the result of continuous action of natural selection on all their traits. In complex organisms, however, many traits do not experience the outside environment: their environment consists of other traits. This implies that fitness is not determined exclusively by how well traits fit the external environment, but also by how well traits are adapted to each other. I will discuss whether the existence of co-adapted trait complexes determines the tempo and mode in evolution of their component traits, and discuss how we could distinguish the extrinsic and intrinsic components of fitness in phylogenetic and experimental studies.

12:10-12:30 Maurizio Casiraghi - Who are You? The Biological Entities in the 21st Century Biology

The identification and classification of living beings is a challenging issue in biology. Since Linnaeus we do have a hierarchical framework universally adopted. However, the currently biologists face several dualisms that needs further consideration: (1) species are the core level of classification, but natural selection is acting largely on individuals or other ranks rather than species. (2) Genome sequencing clearly evidenced that lateral gene transfer and transposition are common events in genome evolution; it seems clear that boundaries among species, at least at the genomic level, are not so strong. (3) Symbiosis deeply challenges the concept of individual; individuals are really evolving alone (i.e. is the real level on which selection acts?) or individuals are rather groups of living beings evolving as a single unit? (4) Since Linnaeus identification and classification of living beings are concurrent, but nowadays identification is separated from classification in many molecular approaches. (5) Is the biodiversity really represented by the three domains of life? Metagenomic approaches on different matrices (ranging from sea water to gut content) reveals the existence of a not negligible quote of biodiversity not clearly falling among Bacteria, Archaea or Eukarya. What is this "biological dark matter"? Is it one (or even more) new domain of life? The overall scenario is much more "fluid" than previously thought. In evolution, the dichotomy among the practical and theoretical contents of classification is well known. However, this is the time in which theoretical issues are deeply influencing practical applications of taxonomy.

12:30-12:50 André Levy - Group Selection and the Relevance of Hamilton's Inclusive Fitness

In 1964, Bill Hamilton proposed a new framework for thinking about fitness that could account for phenomena such as altruism and eusociality: inclusive fitness and kin selection. This framework had a profound effect on our understanding of the evolution of social behavior, particularly in haplodiploid systems such as ants and bees, and played a role in our thinking of the relative importance attributed to individual versus group selection. Recently, Martin Nowak, Ed Wilson – a significant popularizer of Hamilton's ideas – and others have argued that this approach has limitations and that the standard natural selection, based on a form of group selection, represents a simpler and superior approach. These works have re-launched a debate on the importance of group selection and the relevance of Hamilton's inclusive

fitness. We will evaluate the critiques to kin selection and whether it still constitutes a valid and useful approach.

12:50-13:10 **Jorge Carneiro** - The Emergence of Self and Other in Collective Systems: From the Vertebrate Immune System to Distributed Robotic Systems

Understanding how individuality and identity emerge in collective systems is one of the greatest challenges for natural, biological or human sciences alike. The immune system of the vertebrates has a remarkable capacity to eliminate invading microorganisms and extraneous transplanted tissues, while being tolerant to the body's tissues. Tolerance to body's tissues is not hardwired in the organism's genome. It is a developmental process arising from interactions between circulating lymphocytes. This developmental process is so robust and inconspicuous that one only notices it when it fails during so called autoimmune pathologies in which the lymphocytes orchestrate the destruction of organism's tissues. In my seminar I will provide a quantitative framework to understand the causal mechanism of this immunological proto-self. I will first discuss a simple mathematical model describing the ecoevolutionary dynamics of lymphocytes in vertebrates which explains tolerance to body tissue and immunity to invading pathogens. I will then discuss the application of this model to the design of multiagent robotic systems capable of distinguishing self from other.

15:15:45 Plenary Session Afternoon, Chaired by Emanuele Serrelli

15:00-15:45 **Daniel McShea** - The Evolution of "Insideness" and the Architecture of Purpose

The history of life reveals a trend in the depth of organisms, in the number of levels of things inside of things, parts inside wholes. The eukaryotic cell arose as an association of bacterial cells, cells inside a larger cell. Plants and animals arose as associations of eukaryotic cells, cells inside a multicellular individual. Finally, about 480 million years ago, colonies arose – individuals inside a social whole. Evidence suggests that these "major transitions" involve two sorts of change in organismal architecture: 1) Inside individuals diversify, driven partly by biology's First Law (e.g., in animals, an increase in cell types); and 2) inside individuals lose internal structure, becoming simpler even as they diversify. Thus, in the early stages of transitions, inside individuals are very similar and retain much of their primitive autonomy and complexity (e.g., polyps in a coral colony). In later stages, inside individuals are differentiated but lose much of their autonomy and complexity (e.g., ants in a colony). Speculating, these patterns may have implications for the emergence of apparent goal-directedness or purpose in evolution. Apparently purposeful entities are those that lie within larger wholes and are strongly directed by them but still partly free to act independently. The appearance of purposefulness may be a transitional feature of individuals, arising at a halfway point in major transitions, half way between the cumbersome complexity of solitary life and the empty simplicity of life under rigid social control, at the sweet spot between the anomie of individual freedom and the oppressive orderliness of advanced collectivism.

16:00-18:00 **Symposium 2**, Chaired by Cedric Boeckx

What Can an Extended Synthesis Do for Biolinguistics: On the Needs and Benefits of Evo-Devo-Logo

Organizers: Cedric Boeckx & Antonio Benitez Burraco

Taking as its starting point the range of options offered by an Extended Synthesis in biology as outlined in Pigliucci and Mueller (2010, MIT Press), this mini-symposium brings together researchers in biolinguistics in an attempt to distill a research program inspired by Evo-Devo to shed light on the biological foundation of the human language capacity, its evolution and development. After several decades in the shadows, the field of biolinguistics is making a comeback, in part due to the emergence of a 'new' biology. It is often said that, in sharp contrast to the overly adaptationist and genocentric framework provided by the Modern Synthesis (at the heart of Evolutionary Psychology), the conceptual pluralism made available by



the Extended Synthesis could lead to more productive investigations in the domains of language evolution and development. But such promises have yet to be articulated in detail, and the challenges ahead should also be made explicit. This is what this meeting intends to do. It will focus on a range of historical, conceptual, and empirical issues surrounding language and seek to address what evo-devo could do for biolinguistics: Does it lead to new questions? Does it offer new solutions? Does it go back to old insights? Does it force us to abandon traditional assumptions?

16:00-16:20 Antonio Benitez Burraco - When Evo-Devo Makes Comparative Biolinguistics Possible

Variation pervades language, but until recently comparative studies focused on the existence of different languages and different sociologically motivated dialects/idlects, ignoring the deeper layers of variation one finds at the brain levels, and also at the level of the genes regulating the development and functioning of this neural substrate. I argue that to understand this variation, it is necessary to study how developmental dynamics---at the heart of EvoDevo---canalize this variation, resulting in a Faculty of Language FL that is qualitatively equal in all human beings. Language disorders, which plausibly represent a breakdown of this Faculty, do not either manifest randomly, because canalization allows only some impaired, delayed, or deviant FLs to emerge.

