EvolDir

April 1, 2025

Month in Review

Foreword

This listing is intended to aid researchers in population genetics and evolution. To add your name to the directory listing, to change anything regarding this listing or to complain please send me mail at Golding@McMaster.CA.

Listing in this directory is neither limited nor censored and is solely to help scientists reach other members in the same field and to serve as a means of communication. Please do not add to the junk e-mail unless necessary. The nature of the messages should be "bulletin board" in nature, if there is a "discussion" style topic that you would like to post please send it to the USENET discussion groups.

Instructions for the EvolDir are listed at the end of this message.

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Conferences

Auckland GeneticsSocietyAustralasia Jul7-10

Tçnâ koe, hello!

Abstract submission for GSA's 2025 conference is due in just under four weeks, on Monday 7th April. The conference will be held at Waipapa Taumata Rau - The University of Auckland in Aotearoa - New Zealand from 7-10 July 2025.

Our annual conference brings the genetics community from Aotearoa, Australia and the Asia Pacific region together to share fantastic new and innovative research in genetics, covering themes across human genetics, molecular, cellular and developmental genetics, genetics in primary industries, quantitative genetics, microbial genetics, epigenetics, synthetic biology, conservation genetics, evolutionary genetics, comparative genomics, genetics education and more!

We are also excited to be hosting two special symposia - a session featuring Indigenous Early Career Leaders, supported by Genomics Aotearoa, and a Precision Medicine session, supported by The University of Auckland.

- Abstracts are due by Monday April 7th 2025, 23:59 NZST (21:59 AEST). - Early bird registration will close on Sunday May 11th 2025, 23:59 NZST (21:59 AEST). - For more information, see gsa-2025.com.

Abstract submission is generally limited to one abstract per presenter. However, as part of encouraging a community of practice in Genetics Education, we welcome an additional abstract submission to our 'Education and genetics' session. Oral presentations at the session will be eligible for consideration for the GSA Award for Innovation in Education.

In addition to conference attendance, GSA members are eligible to apply for GSA awards, workshop funding, student grants and access to the GSA mailing list to distribute information to members, amongst many other benefits.

This is the preeminent meeting in our field and spans both applied and fundamental genetic research. The conference will also host a diversity of international and national keynote speakers from across the disciplines of genetics, with keynotes from Prof Amanda Black, Prof Alexei Drummond, Prof Matt Littlejohn, Prof Cris Print, Assoc Prof MiloÃ^o Tanurdzic, Dr. Erika Varkonyi-Gasic, and Assoc Prof Phil Wilcox.

Our Indigenous Early Career Leader session features additional keynotes from Dr Alana Alexander, Dr Catherine Collins, Dr Megan Leask, Dawn Lewis, Jordon Lima and Conor Watene O'Sullivan.

Our Precision Medicine session features additional keynotes from Dr Lynsey Cree, Assoc Prof Emma Scotter and Prof Andrew Shelling.

The conference will also feature talks from our GSA Award winners.

We look forward to seeing you in Tâmaki Makaurau - Auckland in July 2025!

Anna Santure On behalf of the Organising Committee - Dr Kimiora Henare, Dr Jessie Jacobsen, Dr Nathan Kenny, Prof Joanna Putterill, Dr Suzanne Reid and Dr Annabel Whibley

Contact email: gsa.conference2025@gmail.com GSA 2025 conference website (includes links to registration and abstract submission): www.gsa-2025.com We acknowledge the generous support of our Platinum Partners Genomics Aotearoa and The University of Auckland, Gold Partner Kiwifruit Breeding Centre, Silver Partner The Center for Computational Evolution, and Bronze Partners Lab Supply, Decode Science, Ngaio Diagnostics, Auckland Genomics, Oxford Nanopore Technologies and AGRF. Partnership opportunities still available!

