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GRADUATE
SCHOOL OF
EVOLUTION

6th Symposium of the

Münster Graduate School of Evolution

in collaboration with the

Center for Philosophy of Science

“Between Science and Philosophy of Science”

Münster, 22nd - 23rd March 2017

6th Annual MGSE Symposium

MÜNSTER GRADUATE SCHOOL OF EVOLUTION

ABSTRACT BOOK 2017

Edited by Joachim Kurtz, François Pellet, Jürgen Gadau, and Vanessa Kloke

Institute for Evolution and Biodiversity

University of Münster

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› BETWEEN SCIENCE AND PHILOSOPHY OF SCIENCE ‹

Dear researchers and colleagues,

Philosophers need to be sufficiently familiar with scientific practices, and their work strongly benefits from having intimate access to modern research methodology and theorizing. On the other hand, also the sciences need to be philosophically investigated, as questions such as “What is a scientific explanation?”, “What is a scientific theory?” or “What is it for an organism to evolve?” cannot be purely empirically answered, but contain an irreplaceable normative dimension that requires conceptual clarification from philosophers. The 6th Symposium of the Münster Graduate School of Evolution (MGSE) - organized in cooperation with the Center for Philosophy of Science (*Zentrum für Wissenschaftstheorie*, ZfW) - will bring together researchers of the natural and life sciences and philosophers to foster a lively interdisciplinary dialogue.

PhD students of the MGSE are invited to present their diverse scientific work in short talks and posters. Their contributions will be embedded into talks by Principal Investigators of the MGSE and public lectures by internationally renowned philosophers of science, who will share their specific expertise and perspectives with the graduate students. The Institute for Evolution and Biodiversity and the northern *Kavaliershäuschen* of Münster’s City Palace will serve as venues for the symposium.

We are looking forward to lively discussions and fruitful exchange in the heart of Münster.

Prof. Dr. Joachim Kurtz	François Pellet
Conference Convenor & former MGSE Speaker	*Conference Convenor & MGSE PhD Student*

MÜNSTER GRADUATE SCHOOL OF EVOLUTION (MGSE)

The MGSE is housed right next to the Institute for Evolution and Biodiversity, in close vicinity to Münster's City Palace (Hüfferstr. 1a).

Prof. Dr. Jürgen Gadau
Speaker of the MGSE

Dr. Vanessa Kloke
MGSE Coordinator

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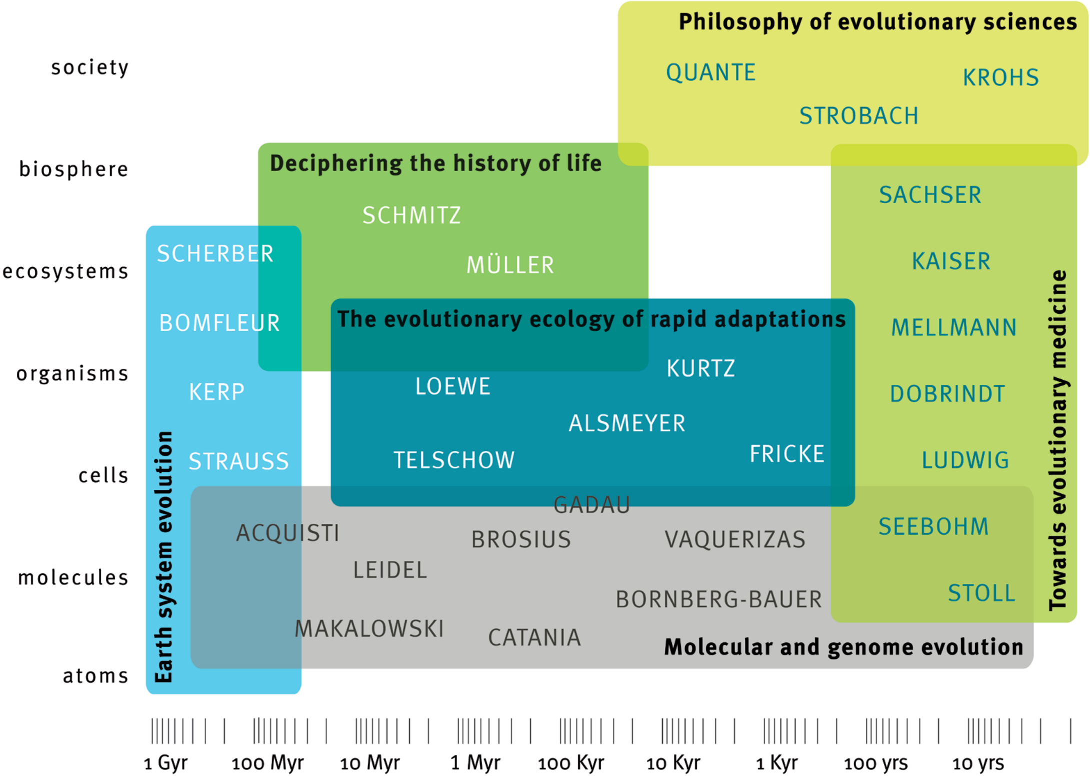
The Münster Graduate School of Evolution (MGSE) provides a structured study program for doctoral students of the University of Münster in the general field of evolution. Researchers from the faculties of Biology, Medicine, Philosophy, Geoscience, and Mathematics contribute to the MGSE, thus forming an interdisciplinary network of excellent scientists studying evolution on multiple scales and levels. The main research areas of the MGSE include earth system evolution, the history of life, the evolutionary ecology of rapid adaptations, molecular and genome evolution, evolution of pathogens, and the philosophy of evolutionary sciences.

Having interdisciplinarity as a leitmotif, the MGSE is continuously striving to increase its collaboration with other humanistic and scientific fields, most notably with Philosophy of Science. A joint symposium of the MGSE and the Center for Philosophy of Science - whose mission is also fundamentally interdisciplinary – provides an ideal platform to pool the expertise of both institutions and allow for a constructive and fruitful exchange of ideas, knowledge, and experiences.