16:20-16:40 Evelina Leivada - Reciprocal Causation, the Triple Helix, and What We Can Learn from EvoDevo about Language Genesis

This paper reconsiders the traditional distinction between Internal-language, viewed as the speaker-internal linguistic knowledge that reflects competence in a given language, and External-language; a socio-cultural construct that refers to similar idiolects from the perspective of an extended synthesis in biology. The distinction between the I- and E-language is often said to depend on adopting a biological vs. an environmental perspective. Exploring properties of recent language emergence in a variety of sign languages, I argue that certain Internal-language properties such as grammaticalization, complexity, and signifier/signified-consistency develop in response to environmental triggers. The environmentally driven emergence of core aspects of Internal-language casts doubt on the robustness of the Internal/External distinction and aligns with conclusions in biology regarding how the environment affects the adaptive development of organisms (cf. phenotypic plasticity).

16:40-17:00 Pedro Tiago Martins - Evo-Devo and Biolinguistics: Business as Usual?

Much like what happens with Evo-Devo, interest in biolinguistics has spawned a fair amount of activity in recent years. However, there seems to be some confusion about what really tells it apart from other approaches to the study of language as a faculty. Following Mueller's (2008) synthesis of the conceptual history of Evo-Devo, three questions might be asked about biolinguistics: i) does it have its own set of specific questions and research methods?; ii) does it solve problems that cannot be solved under other approaches?; iii) does it represent a significant change in the understanding of language development and evolution? This talk argues that answering these questions brings biolinguistics within the fold of an extended synthesis in biology.

17:00-17:20 Lluís Barceló i Coblijn - Alberch's Phenotypic Morpho-Space Applied to the Developmental Level of Language

Pere Alberch proposed a limited space for morphologies of organisms, predicting abrupt transitions between forms, and setting the stage for EvoDevo. In this talk I build on Balari and Lorenzo 2013 and apply Alberch's logic to shed light on the various degrees of complexity one finds at the level of phylogeny and ontogeny in language. Particular emphasis will be laid on experimental results using tools from Complex Systems science to highlight phase transitions in language development.

17:20-17:40 **Victor Longa & Cedric Boeckx** - Lennenber's Evo-Devo Program for Biolinguistics

Lenneberg's (1967) book *Biological Foundations of Language* is rightly regarded as a classic. Like all classics, it deserves to be re-read at regular intervals, not only to appreciate the success (and limitations) of previous attempts at a synthesis among fields, but also to learn things that we all too often forget. It is from this perspective that we go back to Lenneberg's seminal work. Not to stress its importance, for this is already well established in the literature, but rather to make the point that Lenneberg's conception of the biology of language was much more modern than some more current conceptions, and in fact much more modern than one ought to have expected from a work written in the 1960s, in the heyday of Modern Synthesis in biology. In this talk we show how Lenneberg's vision for Biolinguistics was really *Evo-Devo avant la lettre*.

17:40-18:00 **Cedric Boeckx** - Evo-Devo Theses for Language? Sure, But Which Ones?

In some recent papers, Chomsky has pursued analogies between the biolinguistic approach and Evo-Devo. In this talk, I show that some of these parallelisms are not the most fortunate ones that could have been chosen, and I offer a set of new parallelisms that, I argue, provide a more productive conceptual basis to understand the emergence and evolution of the language faculty. This leads me to discard Hauser, Chomsky and Fitch's Faculty of Language Broad/Narrow distinction, and to favor an approach in terms of epigenetic innovation.

16:00-18:00 Session 3, Chaired by Larissa Mendoza Straffon

16:00-16:20 **Haris Saslis-Lagoudakis** - Unifying Phylogenies With Traditional Knowledge to Harness the Potential of Biodiversity

The search for useful products from biodiversity has been closely linked to the study of traditional knowledge of utilization of natural resources. However, the absence of robust tools to optimize the selection of traditionally used biodiversity resources that are more likely to yield novel products has created controversy about the potential of this link. We introduce "phyloprediction", an interdisciplinary scientific field using organismal relationships to synthesize data from traditional knowledge of utilisation of bioresources, in order to inform the search for novel useful products from biodiversity. We apply this framework to test the potential of medicinal plant discovery from traditional knowledge. We reconstruct a genus-level molecular phylogenetic tree representing the 20,000 species found in the floras of three disparate biodiversity hotspots: Nepal, New Zealand, and the Cape of South Africa. We reveal significant clustering of the 1,500 traditionally used species, and provide a direct measure of the relatedness of the three medicinal floras. We demonstrate shared phylogenetic patterns across the floras: related plants from these regions are used to treat medical conditions in the same therapeutic areas. This finding strongly indicates independent discovery of plant efficacy, an interpretation corroborated by the presence of a significantly greater proportion of known bioactive species in these plant groups than in random samples. We conclude that phylogenetic cross-cultural comparisons can focus screening efforts on a subset of traditionally used plants that are richer in bioactive compounds, and could revitalize the use of traditional knowledge in the search of novel useful biodiversity resources. Similar approaches can be applied to various organisms to target a series of desired properties and find novel natural products, such as pesticides and other agrochemicals, specific crop traits, biofuels, as well as undesired properties, such as toxicity.

16:20-16:40 **Lukasz Lamza** - Aspects of Cosmic Evolution Relevant to Biology

The paper discusses the results of a cross-disciplinary statistical analysis of the integrated evolution of cosmological, physical, chemical, mineralogical, geological and biological phenomena. Certain common features of the cosmic "evolution" relevant for biology are discussed: (a) the rapid nature of macroevolutionary change, as demonstrated by early Big Bang chronology, shift in nucleosynthetic regimes in stars, chemical evolution of interstellar gas, geophysical changes in planetary systems, the punctual nature



of macro-evolutionary change etc.; (b) the co-dependence of microscale and macroscale events, whereby changes in physical or chemical composition influence the global behavior of macroscopic systems (e.g. astrophysical or geological), whose evolution induces further microscopic change etc. - the finest example of which is the reciprocal relationship of living organisms and ecosystems (both abiotic and biotic); (c) the co-evolution of matter on all scales, e.g. the parallel changes in nuclear, hydrodynamic and astrophysical phenomena in stellar evolution, the co-occurrence of major chemical, geological, atmospheric and biological changes on Earth, the coexistence of technological, political, artistic and scientific revolutions in human history etc. The aim of the paper is mainly to present the relevant facts and to briefly discuss their possible consequences for evolutionary theory.

16:40-17:00 Paniel Reyes Cardenas - Peirce's Evolutionary Cosmology and the Need to Avoid Circularity in Metaphysics

The explanation of laws is an important problem that probably impinges in the whole account of Peirce's Scholastic Realism. Christopher Hookway presents a trilemma that needs to be sorted out once we recognized that the axiom of "every event has a cause" it is not self-evident. Peirce's emphasis is in the 'why' questions of such trilemma: (i) Why are the laws of physics not different? (ii) Why are there any laws of nature at all? (iii) Why is the world governed by laws to the degree that it is? And the responses to these questions could not possibly be satisfactorily answered using the a purely logical conception of reality, because those concepts could have get us with one of the following responses: either these questions do not have an answer and then the axiom of cause must be rejected altogether, or the naturalistic answer will make laws seem circular (we have laws because we have laws). Peirce tries to avoid nominalism because laws need an explanation that enables prediction; so none of the previous responses to the trilemma seem to be fit for the task. An evolutionary theory of cosmology and categories is needed and convenient because Peirce wanted to account for the steady formation of habits, and the tendency for "habit-taking" gives a non-circular and non-nominalistic answer: our knowledge of laws it's an statistical fact and moreover, not only gives an answer, but permits the way of inquiry been carried further towards a more complete account of categories, and the universal application of those categories to all the spheres/universes of experience.