Nathan Kenny <nathan.kenny@otago.ac.nz>

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BanyulsSurMer France ComparativeAnatomy Jun10-13

Comparative Cartilage & Bone Biology (CCBB) conference 2025

Dear colleagues, we are happy to announce the upcoming Comparative Cartilage & Bone Biology (CCBB) conference to be held in Banyuls (France), 10-13 June, 2025. Please visit the website below for information, aims of the meeting, abstract submission and venue. www.ccbb-conference.com ; please use ccbbconference@gmail.com for all correspondence regarding the conference

CCBB addresses the most interesting topics in comparative skeletal biology and provides space for discussions and networking across disciplines : paleontology, developmental biology and genetics, biomechanics... come and find ideas for future research and studies on many vertebrate species, that can perhaps answer your questions. This friendly and inspiring conference with no more than 100 participants takes place at a beautiful location. Abstract deadline is 16 March and notification on abstract acceptance will be by 31 March, at the latest. Registration fee for students will be maximally 100 €. Registration fee for all others is provisionally set at maximally 300 €. Registration fee only needs to be paid after you have been notified of abstract acceptance.

Finally, please pass on this message to anyone whom you think might be interested!! We look forward to see you at CCBB 2025 in Banyuls!

The Organisers,

Melanie Debiais-Thibaud, University of Montpellier P. Eckhard Witten, University of Ghent Mason Dean, Hong-Kong city U Ann Huysseune, University of Ghent

Melanie Debiais-thibaud <melanie.debiais-thibaud@umontpellier.fr>

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Bordeaux Online MembraneBioenergetics Apr1

Nick Lane (PhD, FRSB, FLS) is Director, Centre for Life's Origins and Evolution and Professor of Evolutionary Biochemistry in the Department of Genetics, Evolution and Environment at University College London (UK). "Why membrane bioenergetics structures cell evolution from the origin of life to agency" April 1st, 2025, 5pm French time (UTC+2) This talk will be hybrid (in person in Bordeaux; Zoom link below) Bordeaux Biologie Sante (BBS) Building, Salle Nord, First floor

Details: https://www.philinbiomed.org/event/nick-lane/ *Abstract:* Life is a surprisingly good guide to its own origins in terms of energy transduction, metabolism and the genetic code. I will give a conceptual overview of our own work on the origin of life in hydrothermal systems, avoiding detailed experimental data. I will outline how an early requirement for membrane bioenergetics to drive CO2 fixation structured later cell evolution, and specifically the singular origin of complex (eukaryotic) life on Earth. Finally I will touch on how these ideas give insights into the physical basis of feelings and their relationship to agency at the level of cells.

Professor Lane's research is on the way that *energy flow has shaped evolution over 4 billion years*, using a mixture of theoretical and experimental work to address the origin of life, the evolution of complex cells and downright peculiar behaviour such as sex. He was a founding member of the UCL Consortium for Mitochondrial Research < http://mitochondria.cs.ucl.ac.uk/cfmr/ >, and is Co-Director of the UCL Centre for Life's Origin and Evolution (CLOE) < https://www.ucl.ac.uk/biosciences/departments/gee/research-centres/ucl-centre-for-life-origins-and-evolution >. He was awarded the 2009 UCL Provost's Venture Research Prize < http://www.ucl.ac.uk/news/news-articles/0910/09102101 >, the 2011 BMC Research Award for Genetics, Genomics, Bioinformatics and Evolution < http://events.biomedcentral.com/bmc-research-awards/ >, the 2015 Biochemical Society Award < http://www.biochemistry.org/Awards/TheBiochemicalSocietyAward.aspx > for his outstanding contribution to molecular life sciences and 2016 Royal Society Michael Faraday Prize and Lecture < https://royalsociety.org/science-events-and-lectures/2017/02/faraday-prize-lecture/ >, the UK's premier award for excellence in communicating science.

Nick Lane is the author of* five* acclaimed books < https://nick-lane.net/books/ > on evolutionary biochemistry, which have sold more than 150,000 copies worldwide, and been translated into 25 languages.