MGSE - Research Areas



society
biosphere
ecosystems
organisms
cells
molecules
atoms

Philosophy of evolutionary sciences
QUANTE
KROHS
STROBACH

Deciphering the history of life
SCHMITZ
MÜLLER

Earth system evolution
SCHERBER
BOMFLEUR
KERP
STRAUSS

The evolutionary ecology of rapid adaptations
KURTZ
LOEWE
ALSMEYER
TELSCHOW
FRICKE

Towards evolutionary medicine
SACHSER
KAISER
MELLMANN
DOBRINDT
LUDWIG
SEEBOHM
STOLL

Molecular and genome evolution
GADAU
ACQUISTI
BROSIUS
VAQUERIZAS
LEIDEL
BORNBERG-BAUER
MAKALOWSKI
CATANIA

1 Gyr
100 Myr
10 Myr
1 Myr
100 Kyr
10 Kyr
1 Kyr
100 yrs
10 yrs

MÜNSTER
GRADUATE
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EVOLUTION

MGSE Principle Investigators

Name, Title	Research Topic	MGSE Research Area
Acquisti, Jun. Prof. Claudia	Evolutionary functional genomics	Molecular and genome evolution
Alsmeyer, Prof. Gerold	Mathematical statistics	The evolutionary ecology of rapid adaptations
Bomfleur, Dr. Benjamin	Paleobotany	Earth system evolution
Bornberg-Bauer, Prof. Erich	Evolutionary bioinformatics	Molecular and genome evolution
Brosius, Prof. Jürgen	Experimental pathology	Molecular and genome evolution
Catania, Dr. Francesco	Evolutionary cell biology	Molecular and genome evolution
Dobrindt, Prof. Ulrich	Microbial genome plasticity	Towards evolutionary medicine
Fricke, Dr. Claudia	Evolution and sexual conflict	The evolutionary ecology of rapid adaptations
Gadau, Prof. Jürgen	Molecular evolution and sociobiology	Molecular and genome evolution
Kaiser, Prof. Sylvia	Behavioural biology	Towards evolutionary medicine
Kerp, Prof. Johannes	Paleobotany	Earth system evolution
Krohs, Prof. Ulrich	Philosophy of science and of nature	Philosophy of evolutionary sciences
Kurtz, Prof. Joachim	Animal evolutionary ecology	The evolutionary ecology of rapid adaptations
Leidel, Dr. Sebastian	RNA biology	Molecular and genome evolution
Löwe, Prof. Matthias	Mathematical statistics	The evolutionary ecology of rapid adaptations
Ludwig, Prof. Stephan	Molecular virology	Towards evolutionary medicine
Makalowski, Prof. Wojciech	Bioinformatics	Molecular and genome evolution
Mellmann, PD Alexander	Hospital and environmental hygiene	Towards evolutionary medicine
Müller, Prof. Kai	Evolution of biodiversity of plants	Deciphering the history of life

Name, Title	Research Topic	MGSE Research Area
Quante, Prof. Michael	Philosophy of ethics and practical philosophy	Philosophy of evolution and education research
Sachser, Prof. Norbert	Behavioural biology	Towards evolutionary medicine
Scherber, Prof. Christoph	Animal ecology & multitrophic interactions	Earth system evolution
Schmitz, PD Jürgen	Experimental pathology	Deciphering the history of life
Seebohm, Prof. Guiscard	Myocellular electrophysiology	Towards evolutionary medicine
Stoll, Prof. Monika	Genetic epidemiology	Towards evolutionary medicine
Strauß, Prof. Harald	Historical and regional geology	Earth system evolution
Strobach, Prof. Niko	Philosophy of logic and language	Philosophy of evolution and education research
Telschow, Jun. Prof. Arndt	Genome evolution	The evolutionary ecology of rapid adaptations
Vaquerizas, Dr. Juanma	Regulatory genomics	Molecular and genome evolution

MGSE Graduate Students

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Sergio Ávila Calero
Marco Chittò
Nicolle Demandt
Kevin Ferro
Frederik Franke
Florian Grziwotz
Yeisson Gutiérrez López
Nadja Haarmann
Niklas Kästner
Matthias Kiel
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Neele Meyer
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François Pellet
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Jürgen Gadau (Speaker)
Johannes Kerp
Tabea Kischka
Ulrich Krohs
Stephan Ludwig
Norbert Sachser
Susanne Sangenstedt

Ex officio members

Francesco Catania, Leader of the ETT
Vanessa Kloke, MGSE Coordinator
Joachim Kurtz, Spokesperson of the DFG-RTG 2220 EvoPAD
Maike Tietjens, Vice-Rector for Strategic Personnel Development

MGSE Ombudsperson

Hans-Dieter Görtz

Equal Opportunity Commissioner

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MGSE PhD Student Retreat, October 2016

Back row: Marco Chittò, April Kleppe, Dr. Tobias Krause (guest from FLI Celle), Dr. Sebastian Leidel (MGSE PI), Prof. Dr. Joachim Kurtz (MGSE PI, Speaker until January 2017), Lars Langhanki, François Pellet, Aaron Lecanda, Sergio Avila, Tabea Kischka, Nadja Haarmann
Front row: Kevin Ferro, Matthias Kiel, Prof. Dr. Jürgen Gadau (Speaker of the MGSE since January 2017), Susanne Sangenstedt, Lena Strauß, Liliya Doronina (MGSE Alumni)

CENTER FOR PHILOSOPHY OF SCIENCE (ZFW)

The Center for Philosophy of Science (*Zentrum für Wissenschaftstheorie,* ZfW) was founded in January 2006. Originally seven departments of the University of Münster were involved, a number that has since then risen to eleven. The ZfW now is an institutionalized, interdisciplinary research association devoted to questions and inquiries in the field of Philosophy of Science.