17:00-17:20 Thomas V. Pollet, Joshua M. Tybur & Willem E. Frankenhuis - What Can Cross-cultural Correlations Tell Us About Human Nature?

Many recent studies in evolutionary psychology and human behavioral ecology have tested hypotheses by examining correlations between group-level (e.g., state, country, continent) variables. Variables collected for each aggregation are often taken to be representative of the individuals present within them, and relationships between such variables are therefore presumed to reflect individual level processes. There are multiple reasons to exercise caution when extrapolating from the macro- to the individual-level. We describe four issues that present substantial obstacles to drawing inferences about individual level processes from analyses conducted at the aggregate level. These are (1) the ecological fallacy, whereby relationships observed at the aggregate level do not accurately represent individual level processes; (2) the use of unequal sample sizes, which gives undue weights to aggregations comprised of smaller number of individuals; (3) non-independence of data points, which violates the assumptions of inferential techniques associated with null hypothesis testing; (4) cross-cultural non-equivalence of measurement (differences in construct validity between groups). We provide examples of how each of these can create problems in the context of testing evolutionary hypotheses about human behavior.

17:20-17:40 Fabrizio Panebianco & Emanuele Serrelli - Eco-Phenotypic Physiologies: A New Kind of Modeling for Unifying Evolution, Ecology and Cultural Transmission

Mathematical modeling can ground communication and reciprocal enrichment among fields of knowledge whose domains are very different. We propose a new mathematical model applicable in biology, specified into ecology and evolutionary biology, and in cultural transmission studies, considered as a branch of

economics. Main inspiration for the model are some biological concepts we call “eco-phenotypic” such as development, plasticity, reaction norm, phenotypic heritability, epigenetics, and niche construction. “Physiology” is a core concept we introduce and translate differently in the biological and cultural domains. The model is ecological in that it aims at describing and studying organisms and populations that perform living, intended as a thermodynamic, matter-energy process concerning resources gathering, usage, and depletion in a spatiotemporal context with given characteristics, as well as with multiplication and space occupation. The model also supports evolution, intended as a dynamics including cumulative change in the features of unique organisms that are connected into breeding populations. The model is then applicable to the economics of cultural transmission in which individuals form their attitudes and patterns of behavior under a complex system of influences derived from their “cultural parents”, other members of the society, and the environment. On the side of biology, an innovative goal is to integrate in a single model all the eco-phenotypic concepts as well as both evolution and ecology. On the side of cultural transmission, eco-phenotypic modeling seems more appropriate in capturing some aspects of cultural systems which are modeled away in the earlier framework based on Mendelian population genetics.

17:40-18:00 **Susana Varela** - Social Learning of Sexual Preferences in *Drosophila* – A Stable Non-genetic Inheritance System?

Organisms require information to make decisions about fitness-affecting resources, such as mates. When choosing mates, animals may base their decisions on innate (mainly genetic) preferences and personal (non-genetic) experience, but also on the social learning (non-genetic social information) of the mating decisions of conspecifics. Mate-choice copying (MCC) by females is a type of social learning that may improve their accuracy in appraising male quality, allowing more adaptive decisions. Experimental studies have shown that MCC occurs in several species of fish, birds and mammals, including humans. In a series of three experiments, I report the first evidence that *Drosophila melanogaster*, an invertebrate species, is also capable of MCC to select mates. *Drosophila* female prospectors (1) increased their time in the attraction zones of the males that they previously observed mating with a model female; they (2) generalized the socially learned information about the copied males to the population of males sharing the same phenotype; and they (3) increased their reproductive investment with the copied males by laying more eggs after mating with them and by laying preferably in their territories. The results provide consistent evidence of the occurrence of MCC in *Drosophila melanogaster*, showing that it is more widespread in nature than previously thought. The results also reinforce the adaptive value of MCC in improving mate quality assessment, by highlighting, for the first time, its role in modulating female allocation decisions. This has consequences to male and female reproductive success and the key question now is how stable and significant this non-genetic inheritance system might be to the rate and direction of sexual selection. The complexity of *Drosophila* decision-making also suggests an unprecedented level of cognition in invertebrates. Here, I will present these results and discuss both the potential of social learning, via MCC, to evolution and the scientific relevance of this finding in an invertebrate species with a miniature brain, like *Drosophila melanogaster*.

16:00-18:00 Poster Session

André F. d'Almeida & Laura Desiré Di Paolo - Be Cool and Look at What Neighbors Do: Niche Construction, Coordination and Sociality in Spreading Inventions

Social transmission of relevant innovations, one of the principal reasons of human success, is relevant in most of primates' behaviors, even if through different learning strategies. Niche Construction perspective, supporting the idea that each individual has a significant role in creating innovations, and Social Learning strategies, understanding the position of each learner in diffusing new techniques, give us the right frame to model the widespread of innovative procedures in a social group. It has been demonstrated that group structure influences the spread of ideas and that primates coordinate their movements in experimental



contexts. We put forward a consideration on how coordination is a vital part of social learning and niche construction.

Christina Behme - Is Language Evolution Threatening Darwinism?

Recent years have seen severe criticism of evolution by natural selection from leading linguists (Chomsky) and philosophers of language (Fodor). These criticisms are based on the premise that evolutionary theorists are not trained linguists and hence unable to fully appreciate the nature of human language. In my paper I will show that many proposed accounts of language evolution are indeed unclear on some fundamental linguistic facts. However, this shortcoming does not imply that accounts based on natural selection are incapable, in principle, to explain language evolution. I argue that we do not need to resort to speculations involving highly implausible 'one-step' saltation as proposed by Chomsky and some of his supporters. What is needed instead is interdisciplinary work that clarifies (i) the nature of human language (the target of evolutionary explanation) and (ii) the biological limitations on the evolution. Given the wealth of work on (ii) I suggest that it is essential for linguists and philosophers interested in language evolution to familiarize themselves with this body of work and to provide criteria based on (i) that allow to test existing theories. Such a refocus would allow linguists to make an important contribution to language evolution debates.

Simon Carrignon - Why Apply Evolutionary Theory to Melodies

We want to show that applying Darwinian theories of evolution to study some social productions can be interesting for various reasons. In order to do so we focus on an experiment we made to measure variation during transmission of a particular kind of musical artifact : melodies. We believe that this kind of study can be valuable because of the following reasons : Following a musicological point of view, it could imply a new method and a new framework for interpretation and modelization of the evolution of melodies when they are orally transmitted in a population. In a context of a theory of "General Evolution" or "Universal Darwinism", it could present a case for which the evolutionary mechanisms acting on non-biological entities are easier to analyze than the usual entities used to illustrate social evolution (i.e. "Ideas", "Concept", "religions" ...). It would give new data to feed research which aim to find out what properties are needed to evolve complex structures. Finally, quantification and modelisation of such evolutionary mechanisms could result in alternative views in regards to studies of biological evolution. The nature of the objects in scope being totally different, it will force scientists to find methods to think about certain concepts which seem easy and already defined in biology (individual, transmission, etc...), thus allowing to throw light on problems often underestimated by biologists.