Zoom link: Zoom Nick Lane < https://u-bordeaux-fr.zoom.us/j/86358907176?pwd=uVPRGfgYgWndYwZf3jZNX9ECSI1ysX.1 >

Sincerely,

Thomas Pradeu CNRS Research Director in Philosophy of Science Immunology Unit ImmunoConcEpT, UMR5164, CNRS & University of Bordeaux Presidential Fellow, Chapman University, CA, USA Team Leader Conceptual Biology and Medicine Team < https://immunoconcept.cnrs.fr/conceptual-biology-medicine/ > Coordinator of the Philosophy in Biology and Medicine Network < https://www.philinbiomed.org/ > (PhilInBioMed)

Thomas Pradeu <thomas.pradeu.list@gmail.com>

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CambridgeUK VisualisingBioData Apr8-11

The 15th international workshop on Visualising Biological Data takes place *online* and *in-person* at Magdalene College, University of Cambridge, from 8th-11th April.

In person registration and poster upload (for registered participants closes 31st March. Sign up at https://vizbi.org/2025/Registration VIZBI 2025 consists of a one-day Masterclass and three-day workshop. Participants are invited to submit posters and lightning talks describing their work, and artistic images for the Art & Biology showcase.

The masterclass is aimed at anyone interested in learning about and improving their skills in data visualisation, visual design and animation. It features talks from Drew Berry (WEHI), Andy Lomas (Goldsmiths), Barbora Kozlikova (Mazaryk), Christian Stolte and Daniel Hahn. See https://www.datavismasterclass.org for more details.

The main workshop features keynotes on the use of visualisation for narrative storytelling (Laura Garrison, Bergen), AI and Machine Learning (Marc Streit, Vienna), and 2D and 3D data visualisation (Tobias Isenberg, INRIA Paris-Saclay). A further 18 plenary speakers will cover the latest tools and techniques for gaining insight into life sciences data from DNA, RNA, Protein, Cells, Tissues & Organisms through to Populations.

We hope to see you in person or online in April!

Jim Procter <j.procter@dundee.ac.uk>

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Edinburgh SimultaneousHermaphrodites May7-8

Dear all,

We have decided to extend registration for the SHOW workshop until March 30th. Please find more information about the workshop below.

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Dear all,

We are delighted to announce this year’s edition of the Simultaneous Hermaphroditic Organisms Workshop (SHOW) in Edinburgh on the 7th and 8th of May at the King’s Buildings campus. This meeting is a forum for researchers studying hermaphroditism to share their findings and plan long-term collaborations. Its relaxed environment encourages early-career researchers to present topics relating to hermaphrodite evolution, including population genetics, gene expression, sexual conflict, mating systems, gamete evolution, and experimental evolution.

Please see our website - https://show2025.github.io/ - where you can find all the information, including directions. If you’d like to attend, please complete the registration form: https://docs.google.com/forms/d/e/-1FAIpQLSeG6P8U2DV5BBCLxzmMI76FQoB9E6IKkSTIQHTQZR4kKx6NJg/-viewform .The deadline for registration is 30th March, and we will let people know if they are accepted in April. It is also possible to attend online. Please note that there is no registration fee. We have space for 50 in-person attendees.

We have included time for discussion in the programme. The topics have not yet been finalised, so if you have any suggestions then please do not hesitate to submit them on the registration form.

Thanks to sponsorship from the Genetics Society, we will be able to offer a Carer’s Award to allow people to attend if they need costs to cover caring responsibilities. If you would like to take advantage of this, please see the registration form. In addition, we are happy to help you find cheaper accommodation if needed; please contact us if you need any advice on this.

We hope to see you soon in Edinburgh. With best wishes from your SHOW 2025 organising team, Elpida Skarlou, Roman Stetsenko, Freya Way, Matthew Hartfield, Chenxi Wang, Fanny Laugier.