The aim of founding the ZfW was to create a center for Philosophy of Science that combines multiple research interests and organizes interdisciplinary events. With this combination and the intensifying research and teaching in the field of Philosophy of Science at the University of Münster, the ZfW seeks to contribute to current debates in Philosophy of Science. Moreover, the ZfW regularly participates in planning and establishing a wide range of courses in Philosophy of Science at the University of Münster, as well as supporting the interdisciplinary structure of the graduate studies in the field of Philosophy of Science.

ZfW
Zentrum für Wissenschaftstheorie

Prof. Dr. Ulrich Krohs
Speaker of the ZfW

Dr. Eva-Maria Jung
Managing Director of the ZfW

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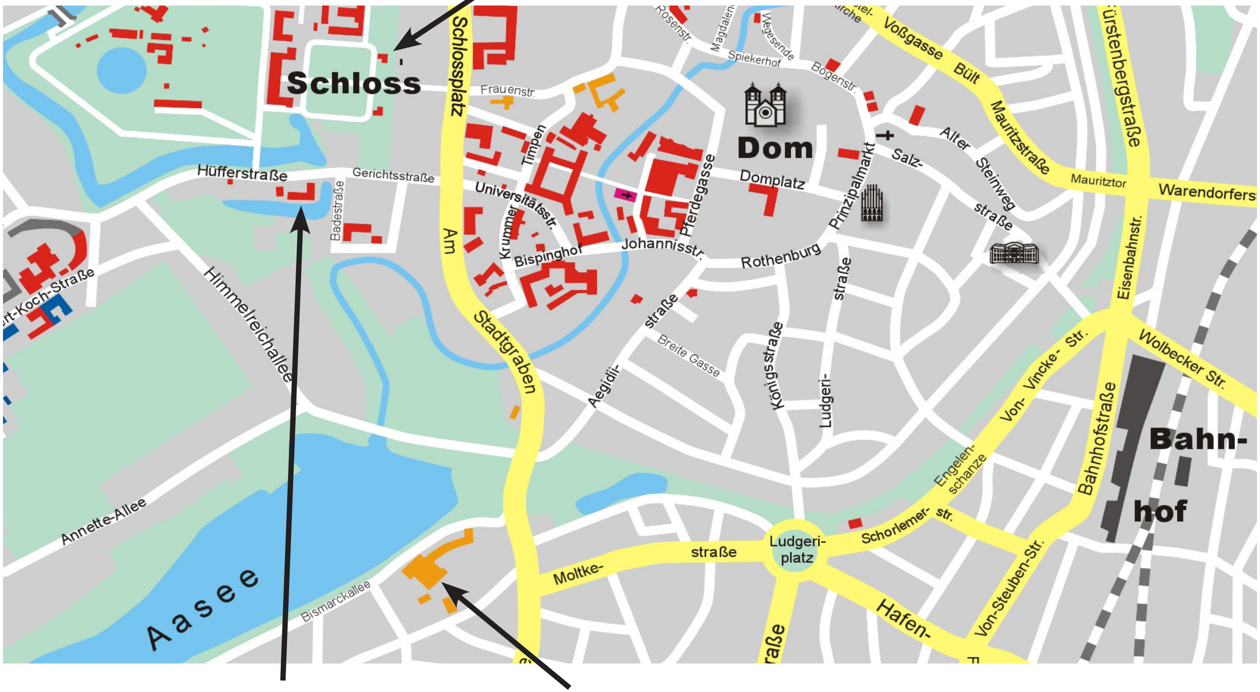
Institute for Evolution and Biodiversity (IEB)

In recent years, evolutionary research has become one of the focus areas of the WWU's research profile. Since its founding in 2005, the Institute for Evolution and Biodiversity (IEB) within the Faculty of Biology covers a diverse research spectrum in evolution and has attracted a number of new professors and junior groups from within and outside of Germany. The IEB currently integrates nine groups working on evolutionary ecology of animals, plants and microorganisms, phylogeny and evolution, aquatic ecology, biocomplexity, and evolutionary bioinformatics. The core question is how biodiversity and biocomplexity at all levels of the biological hierarchy arise through evolutionary processes.

"Kavaliershäuschen" (Schlossplatz 6)

The baroque satellite building of Münster's city palace was originally used as a guardhouse and received its name from the mounted guards ("chévaliers"). Later, the *Kavaliershäuschen* was inhabited by the caretaker of the castle. After its demolition during the Second World War it was reconstructed as home for employees of the district government, so that by the 1950th four families could live inside the house. In 1960, the building became property of the University of Münster and was used by the seminar for musicology. After a fundamental renovation, the *Kavaliershäuschen* is now seat of the University Marketing and Fundraising and the WWU Graduate Centre. The MGSE regularly organizes lectures and workshops in the *Kavaliershäuschen*.

Kavaliershäuschen
Schlossplatz 6



Institute for Evolution and Biodiversity
Lecture Hall HHü, Hüfferstr. 1

Mensa am Aasee
Bismarckallee 11-11b

13.15 - 13.45: Introduction

Lecture hall HHü, Hüfferstr. 1

13.15: Welcome address by the Symposium Convenors, Joachim Kurtz & François Pellet

13.30: Welcome address by the Rector of the WWU, Johannes Wessels

13.45 - 15.45: Public lectures

Lecture hall HHü, Hüfferstr. 1

Chair: Joachim Kurtz

13.45: Philippe Huneman

CNRS / Université Paris I Sorbonne, FR

"Rethinking the macroevolutionary contingency: Gould meets Mandelbrot?"