Laura Desirée Di Paolo, Diego Antonio De Simone & Fabio Di Vincenzo - Learning Creativity: Precision and Flexibility in Social Learning

Social Learning is the apprenticeship of relevant information about foraging techniques and public conducts, that learners take from the context of conspecifics. Without mentioning differences in modalities, learning from the context makes individuals able to efficiently adapt themselves to the environment. This one, built socially by daily activities, is also a selective environment for learners: the good ones survive better into their social context. The constant use of learning strategies, modifying the environment, puts both learners and learning under selection. Consequently, evolution occurs in two directions: on the learning processes and on the apprentices. This process is even more crucial in a cultural scenario, where culture is an outcome of individuals' activities and also learners' selective environment: our aim is to underline how humans are still under biological selection, highlighting that the cognitive correlates, which are pre-requirements of human-like culture, are transmitted and improved by social learning to maximize adaptiveness.

Olga Filatova - Is Killer Whale Dialect Evolution Random?

Killer whale is among the few species in which cultural change accumulates over many generations, leading to the cumulative cultural evolution. Killer whales have group-specific vocal repertoires of stereotyped calls with complex structure, which are thought to be learned rather than being genetically coded. It is supposed that divergence between vocal repertoires of sister pods increase gradually over time due to random learning mistakes and innovations. In this case, the similarity of calls must be correlated with pod relatedness and, consequently, with each other. In this study we tested this prediction by comparing the patterns of call similarity between different matriline of resident killer whales from Eastern Kamchatka. We calculated the similarity of seven components from three call types across 14 matriline. In contrast with the theoretical predictions, units formed different clusters on the dendrograms made by different calls and even by different components of the same call. Similarity patterns were significantly correlated only in two of 21 possible pair-wise comparisons of distance matrices. We suggest three possible explanations of this phenomena. First, it is possible that different call components change in time with different speed and/or in different directions. Second, horizontal cultural transmission of call features may occur between matriline. Third, the lack of agreement between similarity patterns of different components may be the result of some constraints of call structure. In future studies we suggest to check if the similarity patterns of different call features are correlated to prevent errors in estimates of similarity of stereotyped calls.

Daniel Garcia-Rivero - Unraveling Diversity in Archaeology in the Light of Evolution

The systematic application of Darwinian evolutionary theory in archaeology is recent. Particularly in the field of taxonomy, the use of systematic methods based on evolutionary relationships, inheritance principles and the transmission of information barely goes back two decades, and so several key points remain to be thought through. The aim of this presentation is to deal with some of these issues both theoretically and empirically through the analysis of archaeological data, by means of sorting methods based on distance (principal coordinates, correspondence, and network analysis) and based on genealogy (parsimony analysis), as well as through resampling methods (bootstrap analysis). We will thus approach the essentialism/realism dichotomy and the different ways of deriving taxonomic units according to the scales and objectives of the studies; the degree of hierarchical inclusion of archaeological traits and systems to elucidate the main levels and units related to transmission mechanisms and selection; and the influence of different intensities of vertical and horizontal transferences of cultural information. The empirical case study that we will use is a large dataset of symbolic representations made on stone slabs by the populations of the Southwest of the Iberian Peninsula in the Late Neolithic and Chalcolithic I (3250-2700 BC), used as grave goods mainly in megalithic burials and known as 'placas do xisto' by the Portuguese academy and as 'engraved slate plaques' in the Anglo-American literature.

Elena Pagni - Life Phenomena in Phenomenology, Biology and Mathematics

In my paper I will focus on Merleau-Ponty and Patočka's phenomenological readings of the living body, by taking into account those topics that can be extended and compared to some current scientific discussions involved in sketching a pertinent theory of living bodies. My primary attempt is to present a new epistemological view of the living body, in relation to which both philosophy and science could meet. Besides phenomenology, also in science the idea of a new epistemological paradigm of the living body is ever more emerging; this may allow us to understand the body as the fundament of our cognition and scientific frameworks as related to biological development.

Tiago Pereira da Silva - WingPatterns: A Knowledge Base for Butterfly Wings Morphology

The morphological diversity that can be observed on butterfly wings is an excellent example of phenotypic variation. Several butterfly species are becoming established as laboratory model organisms, and a number of natural mutants has already been identified and described. Large image datasets are now potentially available, allowing the detailed characterization of the wild type and mutant phenotypes



observed within a species. We are developing a set of tools named WingPatterns, supported by a structured online database including gene expression (in larval wing discs and pupal wings) and adult wing images. Unlike other model organisms, there are still no such collaborative tools widely available to the butterfly research community. Associated with the database, we are also developing automated image analysis algorithms and data-mining techniques. The WingPatterns knowledge base combines in the same platform the experimental image collections (with the respective associated metadata) and the quantitative analysis results regarding gene expression patterns in embryos, adult pigmentation, vein patterning and wing shape, among other morphometric parameters. Together, these tools enable the definition of objective quantitative classification systems for the described wild types, seasonal variants, and mutant phenotypes, and may also contribute to uncover new relations among the quantified parameters that were previously very hard to address.

Carl Henning Reschke - Strategy and Innovation as Applied Evolutionary Learning in 'Cognitive Landscapes' Strategy, entrepreneurship and innovation involve interpretation and learning to develop and adapt an organization's actions and reactions to 'environmental' challenges. For creative, innovative actors this presents the challenge to overcome traditional, historically grown experience, which are usually systematized in hierarchically organized mental representations of situations. The paper combines concepts from the social and biological sciences to find a common micro-level basis for genetic learning in strategy and innovation as systematization of information in hierarchically organized, modular 'mental systems'. Conceptually, it is based upon a 'epistemological' interpretation of (economic) evolution as learning process that accumulates information and transforms it into 'knowledge' via codification and structural organization of this knowledge. To do so, we refer systemic evolutionary theory and develop a micro-level perspective on genetic learning in actors and develop linkages to the constructs of organizational capabilities and routines.

Diana Soeiro - On Pattern Language: Morphology, Morphogenesis and Sustainability

The ability to establish a pattern is essential to predict and foresee evolution. In that sense: how does our urban built environment relate with our evolutionary biological pattern? Is there a relation between both? Can it be useful to predict how does that relation evolve? The surrounding environment shapes us but, also, we are the ones shaping our environment — nowadays, by gradually making it, predominantly, an urban one. Christopher Alexander (b. 1946), Austrian architect and theorist, decided to take the study of urban morphology as the study of the evolution of a body structure, similar to a living organism. In his book "A Pattern Language: Towns, Buildings, Construction" (1977), he has identified 253 patterns, used throughout times to solve urban morphology related problems. In his four-volumes work, "The Nature of Order: An Essay on the Art of Building and the Nature of the Universe" (2004) he has claimed that patterns are not enough to describe urban morphology dynamics and that we need a morphogenetic understanding of the formation of the built environment. In order to better grasp the growth of cities, and having worked with mathematician Nikos A. Salingaros, Alexander claims the use of fractal theory and biology - hence his name is associated with the "Morphogenetic School". We will frame Alexander's approach with Goethe's concept of morphology and Biomimicry, a contemporary approach on urbanism and architecture. It is relevant to predict how our surrounding built environment and our own body relate, in order to promote a sustainable evolution.