Matthew Hartfield Room 1.19 Institute of Ecology and Evolution The University of Edinburgh Ashworth Laboratories Charlotte Auerbach Road Edinburgh EH9 3FL, UK

Tel: +44 (0)131 650 8632 Email: m.hartfield@ed.ac.uk Web: hartfieldlab.com The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336. Is e buidheann carthannais a th’ ann an Oilthigh DhÃ^{1}n Ãideann, clàraichte an Alba, àireamh clàraidh SC005336.

Matthew Hartfield <m.hartfield@ed.ac.uk>

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ESEB2025 Barcelona HostAssociatedMicrobiomes Aug17-22

ESEB 2025 Symposium: ’The contribution of the microbiome to host adaptation and plasticity’ (S07).

The ESEB 2025 Congress will be held at the International Convention Centre of Barcelona (CCIB) in Barcelona, Spain, from August 17 to 22,2025.

Abstract submission deadline: April 25th 2025 (link below)

We are excited to announce an exciting symposium on the role of microbiomes in host adaptation and plasticity and we invite you to submit your abstracts for contributed talks and posters. Organisers are Melissah Rowe (Netherlands Institute of Ecology), Florent Mazel (University of Lausanne, Switzerland), and Klara Wanelik (University of Surrey, UK), on behalf of the ESEB funded STN on Wild Animal Microbiome Evolution (WAME).

Contribution of the microbiome to host adaptation and plasticity

All organisms host microbial communities in and on their bodies. Over the last 20 years, there has been an explosion in studies characterising the microbial communities associated with a diversity of host sites (e.g. gut, skin, rhizosphere) in a wide range of taxa across the animal and plant kingdoms. Recent studies have shown that these microbiomes can have major impacts on host biology, including effects on digestion, development, immunity, and behaviour. Indeed, it is now widely recognized that microbiomes can play a fundamental role in host ecology and evolution. However, our understanding of the specific role of microbiomes in the evolutionary process by which a host becomes better suited to its environment (i.e. host adaptation) remains relatively limited. Key examples of microbiome-mediated host adaptation are emerging , but the critical next step is to broaden our understanding of the contribution of microbiomes to host adaptation and the role of microbiome-mediated plasticity in this process.

Our proposed symposium will bring together a diverse group of researchers working in this rapidly growing and important field. We will showcase work spanning a wide range of host study systems and including a variety of theoretical, experimental, and field approaches.

We are pleased to confirm as invited speakers - Dr. Hassan Salem (Max Planck Institute for Biology Tübingen, Germany) and Dr. Carola Petersen (Evolutionary Ecology and Genetics, Zoological Institute of Kiel University, Germany).

For more information and to submit your abstract, please visit: < https://eseb2025.com/call-for-abstracts/ >

We are looking forward to seeing you in Barcelona in August, and hope that you will consider our symposium for sharing your research on host-associated microbiomes.

Best Regards, Melissah Rowe (Netherlands Institute of Ecology) Florent Mazel (University of Lausanne, Switzerland) Klara Wanelik (University of Surrey, UK)

Dr. Melissah Rowe Department of Animal Ecology Netherlands Institute of Ecology (NIOO-KNAW) PO Box 50, 6700 AB Wageningen, The Netherlands m.rowe@nioo.knaw.nl (she/her)

“Rowe, Melissah” <M.Rowe@nioo.knaw.nl>

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ESEB Barcelona 3DGenomeOrganisation Aug17-22

Call for contributed talks and posters for symposium on “New Frontiers in Genome Diversity and Evolution: Exploring the 3D Organization and Function of Genomes” (Symposium 38) at ESEB 2025

The ESEB 2025 Congress will be held at the International Convention Centre of Barcelona (CCIB) in Barcelona, Spain, from August 17th to 22nd, 2025.