14.45: Jürgen Schmitz

Institute of Experimental Pathology, ZMBE

"From nets to trees and back again"

15.15: Hans Kerp

Institute of Geology and Palaeontology

"Species and phylogenetic concepts in palaeontology"

15.45 - 16.15: Coffee break

Foyer, Hüfferstr. 1

16.15 - 17.00: Poster talks

Lecture hall HHü, Hüfferstr. 1

Chair: Francesco Catania

17.00 - 18.30: Poster session

First floor, Hüfferstr. 1

18.30 - open end: Dinner buffet

Kavaliershäuschen, ground floor

9.15 - 10.45: Public lectures

Lecture hall HHü, Hüfferstr. 1

Chair: François Pellet

9.15: Rasmus Grønfeldt Winther
UC Santa Cruz, US
"The dangers of anti-pluralism in evolutionary biology"

10.15: Mario Rosario Guarracino
ICAR-CNR, IT
"Mathematical models of supervised learning and their application to biological data"

10.45 - 11.15: Coffee break

Foyer, Hüfferstr. 1

11.15 – 12.15: Talks by PhD students

Lecture hall HHü, Hüfferstr. 1

Chair: Niklas Kästner

11.15: Lena Strauß
Institute of Hygiene
"Phylogenetic comparison of *Staphylococcus aureus* from Germany and sub-Saharan Africa"

11.30: Nadja Haarmann
Institute of Hygiene
"Phenotypic comparison of enterohemorrhagic *Escherichia coli* O104:H4 with enteroaggregative *Escherichia coli*"

11.45 Matthias Kiel
Institute of Hygiene
"Comparative genome analysis to improve detection and typing of Shiga toxin-expressing *Escherichia coli*"

12.00 François Pellet

Department of Philosophy

"The limits of interdisciplinarity between philosophy and science"

12.15 - 13.30: Lunch break

Canteen at the Aasee

13.30 - 14.30: Public lecture

Lecture hall HHü, Hüfferstr. 1

Chair: Ulrich Krohs

13.30: Marie Kaiser

University of Bielefeld, DE

"Normativity in the philosophy of science"

14.30 - 15.00: Farewell coffee

Foyer, Hüfferstr. 1

RETHINKING THE MACROEVOLUTIONARY CONTINGENCY: GOULD MEETS MANDELBROT?

KEYNOTE LECTURE

Philippe Huneman

Institut d'Histoire et de Philosophie des
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CNRS / Université Paris I Sorbonne

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According to the Modern Synthesis (MS), population genetics, as the science of the dynamics of changing allele frequencies in a population, is the core of evolutionary biology since it explains the arising of adaptations by cumulative selection. Its scale is microevolution, namely, evolution of the population of one species within a timescale not too large, defined by a small window of variations and environmental changes. Microevolution contrasts with macroevolution, that is, evolution above the level of speciation, such as the extinction or emergence of species and clades, which involves a longer timescale and therefore may assume large environmental changes. Stephen Jay Gould famously claimed that at levels above the species, or even beyond, the history of life is greatly contingent. This paper will interpret the meaning of Gould's claim in light of various notions of contingency. After having distinguished between biological and mathematical reasons why there could be principled differences between micro- evolution and macroevolution, I will focus on the latter. Considering recent evolutionary research on extinction time I argue that such mathematical reasons concern the modelling of chance events in microevolution: at larger timescales, models of chance (such as Gaussian distribution of fluctuations) may not be any more justified, and other models should be required, though at microevolutionary timescales all models would be in practice equivalent. The view suggested here appeals to the distinction made by mathematician Mandelbrot between "wild randomness" and "mild randomness" as two distinct structures of randomness. I conclude by showing that the mathematical differences between micro and macroevolution are more general, and therefore may challenge the extrapolation thesis even if empirical facts do not support the biological differences.

KEYNOTE LECTURE

Rasmus Grønfeldt Winther

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Consider three episodes of evolutionary biology: *statistical phylogenetics, Fisherian population genetics, and mapping genetics*. Turning to the history of each exposes the normative and philosophical importance of theoretical and methodological pluralism. First, what causal connections obtain between the rise of statistical phylogenetics and the fall of cladistics? Did politics and power silence dialogical, critical rationality? Is a pluralistic future possible, in which we again take seriously morphological characters and the concept of homology, as well as certain taxonomic and documenting practices from cladistic systematics? Second, what is the Fisherian “gene’s-eye” view? How does a Fisherian “inductive” statistical-hacker modeling style pluralistically contrast with more analytical and holistic gene-network modeling styles, such as those of Sewall Wright or Eric Davidson? Finally, how could we construct an *integration platform* of different genetical mapping strategies [e.g., linear genetic maps; gene expression maps; genotype-phenotype (G-P) maps; adaptive landscape maps]? And what happens when we imperialistically universalize and reify only a subset of diverse genetical mapping strategies?

The centrality of critique and pluralism is philosophically articulated by turning to themes from *When Maps Become the World* (University of Chicago Press). My book explores the map analogy and map projection pluralism in philosophy and across the sciences. Inspiration for defending a practice-based pluralistic vision of science is drawn from the work of Nancy Cartwright, Paul Feyerabend, Ian Hacking, Helen Longino, Karl Popper, and Ludwig Wittgenstein, among many other philosophers. To this overarching vision, I inflect map thinking in order to produce a pragmatic cartographic image of science.

NORMATIVITY IN THE PHILOSOPHY OF SCIENCE

The goal of this talk is to clarify what it means for philosophy of science to be normative. I argue that normativity is a multifaceted phenomenon rather than a feature that a philosophical theory about science either has or has not. I distinguish three major kinds of normativity. Statement-normativity arises from the kind of statements that a philosophical theory about a given object of study contains. Some philosophers make normative claims about science as it should be, rather than (only) about science as it actually is. Methodological normativity can be found even in philosophical accounts that aim at describing actual scientific practice. This kind of normativity is due to normative methodological assumptions that are made in selecting, interpreting, and evaluating the relevant empirical information on the basis of which a philosophical theory is developed. Object-normativity emerges from the fact that sometimes the object of philosophical theorizing X, itself, is normative, namely, if a philosophical theory refers to epistemic or social norms and their roles in scientific practice. By distinguishing these three kinds of normativity and relating them to each other a more comprehensive and clear view of normativity in the philosophy of science emerges.