Gabi Lipede - The End of Aesthetic Evolution: Toward a Macroevolutionary Model of Adaptive and Null Intersexual Selection Mechanisms

In this paper I will show that the projected long-term effects of adaptive intersexual selection mechanisms, expressed in terms of constrained evolvability within and between populations, are structurally homologous to the projected evolutionary trends which emerge from the late Collin Martindale's most recent model of the psychodynamics of creative ideation and aesthetic reception (Martindale, 1990, 2009). Martindale anticipates the end of art. He conceives this broadly in terms of an evolutionary

threshold beyond which the production of new aesthetic variants will no longer be able to keep pace with the aesthetic mandate of "meaningfulness" on which positive, hedonic evaluations of a given artwork depend. This Hegelian tragedy of sorts (Martindale, 2009), which pits art's relative novelty against its communicative value, receives indirect support from the application of the theory of costly signaling to art and aesthetics insofar as costly signals tend toward the elimination of aesthetic variants in favor of communicative value. However, I will argue that the observations Martindale evokes in his argument for an upcoming "end of art" can be understood differently, in terms of the immanent vulnerability of human and biotic art worlds to the establishment of the LK-null mechanism (Prum, 2010) and, in the human art world, of the consequent inauguration of a new era of intrinsic, coevolutionary aesthetic evolution.



Wednesday, May 29th

9:30-11:00 Plenary Sessions Morning, Chaired by Luís Correia

9:30-10:15 **Richard A. Watson** - The Evolution of Symbiotic Partnerships and the Algorithmic Principles underlying the Major Evolutionary Transitions

The evolution of symbiotic partnerships has had dramatic consequences for evolutionary history and a significant role in the origins of biological complexity. In some cases the evolution of such partnerships has been instrumental in the major evolutionary transitions by creating new selective units, e.g., via the vertical transmission of a symbiont. Rather than treating the unit of selection as a fixed parameter, the evolution of such symbiotic partnerships requires that we treat the unit of selection as a dynamic variable, affected by the evolving relationships between species. Moreover, the selective pressures on those relationships are in turn determined by their ecological context. These interactions are not easily accommodated in existing ecological or evolutionary models. Here we begin to explore the interaction of symbiotic partnerships and ecological dynamics given individual traits that change the unit of selection. We find that, under some ecological conditions, the potentially complex eco-evolutionary interactions involved can be understood using simple principles of associative learning that are well understood in the context of neural networks – thus, in a manner analogous to 'neurons that fire together wire together' here species that assort together (i.e., co-occur at high density in the ecological dynamics) 'wire' together via evolved partnerships. This is essentially a very simple positive feedback principle acting on inter-specific relationships, but the algorithmic capabilities of such a system, involving processes that dynamically restructure the unit of selection, are significantly different from those with fixed units of selection. In fact, the ecosystem of evolving partnerships collectively implements a quite sophisticated distributed optimization algorithm that discovers and exploits implicit modularity in the network of fitness dependencies between species. This suggests that there are general organizational principles that can help us understand how ecological and evolutionary dynamics interact – and specifically, interact in a manner that systematically predisposes the formation of new evolutionary units that are adaptively significant at a higher level of biological organization. Far from being aberrant curious in an otherwise exclusively gradual picture of evolutionary change, this suggests that the major transitions in evolution may admit systematic algorithmic descriptions that expand our understanding of evolutionary adaptive processes into a multi-scale framework.

10:15-11:00 **Tal Dagan** - Networks Approach to Evolutionary Dynamics of Genomes and Languages

Phylogenomics is aimed at studying functional and evolutionary aspects of genome biology using phylogenetic analysis of whole genomes. Current approaches to genome phylogenies are commonly founded in terms of phylogenetic trees. However, several evolutionary processes are non tree-like in nature, including recombination and lateral gene transfer (LGT). Phylogenomic networks are a special type of phylogenetic networks reconstructed from fully sequenced genomes. The network model, comprising genomes connected by pairwise evolutionary relations, enables the reconstruction of both vertical and LGT events. Modeling genome evolution in the form of a network enables the use of an extensive toolbox developed for network research. The structural properties of phylogenomic networks open up fundamentally new insights into genome evolution. Genome evolution has a lot in common with language evolution. Both processes entail evolving elements – genes or words – that are inherited from ancestors to their descendants. The parallels between biological and linguistic evolution were evident both to Charles Darwin, who briefly addressed the topic of language evolution in *The Origin of Species*, and to the linguist August Schleicher, who in an open letter to Ernst Haeckel discussed the similarities between language classification and species evolution. Charles Darwin pictured the history of life as a tree. However, genes can be acquired laterally (not by inheritance), while words can be borrowed between different languages.

Phylogenetic trees cannot be used to model such lateral transfers. Phylogenomic networks may offer an alternative model.

11:30-13:30 Invited Speakers Session, Chaired by Luís Correia

11:30-11:50 Andreas Bohn - Integrative Ecoinformatics of Phototrophic Biofilms: Joining Perspectives on the Dynamics of Cities of Microbes

Biofilms are surface-attached microbial communities, encased in a matrix of extracellular polymeric substances. In natural environments this sessile form of microbial existence is generally dominant over the detached, planktonic form. Understanding the long-term dynamics of these communities requires the integration of knowledge from many heterogeneous, complementary sources. Developing predictive models based on the outcome of i) laboratory studies of molecular regulatory networks, addressing the "how" of microbial behavior, and ii) ecological and biosociological studies of species competition, giving clues to the "why" of the observed community-level processes, involves a significant amount of "science friction" and represents a fundamental challenge to emerging discipline of ecological informatics.

In this context I will present our work related to a former European project on phototrophic biofilms, microbial communities with a significant presence of photosynthesizing organisms. I will present the implementation of a database prototype for semantic data management, the integration of several biostatistical studies in a qualitative model and the quantitative minimal description of the often observed boom-and-bust growth dynamics. Considering these different tools as nodes in a knowledge network, I will discuss the role of semantic annotations and metadata as possible links between the nodes and their capacity to catalyze the evolution of systems-level knowledge in biofilm research.

11:50-12:10 Claudine Chaouiya - The Logic of Gene Regulatory Networks

Over the last decade, great progresses have been made to elucidate intricate regulatory networks that orchestrate core cellular processes. Although structural analysis provides valuable insights, it is not enough to fully understand how these networks control cell behaviors depending on external environment. In this context, logical modeling proved useful to convey qualitative, dynamical analysis of regulatory networks. I will briefly present the mathematical formalism and discuss current challenges for analyzing the dynamical properties of large regulatory networks. I will then illustrate how simple regulatory modules behave differently, depending on the regulatory functions that define, for each gene, the contributions from its regulators. I will particularly focus on regulatory circuits known to play a crucial role in the dynamics, and prove that variation in regulatory functions may greatly impact crucial properties related to multi-stability and sustained oscillations.