Within this congress, we are excited to announce a symposium on the evolution of 3D genome organisation, and we invite you to submit an abstract for a talk or poster presentation. Symposium organisers are Aurora Ruiz-Herrara (Universitat Autonoma Barcelona), Thea Rogers (University of Vienna) and Rui Faria (University of Porto).

Symposium description

The study of genome structure and function across diverse phylogroups is key for our understanding of evolutionary dynamics and their role in speciation and the generation of biodiversity. In this context, the evolution of chromatin conformation is fundamental for deciphering the mechanisms underlying the origin and evolvability of genome architecture, opening new frontiers in comparative genomics and evolution.

This rapidly accelerating research field is fueled by significant recent progress in genomic resources, including the generation of complete genomes. Consequently, this symposium will delve into a cutting-edge area of evolutionary biology, exploring the relationships between 3D genome organization and the evolution of novel genomic, recombination and regulatory patterns. It will provide a forum to discuss topics ranging from local regulatory architecture focusing on the intricate interactions between genes to large-scale genomic processes that can shape the evolution of regulatory regions.

Topics will include, but are not limited to, large-scale genome rearrangements, transcriptional regulation through long-distance enhancer-promoter interactions and chromosome-scale phenomena such as meiosis and dosage compensation. The symposium will also cover functional and comparative genomics, examining the conservation and divergence of genome topology across species. This comparative approach will shed light on the distinct evolutionary trajectories of lineages and offer valuable insights into the genetic underpinnings of species' adaptation and innovation.

We have two exciting invited speakers presenting at this symposium, Claire Mérot, University of Rennes (France), and Harris Lewin, Arizona State University (USA).

For more information and to submit your abstract, please visit: https://eseb2025.com/call-for-abstracts/ We look forward to seeing you in Barcelona in August 2025 and hope you will consider presenting your research on the evolution of the 3D genome at our symposium.

Kind regards,

Thea Rogers (thea.rogers@univie.ac.at)

Aurora Ruiz-Herrera (Aurora.RuizHerrera@uab.cat)

Rui Faria (ruifaria@cibio.up.pt)

Thea <thea.rogers@univie.ac.at>

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ESEB Barcelona AdaptivePolymorphisms Aug17-22

Call for abstracts for the symposium on "The maintenance of adaptive polymorphisms" (Symposium S48) at ESEB 2025, taking place from 17-22 August in Barcelona, Spain.

ABSTRACT SUBMISSION DEADLINE 25th April 2025 https://eseb2025.com/call-for-abstracts/ In the face of decades of work, the maintenance of heritable variation for fitness remains an unresolved question in population genetics. Natural populations often display much more fitness variance than mutation-selection balance or single-locus heterozygote advantage alone can account for. To explain this surplus variance, alternative processes, such as negative frequency-dependent selection, multi-locus balancing selection, spatially or temporally varying selection, antagonistic selection, or genotype-by-environment interactions, have been invoked, yet fundamental questions about the role of these mechanisms in maintaining polymorphism remain open.

Despite growing theoretical and empirical interest, we still lack a comprehensive understanding of such "non-classical" forms of balancing selection and their relative contributions to the maintenance of genetic variance. This symposium aims to spotlight emerging examples of non-classical balancing selection and to address key outstanding questions: (1) How prevalent are these processes in natural populations, and how frequently do they interact? (2) Do they produce distinct population genetic signatures? Can we disentangle such signatures in genomic data? Alternatively, can we devise experiments to identify the type of balancing selection at play?

To foster a discussion of these fundamental issues, our symposium aims to bring together theoreticians and empiricists studying a variety of processes and systems that result in balanced polymorphisms. We welcome contributions from researchers at any career stage.

Invited Speakers Meike Wittmann, Bielefeld University. Bielefeld. Germany Karl Grieshop, University of East Anglia. Norwich. England

Organizers Dr. Hannah Augustijnen, University of Fribourg. Fribourg. Switzerland. Dr. Harshavardhan Thyagarajan, University of Fribourg. Fribourg. Switzerland.