KEYNOTE LECTURE

Marie I. Kaiser

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FROM NETS TO TREES AND BACK AGAIN

In the world of bacteria, it is not easy to find traces of clear, bifurcating evolutionary relationships because their genes can be easily exchanged via horizontal transfer. Therefore, bacterial phylogeny is best presented as a network or mosaic of affiliations. Introduction of the nucleus in our eukaryotic ancestor provided a barrier limiting horizontal genetic transfer, and genetic exchange was subsequently more or less restricted to vertical exchanges from generation to generation. Thus, the phylogenetic relationships of eukaryotes were easier to decipher and their reconstructions to display as phylogenetic trees with ancestral roots and internodes bifurcating into branches with terminal species. Traditional and modern reconstruction methods were developed to more or less force datasets into tree-like structures. However, the ever increasing amounts of molecular data brought more apparent exceptions to such simple bifurcations to light, and finally, despite the virtual absence of horizontal transfer, networks often better describe the phylogenetic relationships of also many eukaryotic lineages. We will present some of the nicest trees and most complex nets representing bird and mammal evolutionary relationships and evaluate these differences in the underlying data. In such cases, the shared presence or absence of jumping genes/retroposed elements has dramatically aided our reconstruction of nearly homoplasy-free signals of order (trees) and chaos (nets).

Jürgen Schmitz

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Hans Kerp

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Modern biologists have the great advantage that they are working with living material. They have developed a wide array of methods to define and recognize species and reconstruct phylogenies. Palaeontologists have the great disadvantage that they are working with dead material, usually representing taxa that are extinct. In addition to the fact that a number of methods currently applied in modern systematics, e.g., molecular studies, cannot be used, the preservation of the material is often problematic. Usually only the hard durable parts are preserved; only in very rare occasions so-called soft-bodied organisms are found. The fragmentation of larger organisms is also a problem. Only very few larger organisms are preserved completely. Many plants even shed organs annually, e.g., leaves, fruits, seeds, as part of their life cycle. This presentation will give an idea, which difficulties palaeontologists are facing studying fossil organisms and the species concept(s) in palaeontology will be discussed briefly. These problems inherent to the nature of the organisms and the preservation of course also affect phylogenetic reconstructions, as will be shown by some examples.

MATHEMATICAL MODELS OF SUPERVISED LEARNING AND THEIR APPLICATION TO BIOLOGICAL DATA

Supervised learning refers to the ability of a system to learn from examples, represented by a set of input / output pairs, called the training set. A trained system provides the answer (output) to each new question (input). The term supervised is used when an expert provides the answer for all training questions.

Among supervised learning algorithms, the so-called Support Vector Machines (SVMs) provide accurate solutions and low training time. These are based on the statistical learning theory and compute the solution by minimizing a quadratic type cost function. SVMs, in conjunction with the use of kernel methods, provide non-linear classification models, namely separations that cannot be expressed using inequalities on linear combinations of parameters.

It is also possible that the training sets change over time, for example, because data are added and modified as a result of new tests or new knowledge. In such a case, many techniques cannot capture the changes, but need to restart the learning process from scratch. Those techniques, which extract only the new knowledge contained in the incoming data and provide the learning model in an incremental way, have the advantage of taking into account only new data that are really useful.

Finally, since the supervision process can be expensive and time consuming, some techniques take advantage from unlabeled points, under some assumptions on the probability distribution of data.

In this talk, we describe some solutions to these problems, with the support of numerical experiments, and some applications of biological interest.

Mario Rosario Guarracino

High Performance Computing and
Networking Institute – Italian National
Research Council, Naples

Fellow of the Evolution Think Tank

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PHYLOGENETIC COMPARISON OF STAPHYLOCOCCUS AUREUS FROM GERMANY AND SUB-SAHARAN AFRICA

Staphylococcus aureus is a bacterium that asymptomatically colonizes 25-35% of the human population, but may also cause mild to severe diseases under appropriate conditions. Although *S. aureus* infections are common in countries of sub-Saharan Africa, little is known about the bacterium's regional population structure and molecular characteristics, especially in comparison to other world regions. We performed whole genome sequencing (WGS) of 1,162 community-associated *S. aureus* isolates from Germany (n=418), Gabon (n=192), Mozambique (n=171), Tanzania (n=196) and the Democratic Republic of Congo (n=185). Isolates were obtained from patients (n=569) and healthy volunteers (n=594). Using the allele types of 1861 conserved genes, we reconstructed a neighbour-joining (NJ) phylogeny of all 1,162 isolates. Moreover, we performed *in silico* multilocus sequence typing (MLST). Our 1,162 isolates were assigned to 145 different MLST sequence types (ST), indicating high genetic diversity. Eight samples were non-typeable due to sequencing / assembly errors. Fifty-four STs were exclusively found in Africa (n=220), while 74 ST were exclusively found in Germany (n=170). Only 17 ST were found in both regions, but these ST comprised the majority of isolates (n=764). All STs could be summarized in 37 clonal complexes (CC). CC25 and CC45 are of particular interest for future research, because they show regionally specific diversifications of "German" and "African" *S. aureus*. We conclude that there are few globally successful clones of *S. aureus* as well as diverse local populations.

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PHENOTYPIC COMPARISON OF ENTEROHEMORRHAGIC ESCHERICHIA COLI O104:H4 WITH ENTEROAGGREGATIVE ESCHERICHIA COLI

Nadja Haarmann
Petya Berger
Andreas Bauwens
Michael Berger
Helge Karch
Alexander Mellmann

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Escherichia coli O104:H4 was identified as the pathogen causing the largest outbreak of bloody diarrhea and hemolytic uremic syndrome (HUS) in Germany in 2011. It is hypothesized that the exceptional pathogenicity of this strain derives from the hybrid character of this strain i.e. from the combination of virulence determinants originating from enterohemorrhagic *E. coli* and enteroaggregative *E. coli*, respectively. Here, we phenotypically compared the outbreak strain with other typical EAEC strains in order to assess the contribution of enteroaggregative virulence factors on its pathogenicity.

In this study, we compare *E. coli* O104:H4 C227-11 Φcu with the prototypical EAEC strains 55989 and 042. Growth characteristics were monitored in LB medium, in a cell culture medium (DMEM) and in a medium mimicking the conditions in the colon (SCEM). Moreover, the production of different virulence determinants were measured using semi-quantitative Western blot analysis. Finally, the strains were further phenotypically characterized using qualitative and quantitative adherence, biofilm, and cell cytotoxicity assays.