12:10-12:30 Margarida Matos - The Role of Selection, Chance and History during Adaptation to a Novel Environment

Experimental Evolution is Evolutionary Biology in its most empirical sense, as it allows the direct characterization of micro-evolutionary patterns and processes. It is thus a powerful tool to address essential evolutionary questions such as: How fast do populations adapt to a novel environment? What constrains adaptive evolution? What is the role of History, Chance and Selection during local adaptation? For almost two decades now my team has been studying the evolutionary dynamics of laboratory populations of *Drosophila subobscura* derived from repeated collections in the wild. The rationale of our studies is that the lab is just a novel environment to which populations may adapt, and as such the analysis of how populations change through time since foundation contributes to a general characterization of evolutionary patterns and processes during adaptive evolution. We show that populations are able to adapt to the novel environment, though evolutionary contingencies due to founder effects and genetic drift during the earliest generations affect the details of the adaptive patterns. We also found that selection is able to overcome the signature of History in populations highly differentiated at the start of



colonization. Future studies testing for repeatability of the later findings will allow the study of how much History interacts with Chance events during Adaptation.

12:30-12:50 Sven Steinmo - Institutional Change as an Evolutionary Process

I argue that institutional change can be understood as an evolutionary process. Whereas it is often suggested that evolutionary theories do not apply to human history or institutions because of our conscious capacities and intelligence, I submit that human's advanced cognitive capacities are key to understanding why human institutions can evolve so quickly. Human beings creative intelligence and proclivity to misunderstand or misinterpret are the key sources of variation in this model. Human's ability to learn from one another is the mechanism for selection. Finally, we build institutions in order to reproduce and reinforce the social rules selected.

12:50-12:13:10 Luis Mateus Rocha - Turing's Tape, Biosemiotics, and the Cybernetics of Biocomplexity

Many have argued that life and open-ended evolution depend on a semiotic closure, or a complex interplay, between separated symbolic information and molecular dynamics components. Alan Turing also showed that the separation between data and program is essential to achieve universal computation. Many, at least since John Von Neumann, have argued that this separation between information/data and dynamics/program is an evolutionary system that is more general than computation, and indeed defines life as we know it. In this talk I will review this idea and argue that many important systems and events in our evolutionary history constitute a re-discovery of this evolutionary principle of organization. In particular, I will discuss how it manifested in genomic organization, vertebrate immune complexity, human cognition and culture.

15:00-15:45 Plenary Session Afternoon, Chaired by Luís Correia

15:00-15:45 Carl Knappett - Using Network Thinking to Understand Transmission and Innovation in Ancient Societies

Are biological models suitable for understanding socio-cultural evolution? While they may have introduced some much-needed methodological rigor into humanities research, and represent an important area of thoroughgoing interdisciplinarity, they fail to capture some key aspects of cultural transmission. In particular, innovations that are combinatorial, or require some depth of learning for adoption, seem largely intransigent to biological models. As innovations of this kind — such as the spread of new technologies like bronze metallurgy or the potter's wheel — are key features of prehistoric social change, we should work on developing models that can capture the dynamics of their horizontal and vertical transmission. I shall argue for a multi-scale cognitive model for innovation that has two central tenets. The first is that learning is critical in innovation, and plays out at three basic levels: that of the individual who must learn the technique, that of the community of practice in which individual learning is invariably embedded, and that of inter-community interactions which allow for innovations to spread from one region to another. The second is that, as a cognitive, decision-making process, it involves a complex interplay of information, data and knowledge.

16:00-17:40 Session 4, Chaired by André Levy

16:00-16:20 Filipa Alves - Modeling and Classifying Variation in Butterfly Wings

The morphological diversity that can be observed on butterfly wings is an excellent example of phenotypic variation. Several butterfly species are becoming established as laboratory model organisms, and a number of natural mutants has already been identified and described. We are using a theoretical modeling approach to study the interplay between the biophysical mechanisms and the gene regulatory networks underlying wing morphology and pigmentation patterning. We are especially interested in how this

interplay both generates and constrains the phenotypic variation observed within and among species. Our theoretical models are mainly focused on formulating organized hypotheses and making testable predictions. The gene regulatory networks are defined by partial differential equations and the spatial gene expression patterns are represented in 2D using finite differences methods. By evaluating the model's results agreement with the experimental data, we are testing different possible network topologies and candidate genes. Furthermore, as this model calibration and validation is strongly dependent on quantifying and estimating the biological parameters involved, we are also developing image analysis tools and databases, and implementing parameter optimization algorithms. Our results provide testable hypotheses for how the observed variation on the wing morphology and pigmentation patterns may depend on subtle changes on specific biophysical parameters, opening interesting perspectives to understand the evolution of these mechanisms.

16:20-16:40 Magnus Magnusson - Structural and Functional Analogies Between Real-time Patterns in Neuronal, Animal and Human Interactions and DNA Sequences

Real-time event-streams in human and animal behavior pose a challenge no less than the detection of patterns in DNA and the detection of hidden interaction patterns presupposes adequate hypotheses concerning the inherent structure. The T-system is a set of related concepts for the description and detection of often hidden patterns within continuous real-time streams of numerous kinds of behavioral and/or environmental events. A special interval relationship, relating a pair of 1-dimensional point series underlies the definition and detection of the central t-pattern type, a particular statistical pseudo-fractal. T-patterns characterized simultaneously by order and intervals between events. They are often invisible even to trained observers under ideal conditions, but the especially developed Theme software (Magnusson, 1996, 2000) has allowed the detection and analysis of complex t-patterns in many kinds of human, animal, and neuronal interactions (Nicol, Magnusson & Kendrick, 2005) and on DNA molecules. Syntactic structure and symmetry come increasingly into focus. While centered on the repeated, temporally and sequentially constrained self-similar t-patterns, the T-system also involves non-sequential (T-packets) and non-repeating (T-composition) patterns types, which are also defined and illustrated. The detection algorithm uses bottom-up binary-tree detection of specially defined critical interval relationships between (1-D) point series to connect primitives and/or patterns into higher patterns. An evolution method based on pattern completeness competition is used to evolve maximally complete versions of underlying patterns. Striking structural and functional analogies between t-patterns in DNA and social behavior have been noticed and evoked among other in an essay on the evolution of religious behavior (Magnusson, 2003, 2004, 2005, 2006, 2009).

16:40-17:00 Emanuele Serrelli - Integration Between Ecological and Genealogical Patterns: Where Are We?

Genealogical patterns are those that can be followed and fully captured by following 'bloodlines', related lineages, and their common ancestry. Ecological patterns instead can be captured by following physical and chemical flows and cycles. Ecology is the science of ecological patterns, commonly divided into two fields: community ecology, studying the composition and assembly of populations, communities, and metacommunities; and ecosystem science, studying organisms and their environment as parts of an interactive system with 'functions' such as primary productivity, food chain efficiency, and decomposition. Genealogy and its patterns such as the neo-Darwinian natural selection, drift, speciation, and phylogeny were inscribed the powerful framework of the Modern Synthesis in evolutionary biology. As a side consequence, ecological assemblies were seen as aggregations among genealogies, characterized by secondary, derived patterns: they are the 'stage' for the evolutionary play, summarized at best as 'selective pressures'. Evolutionary ecology, 'macroevolutionary consonance', the dual hierarchy theory, thermodynamic-informational evolutionary theories, and niche construction theory are some of the 20th Century pleas and attempts towards a science that better integrates ecological and genealogical patterns.