Best regards,

Hannah Augustijnen Postdoctoral researcher Department of Biology University of Fribourg Switzerland

Hannah.augustijnen@unifr.ch

AUGUSTIJNEN Hannah <hannah.augustijnen@unifr.ch>

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ESEB Barcelona EvolutionaryAdaptation Aug17-22

Call for abstracts: symposium on Genomic insights into evolutionary adaptation and species movements in a changing climate at ESEB 2025

ESEB 2025 Congress will be held at the International Convention Centre of Barcelona (CCIB) in Barcelona, Spain, from August 17 to 22, 2025.

Danielle Davenport and Ian Bradbury from Fisheries and Oceans Canada and Samantha Beck of UHI Inverness are pleased to announce the upcoming symposium On Genomic insights into evolutionary adaptation and species movements in a changing climate at ESEB 2025.

Rapid environmental change is altering biodiversity and driving shifts in species' ranges. These changes can lead to phenological mismatches, heightening population vulnerability and disrupting ecological interactions. Genomic tools provide powerful insights into the genetic architecture of adaptive traits, particularly those linked to phenology, helping to understand the vulnerability of populations to climate change and their capacity for range shifts. In this symposium, we highlight our current understanding of the genomic basis of adaptation to climate change, with focal areas of research covering genomic forecasts and traits linked to phenology. By bringing together a diversity of researchers using novel genomic tools to address fundamental conservation concerns, we hope that this symposium inspires collaboration among researchers and promotes the development of innovative methods and strategies for conservation and evolutionary rescue. Our goal is to advance the application of genomic insights to predict species' responses to environmental changes and to inform management practices that support biodiversity and ecosystem resilience in an increasingly unpredictable climate.

We are pleased to confirm as invited speakers Matthew Fitzpatrick, University of Maryland Center for Environmental Science, who will speak on "Can ecological genomics predict population maladaptation under climate change? Lessons learned from 10 years of working with genomic offsets" and Shawn Narum, Columbia River Inter-Tribal Fish Commission/University of Idaho who will speak on "Genetic variation associated with adult migration timing in lineages of Steelhead & Chinook Salmon".

Deadline for abstract submission: 25 April 2025.

For more information and to submit your abstract, please visit: https://eseb2025.com/call-for-abstracts/ Don't miss the opportunity to share your research, engage in stimulating discussions, and network with peers in this exciting area of genomics!

Best regards,

Dr. Danielle Davenport, Fisheries and Oceans, Canada Dr. Samantha V. Beck, UHI Inverness, Fisheries and Oceans Canada, Dalhousie University Dr. Ian R. Bradbury, Fisheries and Oceans Canada

Danielle Davenport (she/her|elle/la) Research Scientist | Chercheur

Fisheries and Oceans | PÃÂches et Océans Canada danielle.davenport@dfo.mpo.gc.ca | 902-580-7049

"Davenport, Danielle (DFO/MPO)" <Danielle.Davenport@dfo-mpo.gc.ca>

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ESEB Barcelona EvolutionaryRates Aug17-22

Call for contributed talks and abstracts for symposium on "Time-dependency in micro- and macroevolutionary rates" (Symposium S49) at ESEB 2025

The ESEB 2025 Congress will be held at the International Convention Centre of Barcelona (CCIB) in Barcelona, Spain, from August 17 to 22,2025.

Within this congress, we are happy to announce this exciting symposium on time-dependency in evolution and we invite you to contribute with talks and posters. Organizers are Erik Svensson (Lund University, Sweden), Stephen DeLisle (Karlstad University Sweden) and Lesley Lancaster (Aberdeen University, UK).