The growth experiments showed similar growth characteristics for the strains C227-11 Φcu and 55989. Even though EAEC 042 showed the lowest final bacterial density under the conditions tested, it produced twice as much Dispersin as EAEC 55989, and three fold more than C227-11 Φcu. The qualitative adherence assay confirmed the typical “stack-bricked” pattern of EAEC. The biofilm formation of EAEC 042 in DMEM was five (55989) to twelve (C227-11 Φcu) times higher than in the other strains but two (55989) to four (C227-11 Φcu) times lower in SCEM.

COMPARATIVE GENOME ANALYSIS TO IMPROVE DETECTION AND TYPING OF SHIGA TOXIN-EXPRESSING ESCHERICHIA COLI

Escherichia coli (*E. coli*) is usually a mutual member of the human microbiota. Nevertheless, several pathogenic *E. coli* pathotypes exist. Especially foodborne infections with Shiga toxin-expressing *E. coli* (STEC), which can lead to bloody diarrhoea and the severe haemolytic uremic syndrome (HUS), are a worldwide health concern. To ensure the best treatment of patients and to facilitate strain typing and risk assessment a quick and reliable DNA-sequence-based detection method for STEC is important.

To ensure an unbiased search for possible STEC biomarkers, genome sequences of *E. coli* were collected from the NCBI Sequence Read Archive. The sequences were used for a molecular epidemiological analysis including Multi Locus Sequence Typing (MLST) and virulence gene profiling. Based on these results and metadata analysis, 248 sequences were grouped into STEC, other diarrheagenic *E. coli*, extraintestinal pathogenic *E. coli* (ExPEC) and commensal genomes. These groups were screened for putative biomarkers using a bioinformatics pipeline. Our results indicate a high genomic diversity among STEC strains. As a consequence, a general biomarker set specific for all used STEC variants could not be identified. Nevertheless, further subdividing of the genomes according to clonal lineage or serotype led to the discovery of 54 putative group-specific biomarkers. Following the *in silico* identification of these biomarkers, a multiplex PCR was established which reliably detects the “Big Five” and additional clinically important STEC subgroups. Thus, our improved DNA-based typing method can facilitate STEC typing and risk assessment in routine surveillance as well as in the food industry.

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Alexander Mellmann[1]
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Francois Rechenmann[4]
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THE LIMITS OF INTERDISCIPLINARITY BETWEEN PHILOSOPHY AND SCIENCE

François Pellet

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It is acknowledged today that philosophy and science should be interdisciplinarily investigated. However, it is rarely clear how to pursue this interdisciplinarity and what its limitations are.

The purpose of this talk is to argue that a model of how this interdisciplinarity could be pursued fails. The talk is divided into two parts. The first part presents such a model; the second part argues that this model fails.

It is obvious that any model of interdisciplinarity between philosophy and science should explain how philosophy brings constraints on science and vice versa. These constraints are put in terms of the relationship between philosophy of science and science, where philosophers are interested in foundational issues of science, and between psychology and philosophy of mind, where philosophers of mind provide the possession conditions for concepts and psychologists the realization conditions necessary for the possession conditions.

The second part argues that this model fails, by sustaining a neutrality principle: even if there are ontological relations between philosophy and science, these two disciplines are mutually independent, because for a theory belonging to the discipline x to be correct is for it to resist to the attempts to falsify it by using any plausible theory that may belong to another discipline y – and thus, not by using a correct theory belonging to y. This argument proceeds by showing that, once we distinguish between a theory being correct and plausible, the interactions between philosophy and science cease to be of mutual support.

EGG ANTIBACTERIAL ACTIVITY IN DROSOPHILA MELANOGASTER

Insects have evolved a wide repertoire of strategies to protect themselves from infections by pathogens and parasites. From all developmental stages, eggs are the most vulnerable ones since they are not able to move in order to escape from these menaces. A few species of arthropods possess an antimicrobial protection that could increase their probabilities of survival in highly contaminated environments. In some cases, this antimicrobial activity comes from inside of the eggs, but in some others females are able to coat the surface of their eggs with antimicrobial peptides. Among insects, *Drosophila melanogaster* is one of the most studied species given the wide set of methodological tools available for it. Although a lot of research on immunity of *D. melanogaster* has been done, not much is known about the antimicrobial activity of their eggs. Therefore, we used the zone of inhibition assay, an easy-to-perform assay which requires low quantity of samples, to quantify the antibacterial response of the eggs of *D. melanogaster* against the bacterium *A. globiformis*. The results show for the first time that the eggs of this species of fly are able to inhibit the growth of *A. globiformis*. These results open the possibility to deepen the knowledge of the evolution of mating and immunity in insects.

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INSIGHTS INTO A 260 MILLION-YEAR-OLD-ECOSYSTEM THROUGH CUTICULAR ANALYSIS

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Cathaysia is one of the four major late Palaeozoic floral provinces and includes the palaeotropical plant assemblages from present-day China and East Asia. It was originally established based on plant fossils from the Permian of central Shanxi Province, China. The taxonomy is primarily based on macromorphological criteria and relationships of taxa often remain unclear. Thus, detailed studies of the Cathaysia flora are necessary for a better understanding of its relationships to other floral provinces. Cuticular analysis not only allows a precise definition and delimitation of individual taxa, but it also provides important information on the palaeoecology and -climate on the basis of biological criteria, i.e. the epidermal anatomy. Newly identified plant-bearing horizons from the Palougou section in Shanxi, which is generally regarded as a standard reference section for the Cathaysia flora, reveal a diverse and well-preserved macroflora with in situ cuticular preservation of different taxa. Here we present the first results of cuticular analyses of in situ and bulk-macerated material including cuticles of typical Cathaysian plant taxa. Our on-going study promises to yield important new insights about the taxonomy and palaeoecology of these plants.