The talk reviews and assesses such proposals, gives a glance to the present achievements, and outlines some future challenges.

17:00-17:20 Haris Saslis-Lagoudakis & Julie Hawkins - Medicinal Plant Use in Nepal Is More Strongly Influenced by Environment than Ethnicity

Traditional herbal medicine is important in many human societies, and approximately 60-80% of the world's population depends on traditional healthcare. Here we describe research investigating horizontal and vertical evolution in cultural adoption of medicinal plants, using Nepalese traditional medicine as a case study. We investigated the influence of ethnicity on the medicinal plants selected and used by people belonging to 12 ethnic groups in Nepal. The influence of ethnicity is realized through vertical transmission, and more closely related ethnic groups would share more medicinal plant use if vertical transmission predominates. Conversely, ethnic groups that are nearest geographical neighbors have the opportunity to harvest the same plants from their local environment, or to share traditional knowledge, so geographical proximity could shape medicinal floras. The similarities of the 12 medicinal floras were calculated, as were the similarities of the whole local floras that the 12 ethnic groups are exposed to. Using traditional taxonomic and phylogenetic approaches, we reveal a positive and strongly significant correlation between medicinal and total floras, and a positive but insignificant correlation between linguistic relatedness and medicinal floras. Medicinal floras converge in similar environments, and do not reflect linguistic relationships. This finding is counter to many which have shown that ancestry is more influential than geography for cultural traits, and could be attributed to horizontal transfer of cultural plant use or to independent discovery of the same plant groups for medicinal purpose in the local environment.

17:20-17:40 Susanna Manrubia & José A. Cuesta - Evolution on Genotype Networks Leads to Phenotypic Entrapment

The relationship between genotype and phenotype is many-to-many. In particular, genotypes encoding a particular phenotype form vast, connected networks that often span the whole space of possible genotypes. Regarding their topological properties, genotype networks are highly heterogeneous in degree and, in most known cases, assortative (as in RNA and proteins). These properties have important effects on the dynamics of populations evolving on genotype networks. In this contribution we demonstrate that, as time elapses, the probability that a population visits nodes of increasingly higher degree augments. In evolutionary terms, this implies that the probability that a population changes phenotype depends in a non-trivial way on the time the population has maintained its current phenotype. We derive a mathematical theory that explicitly quantifies this phenotypic entrapment and explicitly shows the dependence on measurable quantities such as network size, mutation rate, or fitness of the phenotype. Numerical simulations of dynamics on RNA genotype networks are used to illustrate the phenomenon and the predictive power of the theory.

16:00-17:40 Session 5, Chaired by Matthis Krischel

16:00-16:20 Matthis Krischel - The Many Faces of Konstantin Mereschkowski: A Contribution to the Historiography of Symbiogenesis

In this contribution, I aim to present an overview of the biographical works and sketches concerned with the life and work of the Russian biologist Konstantin Mereschkowski (1855-1921). I will show how Mereschkowski rose to fame as a historical figure with the rise of symbiogenesis as a field of biological research from the 1970s onward. Emphasis will be placed on different biographical approaches used by biologists writing the history of their own discipline and later contributions by cultural historians.

16:20-16:40 **Marianna Teräväinen** - Tracking Cultural Evolution With Cladistics: The Medicinal Use of Invertebrates in Northern Vietnam

The evolution of the use of invertebrate-based remedies among ethnic minorities in northern Vietnam is analyzed. Local ethnic groups rely on self-made natural medicines, including ones made from insects, arachnids, snails, and earthworms. Northern Vietnam is a region where phylogenetic or vertically branching transmission is evident by the numerous ethnic groups having retained their unique identities in the form of dialects, clothing and adornment styles. However, their close geographic proximity and equal living standards are thought to contribute to the sharing of knowledge, leading to ethnogenetic or horizontal blending of innovations. The evolution of this medicinal practice and the contributions of the two modes of transmission are examined.

16:40-17:00 **Nicholas Tebben & John Waterman** - Epistemic Free Riders and Reasons to Trust Testimony

A traditional problem facing epistemology is how to give a naturalistic account of the normative force of epistemic terms of evaluation like “rational” and “irrational.” We argue that the function of these terms is to express an evolved practice of encouraging and discouraging epistemic behaviors. We first present an exchange-based account of testimony, where individuals trade information with other members in an epistemic group. We then show that the exchange-based account of testimony would be evolutionarily useful, but vulnerable to free-riders. We then argue that an expressive account of epistemic terms of evaluation, combined with an account of epistemic reputation, not only resolves the free-rider problem, but also explains the normative authority of epistemic evaluations as markers of the exchange value of testimony. We then conclude that the ultimate authority of epistemic terms of evaluation derives from their expression of an efficient equilibrium in the practice of exchanging testimony. A virtue of this view is that it offers an account of the basis of rational authority by grounding it in practical concerns.

17:00-17:20 **Marco Pina** - Behavioral Epigenetics: A Biomedical and Epistemological Assessment

The young discipline of Behavioral Epigenetics (BE) aims at elucidating to what extent epigenetic mechanisms influence and determine behavior in animals and humans. Although the seminal works of British biologist C.H. Waddington on the epigenotype and epigenetics already date from the late 1930s, it wasn't until very recently that the study of the role of epigenetic mechanisms in behavior started to gather some attention. Epigenetic mechanisms can be described as the complex set of cellular devices that participate in the regulation of gene expression. They are thought not to act independently, but to participate in a complex web of interactions and feedbacks where the genome and environmental factors (such as nutrients, toxins, emotional states and other psychological factors) also step in.

In the field of behavioral research, in the 2000s, scientists like Meaney and Szyf have studied in rats how maternal care affects the epigenomic regulation of gene expression leading to different stress responses of the offspring. Similar data have accumulated over time suggesting what seems to be an association between (social) environment, epigenome, genome and the development of specific behavioral traits -- including illness. In fact, in human psychology, as Murgatroyd and Spengler (2011) write, “understanding how early life experiences can give rise to lasting epigenetic marks conferring increased risk for mental disorders, how they are maintained and how they could be reversed, is increasingly becoming a focus of modern psychiatry”.

In spite of all the limitations it faces, could BE work as a connector between biology and psychology, thus allowing for a solid integrated approach to the study and understanding of psychological development?

17:20-17:40 [Cancelled] **Juan F. Poyatos** - Plasticity Facilitates Sustainable Growth in the Commons

In the commons, communities whose growth depends on public goods, individuals often rely on surprisingly simple strategies, or heuristics, to decide whether to contribute to the shared resource (at risk of exploitation by free-riders). Although this appears a limitation, I will discuss in this talk how four heuristics lead to sustainable growth when exploiting specific ecological constraints. The two simplest ones—contribute permanently or switch stochastically between contributing or not—are first shown to



bring sustainability when the public good efficiently promotes growth. If efficiency declines and the commons is structured in small groups, the most effective strategy resides in contributing only when a majority of individuals are also contributors.