Time-dependency in micro- and macroevolutionary rates

In recent years, there has been an increasing interest in the possible role of time-dependency in evolutionary rates. Such putative time-dependency include systematic slowdowns or accelerations of phenotypic change, speciation and extinction rates estimated from phylogenies, morphological rates in the fossil record and rates of molecular evolution. The strength and generality of these associations has led some researchers to argue that rates of evolution appears to be slower over longer (macroevolutionary) temporal scales, or conversely, rates appear to be faster over short timescales. If rate shifts are real, systematic time-dependency of evolutionary rates will have major consequences for our understanding of the temporal scaling of evolution and for efforts to build bridges between micro- and macroevolution. However, claims for systematic time-dependency have also been criticized, and some researchers argue that such (perceived) time-dependency could result from statistical or methodological artefacts. Thus, it is unclear the degree to which rate-time scaling reflects actual time-dependence of the evolutionary process.

In this symposium, we will discuss the problem of time-dependency across temporal scales, aiming to clarify what may be artefact versus real patterns and how it will affect our understanding of evolution. We invite evolutionary ecologists, comparative biologists, developmental biologists, molecular evolutionists, paleontologists and all other researchers interested in the problem of time-dependency to this cross-disciplinary and highly integrative symposium. We will discuss the methodological and statistical challenges of studying time-dependency in evolution in both extant and extinct organisms. One of our aims with this symposium is to stimulate further discussion of time-dependency in micro- and macroevolution. We will cover methodological, empirical and statistical aspects as well as more conceptual and theoretical issues. We also aim to prepare the ground for a joint review article or theme issue in e.g. Journal of Evolutionary Biology.

We have two exciting invited speakers to this symposium, namely Jeremy Michael Beaulieu (Department of Biological Sciences, University of Arkansas, USA) and Rosana Zenil-Ferguson(Department of Biology, University of Kentucky, USA).

Deadline for abstract submission: 25 April 2025.

For more information and to submit your abstract, please visit: https://eseb2025.com/call-for-abstracts/ We are looking forward to see you in Barcelona in August 2025 and hope that you will consider our symposium for sharing your research on evolutionary rates.

Best regards,

Prof. Erik Svensson, Department of Biology, Lund University, SWEDEN (erik.svensson@biol.lu.se)

Dr. Stephen De Lisle, Dept. Environmental and Life Science, Karlstad University, SWEDEN (stephen.de.lisle@kau.se)

Prof. Lesley Lancaster, School of Biological Sciences, University of Aberdeen, UK (lesleylancaster@abdn.ac.uk)

Erik Svensson Professor (Division for Biodiversity and Evolution) Department of Biology Lund University SWEDEN Homepage: https://portal.research.lu.se/en/persons/erik-svensson Research lab: https://portal.research.lu.se/en/organisations/population-biology-micro-and-macroevolution Research Gate: https://www.researchgate.net/profile/Erik-Svensson-3 Google Scholar: https://scholar.google.se/citations?user=-66nqTEAAAAJ&hl=sv Erik Svensson <erik.svensson@biol.lu.se>

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ESEB Barcelona HabitatFormingSpecies Aug17-22

Dear Colleagues,

on the behalf of my co-organiser Jean-Baptiste Ledoux, I would like to bring your attention to the symposium we are organizing in the upcoming ESEB congress < https://eseb2025.com > in Barcelona. The symposium entitled "S31 | Habitat-forming species and global change: a multidisciplinary perspective on their evolution and adaptive potential to improve their conservation." aims to discuss the evolution of terrestrial and marine habitat-forming species impacted by global change, including climate change.

The two confirmed invited speakers are Dr. Ophelie Ronce (ISEM) and Prof. Thorsten Reusch (GEOMAR).

We encourage studies adopting a multidisciplinary perspective combining for instance population genetics, genomics, transcriptomics, experiments (common gardens or reciprocal transplants), long term in situ monitoring, symbiotic interactions, genomic offset and modeling.

Abstracts can be submitted here < https://eseb2025.com/call-for-abstracts/ > until the 25th of April 2025.