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A LATE PERMIAN TROPICAL COCKTAIL - THE ‘MIXED FLORA‘ OF THE UM IRNA FM., JORDAN

The Um Irna Formation, an up to 85 m-thick-succession of Permian continental sedimentary deposits exposed along the Dead Sea Coast of Jordan (Bandel and Koury, 1981), has yielded remarkably well preserved plant-fossils. Studies have so far focused on species of the seed-fern frond *Dicroidium*; however, during recent field work, rich and diverse assemblages of typical Cathaysian elements (e.g., *Gigantonoclea*) as well as Angaran and more cosmopolitan taxa (e.g., *Qasimia*, *Pecopteris*, ?*Saportea*, ?*Rissikia*, *Elatocladus*, *Lobatannularia*, *Rhipidopsis*, *Taeniopteris*) were collected. The plant-fossil assemblages vary markedly in systematic composition. In total, six distinct associations can be distinguished. Some are dominated by *Dicroidium* or by hygrophilous floral elements (e.g., ferns), whereas others are dominated by xeromorphic floral elements (e.g., conifers). In general hygrophilous associations seem to be dominated by Angaran and cosmopolitan taxa (e.g., *Qasimia*, *Taeniopteris*) with *Dicroidium* being absent. Meso- to xerophilous assemblages are either dominated by *Dicroidium*, with rare occurences of *Rhipidopsis* and *Taeniopteris* or by *Elatocladus* and *Rissikia*. We interpret these differences to reflect a mosaic of locally restricted, contemporaneous plant communities rather than climatic changes. Although some of these elements were briefly reported already by Mustafa (2003), our report shows that the diversity of plant communities is much higher than previously thought, and contains a wide variety of hygrophilous to xeromorphic plants. We are confident that continued work on these remarkable floras will yield even further insights into Late Permian plant-ecosystems, and deepen our understanding of the palaeogeographic significance of the peculiar ‘mixed floras’ of the Permian palaeotropics.

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EVOLUTION OF BACTERIAL GENOMES: THE ROLE OF PATHOGENICITY ISLAND-ENCODED INTEGRASE GENE EXPRESSION

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Pathogenicity islands (PAIs) are mobile integrated genetic elements (MIGEs) that contain a diverse range of virulence-associated genes and that play an important role for the evolution of pathogenic bacteria. Horizontal gene transfer is an important aspect of microbial genome evolution and it is responsible for the global spread of antibiotic resistance. Horizontal acquisition and the loss of PAIs play key roles for bacterial evolution and the adaptation of pathogens during pathogen-host-interaction. P4-type integrases are involved in the chromosomal insertion as well as the excision of PAIs, and they usually specifically recognize their encoding PAI. Growth conditions, which affect the differential regulation of integrase gene expression and factors, which contribute to the DNA sequence specificity of the integrases are not extensively studied. To increase our knowledge of fundamental mechanisms involved in bacterial genome plasticity, we therefore investigate (i) growth conditions which modulate expression of integrase-encoding genes in Escherichia coli, and (ii) the impact of “xenogenic silencing” on regulation of integrase genes. For this purpose, reporter gene fusions were generated in the chromosome of uropathogenic E. coli strain 536 to monitor promoter strength and regulation of the P4 integrase-encoding genes of PAI I_{536} to PAI V_{536}. The corresponding promoter sequences were fused to a promoterless yfp gene plus a selectable marker (cat). The data collected on the integrase promoter activity showed that the promoter of the integrase gene of PAI I_{536} is the most active followed by the promoter of the integrase genes of PAI II_{536} and PAI III_{536}, while the activity of the promoters of the integrase genes of PAI IV_{536} and PAI V_{536} are very weak under the conditions tested so far. With this project, I will increase the knowledge regarding environmental factors and signals, which regulate integrase gene expression thus affecting the genetic and phenotypic variability of pathogenic bacteria.

A TIME TO WEAN? IMPACT OF WEANING AGE ON ANXIETY-LIKE BEHAVIOUR AND STABILITY OF BEHAVIOURAL TRAITS IN FULL ADULTHOOD

In mammals, weaning constitutes an important phase in the progression to adulthood. It comprises the termination of suckling and is characterized by several changes in the behaviour of both mother and offspring. Furthermore, numerous studies in rodents have shown that the time point of weaning shapes the behavioural profile of the young. Most of these studies, however, have focused on 'early weaning', while relatively little work has been done to study 'late weaning' effects. The aim of the present study was therefore to explore behavioural effects of 'late weaning', and furthermore to gain insights into modulating effects of weaning age on the consistency of behavioural expressions over time. In total, 25 male and 20 female C57BL/6J mice, weaned after three (W3) or four (W4) weeks of age, were subjected to a series of behavioural paradigms widely used to assess anxiety-like behaviour, exploratory locomotion, and nest building performance. Behavioural testing took place with the mice reaching an age of 20 weeks and was repeated eight weeks later to investigate the stability of behavioural expressions over time. At the group level, W4 mice behaved less anxious and more explorative than W3 animals in the Open Field and Novel Cage, while anxiety-like behaviour on the Elevated Plus Maze was modulated by a weaning-age-by-sex interaction. Furthermore, weaning age shaped the degree of behavioural stability over time in a sex-specific way. While W3 females and W4 males displayed a remarkable degree of behavioural stability over time, no such patterns were observed in W3 males and W4 females. Adding to the existing literature, we could thus confirm that effects of weaning age do indeed exist when prolonging this phase, and were furthermore able to provide first evidence for the impact of weaning age and sex on the consistency of behavioural expressions over time.

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EVOLUTIONARY EFFECT OF TRANSLATIONAL ERRORS

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During translation the genetic instructions are passed from DNA via mRNA to the ribosome to assemble a protein chain. Synthesis of this chain is terminated by a stop codon in the mRNA. Recent research find that stop codons are occasionally ignored by the ribosome and that translation continues into the untranslated region (3'-UTR). This process, called translational readthrough (TR), yields a protein that becomes longer than one would predict from the DNA sequence alone.