In contrast, when group size becomes large, the most effective behavior follows a minimal-effort rule: contribute only when it is strictly necessary. Both plastic strategies are observed in natural scenarios across scales what present them as relevant social motifs for the sustainable management of public goods. Overall, these findings stress that sustainability in the commons should be understood as the appropriate integration of ecological dynamics and individual information-processing abilities.

16:00-17:40 Session 6, Chaired by Luís Borda-de-Água

16:00-16:20 Luís Borda-de-Água & Stephen Hubbell - The Relative Abundance of Languages: Neutral and Non-neutral Dynamics

Credible estimates predict that upwards of 90% of the nearly 7,000 languages could go extinct this century, a prospect with profound cultural, socioeconomic, and political ramifications. Despite its importance, we still have little predictive theory for language dynamics and richness. Several hypotheses invoke cultural and environmental mechanisms to explain the number of languages in language families and different geographic regions of the world. More critical to the language extinction problem, however, is to understand the dynamics of the number of speakers of languages, the dynamics of language abundance distributions (LADs). Here we show that LADs can be understood as an equilibrium or disequilibrium between stochastic rates of origination and extinction of languages. Many regional LADs are very similar to the bell-shaped distributions of relative species abundance predicted by neutral theory in ecology. The hypothesis of neutral language dynamics yields a particularly good fit in Africa, Papua New Guinea, Laos, and many island archipelagos of Polynesia. However, neutral theory does not fit some regional LADs, which can be explained if the number of speakers has grown systematically faster in some languages than others, due to cultural factors and other non-neutral processes. The LADs for Asian countries illustrate non-neutral processes in language dynamics. Only two LADs, for Australia and the United States, deviate from a bell-shaped pattern. These deviations are due to the documented higher, non-equilibrium extinction rates of low-abundance languages in these countries.

16:20-16:40 Outi Vesakoski & Terhi Honkola - Micro- and Macroeolution of Languages: Finnish Dialects and Uralic Languages Revised

In the BEDLAN project (Biological Evolution and Diversification of Languages) we study language diversification in the framework of biological micro- and macroevolution. In the macroevolutionary approach we apply different speciation models (Red Queen, Court Jester) to the evolutionary pattern of Uralic languages. The divergence time estimates are compared to studies in historical linguistics. We suggest that climate fluctuation may be the primary reason for prehistorical language speciation - by triggering cultural alterations and migrations. The language speciation is studied with basic vocabulary and phylogenetic tree models, which are further compared with network models and “less-basic-vocabulary” which allow for illustrating also secondary contacts in the language family history. We put forward an analogy between microevolution of language and divergence of biological populations and test this by analyzing an extensive, 90 years old data of Finnish dialects with population genetic methods. The data behaves as frequency data and allows measuring linguistic variation between dialectal areas (dialects = populations derived from Structure software and K-means cluster, which corresponds amazingly well with earlier results in Finnish dialectology) with values based on F_{st} and heterozygosity calculations. Also e.g. linguistic diversity index (Shannon-Wiener diversity index) is calculated for municipalities (corresponding here to individuals in biological data). Finally, we adopt landscape genetics approach and exploit GIS-tools to compare linguistic variation with abiotic, biotic and cultural variation to locate the factors behind

linguistic barriers or diversity. Next phase is to add more depth to the studies and compare the linguistic variation to that of genetic and (pre)historic.

16:40-17:00 Erich Round - Three Principles for Improved Linguistic Datasets

Applications of new (bio)statistical methods to linguistic data have sparked debate over their detection of vertical versus horizontal transmission, and the merits of various computational methods. However, little research has considered how linguistic datasets should be designed. Statistical methods place stringent constraints on input data, often requiring variables to be independent. Yet in linguistics, discipline-internal factors have historically favored analytic units (such as “phonemes”) whose logical parts are highly interdependent. Unchecked, these dependencies carry over into computational datasets, degrading or invalidating statistical results. We illustrate this concern using a published study of 121 languages × 160 characters (Reesink et al. 2009). We then propose the following methodological principles: 1. “Use micro characters rather than macro”. Though well established in linguistic theory, ‘macro’ characters, such as [A] below, effectively summarize the states of multiple, finer-grained ‘micro’ characters, such as [B] and [C], among others. Using macro states is needlessly lossy, and can be misrepresentative, as languages can share a macro state despite none of the underlying micro states matching. [A] Are there prenasalised stops? [B] Does nasal+stop appear word initially? [C] Does [nasal+stop] contrast with [nasal]+[stop]? 2. “Identify and minimize dependencies”. Identifying sets of characters that are logically dependent on shared third factors presents a particular challenge, and represents a priority for research. 3. “Track remaining dependencies”, to allow sampling of multiple subsets of reliably independent data. The potential of new methods in evolutionary linguistics will only be realized once such issues of data design are attended to.

17:00-17:20 Thomas Dougherty - A Theoretical Look at Characters in Phylolinguistics as Applied to the Japonic Languages

The only widely accepted method of demonstrating how languages are related to one another is through shared innovations—that is, changes unique to a group of languages since their divergence from a common ancestor (Campbell 2004:190-191). Historical linguistics has generally taken a holistic approach, utilizing innovative changes in the phonology (the sounds), morphology (the structure of individual words), and syntax (the arrangement of words with one another in phrases and sentences) of the languages in question (Campbell 2004:196). In supplement to the comparative method, new techniques using computational phylogenetics have also emerged (e.g., Warnow et al. 1995, Gray and Atkinson 2003). These approaches have generally relied on innovations within a set of so-called basic vocabulary, on the assumption that it is an adequate proxy of linguistic evolution. In recent discussion on these methods, Donohue et al. (2012) argue that by using only lexical items, these computational methods do not take into consideration an adequate number of innovations to accurately subgroup languages (Donohue et al. 2012:541-542). In this regard, we agree with Donohue et al., and, as a case study, we will re-analyze the data and conclusions of Lee and Hasegawa (2011)’s phylogenetic reconstruction of Japonic. Based on incongruities with previous reconstructions, as well as phonological, morphological, and syntactic, and philological evidence, we will analyze—qualitatively—the source of errors in Lee and Hasegawa (2011)’s reconstruction, and suggest possible solutions in terms of character choices, and use this as a springboard to discuss what kinds of characters are appropriate proxies for modeling linguistic evolution.

17:20-17:40 Larissa Mendoza Straffon - Human Cooperative Behavior as a Key Selective Pressure for the Evolution of Visual Art

Recent thinking about biological communication has turned on the paradigm that animal communication is a process in which signalers basically seek to manipulate receivers for their own benefit. Current views, instead, see communication as an operation whose goal is to coordinate behavior between sender and receiver. This sets cooperation alongside competition and conflict of interest as an important selective pressure for communication. In group-living social animals, especially, cooperation towards common goals



seems to be a key incentive in evolving communication systems. Topical views in language studies indicate that this seems to be particularly true in the human case. In this paper, I argue that visual art should be understood as a component of human communication and, as such, must have evolved under pressure for cooperative behavior. The archaeological record further supports the suggestion that visual art coevolved with typically human reciprocal relations, as an index of identity and reputation. In this manner, visual art played an important role in the constitution and maintenance of large-scale cooperation networks in the Pleistocene, which proved an important adaptive strategy for modern humans.

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