We would like to understand how frequent these errors are, if they can be induced e.g. when a longer protein sequence is needed and if there is an hitherto unknown evolutionary pressure to maintain and maybe even adapt the UTR such that the synthesised protein has additional functionality.

We analyse ribosome profiling data in yeast to establish the TR-rate, homology, and sequence features for 3'-UTRs and their respective parent-genes.

We find a relatively high abundance of TR and that TR is consistent in non-essential genes involved in metabolism and stress regulatory processes.

We suggest errors like TR are more tolerated in genes that are not risking immediate fitness costs.

Upcoming research will concentrate on establishing the evolutionary relationship between mutational robustness and evolvability.

SOCIAL NICHE AND REPRODUCTIVE SUCCESS - A STUDY IN GUINEA PIGS

Individuals of the same species can find themselves in different social niches. They can live at high or low population numbers and they can fill different social positions. The occupied social niche in turn can have profound fitness consequences. The aim of the present study was to investigate the effects of social niche on reproductive success in male guinea pigs. For this purpose a low and a high individual number situation were explored with males living either together with one female in pairs (P) or in large age graded mixed-sex colonies (C). Paternities were determined via DNA-fingerprinting and as potential factors influencing reproductive success age, weight, and in colonies also dominance rank were assessed. The main results were that P males, having unrestricted access to a female, had their first successful conception at about 78 days of age, hence around sexual maturity. In contrast, C males were significantly older at first successful conception (about 200 days old) and also the variance of age at this date was much larger. Furthermore, in colonies a significant positive correlation was found between reproductive success and dominance rank, whereby age and weight appeared to play a major role in gaining a high social status. Still, some males were able to reproduce before 200 days of age, which might have been facilitated by the considerable amount of multiple paternities (up to 50 %). The present study clearly emphasises the complex relationship between social niche, behavioural strategy, and reproductive success.

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DOES THE EARLY SOCIAL ENVIRONMENT PREPARE FOR THE FUTURE? ADAPTATIONS TO LOW DENSITY POPULATIONS

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Animals living in a low density population rarely face high competition levels due to sufficient resources and a stable social environment. In contrast, animals living in a high density population regularly face high competition levels due to scarce resources and an unstable social environment. Parents can pass on information about the current social environment in order to prepare their offspring to fit future challenges. In the present study, we mimicked the settings of high and low density populations by creating unstable and stable social environments. We tested 22 wild cavy (*Cavia aperea*) daughters, which were born in either of the two environments, in a low density condition with sufficient resources. Our hypothesis was that daughters born in a stable social environment with low competition levels will be better adapted to similar conditions in later life than daughters born in an unstable social environment with high competition levels. In order to detect adaptations, we measured fitness proxies such as dominance relations, stress hormone levels, body weights and behavioural profiles. Body weights and the number of daughters which became dominant did not differ between the two groups. However, higher stress hormone and activity levels indicated that daughters born in an unstable social environment were significantly more stressed in a low density condition than daughters born in a stable social environment. Thus we conclude that daughters born in a stable social environment are better adapted to similar conditions in later life than daughters born in an unstable social environment.

INVESTIGATING THE ROLE OF tRNA METHYLTRANSFERASE (DNMT2) IN THE RED FLOUR BEETLE TRIBOLIUM CASTANEUM

Epigenetic regulation enables rapid phenotypic adaptation to environmental change. Cytosine methylation of small RNAs is an important epigenetic mechanism, generated by an evolutionarily conserved enzyme, tRNA methyltransferase (Dnmt2). For a long time Dnmt2 was thought to be involved in DNA methylation, because of its sequence similarities to the two other known DNA methyltransferases (Dnmt1 and 3). But, recent studies have shown that Dnmt2 is responsible for methylating RNAs, especially tRNA.

The genome of the red flour beetle *Tribolium castaneum*, encodes for Dnmt1 and 2 but lacks a copy for Dnmt3. Additionally, there is an ongoing debate, whether the beetle exhibits functional cytosine DNA methylation. We therefore investigated the status of Dnmt2, to determine whether it could contribute to the phenotypic plasticity observed in the beetles.

Dnmt2 is expressed across all stages and in the gonads. Furthermore, parental RNAi in male and female pupae led to a significant systemic downregulation. However, development and fitness were unaffected by the downregulation of Dnmt2.

Although Dnmt2 is expressed during the entire life of the beetle and in the germline, its expression does not seem essential for the survival of the beetle under ad libitum conditions. In the future, we plan to investigate the status of tRNA methylation in *T. castaneum* and the effect a knockdown of Dnmt2 has on phenotypic plastic traits, e.g. trans-generational immune priming.

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INCREASING DATA ACCESSIBILITY AND REUSE IN PHYLOGENETICS BY EMPLOYING EXTERNALLY DEFINED ONTOLOGIES

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In philosophy, ontology is defined as the study of the nature and relations of being. Information sciences apply this concept to create naming conventions describing types, properties and interrelationships of certain entities. Ontologies aim to limit complexity and organize information. In phylogenetics, they allow scientists to provide semantic information on data in a machine-readable way. Using fixed vocabularies from external ontologies makes the data more easily accessible for other researchers and facilitate its reuse. This is becoming more and more important with a rapidly increasing amount of biological data available in online sources. Here we present three software projects from our group that foster the use of external ontologies, enabling users to handle semantic metadata annotations much more elegantly than possible with current software solutions.
JPhyloIO is a software library that allows developers to support reading and writing different phylogenetic file formats (modeling alignments and trees), including full support for the formats' metadata models and the use of externally defined ontologies. LibrAlign and TreeGraph 2, on the other hand, allow to process and visualize such metadata in bioinformatical software applications. LibrAlign is a library providing GUI components to display and edit multiple sequence alignments, allowing externally implemented data areas for metadata described by externally defined ontologies. Different types of branch labels available in TreeGraph 2 offer a similar functionality for phylogenetic trees. In combination, our software components simplify the use of metadata from externally defined ontologies both in data storage and data processing for the main phylogenetic data types, thereby facilitating accessibility and reuse.

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ABSTRACT BOOK

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