Please feel free to forward this message to interested individuals in your research group and wider community. And please also feel free to write to any of us if you have questions.

Best regards, Didier Aurelle

AURELLE Didier <didier.aurelle@univ-amu.fr>

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ESEB Barcelona LinkageDisequilibrium Aug17-22

Call for abstracts for the ESEB 2025 symposium S02 "Addressing new and long-standing evolutionary questions with linkage disequilibrium based approaches".

The ESEB 2025 Congress will be held at the International Convention Centre of Barcelona (CCIB) in Barcelona, Spain, from August 17 to 22,2025. Within this congress, we are happy to announce this symposium on approaches based on linkage disequilibrium to advance our understanding of evolution and we invite you to contribute with talks and posters.

Many evolutionary processes, such as admixture, selection, drift, structural rearrangements and genetic incompatibilities, can result in non-random associations between loci (linkage disequilibrium), even in the absence of physical linkage. The availability of extensive genomic data for both model and non-model species has fuelled the development of novel and powerful methods to address fundamental questions in evolutionary biology using two-locus statistics, such as correlations in allele frequencies and variance in heterozygosity. These approaches have revolutionized our ability to infer demographic history across various organisms, including humans, expanded our ability to identify genetic incompatibilities underpinning speciation events, enhanced the power of genome-wide association studies (GWAS) and quantitative trait loci (QTL) mapping, and opened new avenues for investigating parallel evolution in non-model taxa, even when the traits under selection are unknown. In this symposium, we aim to showcase how the analyses of genome-wide patterns of linkage disequilibrium allow evolutionary biologists to answer exciting long-standing and new questions.

Invited speakers Aaron Peace Ragsdale (University of Wisconsin-Madison, USA) Claudia Bank (University of Bern, Switzerland).

Organizers Francesca Raffini, Department of Biology and Evolution of Marine Organisms, Stazione Zoologica Anton Dohrn Paolo Momigliano, Department of Ecological and Biological Sciences, Tuscia University; School of Biological Sciences, The University of Hong Kong Paolo Franchini, Department of Ecological and Biological Sciences, Tuscia University

Deadline for abstract submission 25 April 2025

For more information and to submit your abstract, please visit: https://eseb2025.com/call-for-abstracts/ We are looking forward to seeing you in Barcelona in August 2025 and hope that you will consider our symposium for sharing your research.

Best wishes,

Paolo, Francesca and Paolo

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ESEB Barcelona MicroevolProcesses Aug17-22 CallForAbstracts

Call for abstracts: symposium on microevolutionary processes and macroevolutionary patterns at ESEB 2025

ESEB 2025 Congress will be held at the International Convention Centre of Barcelona (CCIB) in Barcelona, Spain, from August 17 to 22, 2025.

Carolin Kosiol from the University of St Andrews, Thibault Latrille and Th??o Gaboriau from the University of Lausanne are pleased to announce the upcoming symposium on microevolutionary processes and macroevolutionary patterns at ESEB 2025. Recent advancements in phylogenetics, phylogenetic comparative methods, and high-throughput genotyping and phenotyping tools provide unprecedented opportunities for studying evolution across different evolutionary time scales. The wealth of emerging molecular and phenotypic data and new integrative statistical tools enable us to address one of the most enduring questions in evolutionary biology: whether and how evolutionary processes observed at population levels scale up to the diversity observed at higher taxonomic levels. This symposium will bring together a variety of topics and approaches that aim at addressing the interface between microevolution and macroevolution. We aim to thrust the field forward by showcasing state-of-the-art approaches that make inferences about macroevolutionary patterns and processes from microevolutionary mechanisms, with an overarching goal to stimulate the use of these powerful approaches for wider fields of evolutionary biology. This symposium will also connect researchers exploring the same questions and raise awareness about model systems that help answer these fundamental questions. We are pleased to confirm as invited speakers Lee Hsiang Liow from the Natural History Museum. Oslo. Norway and Jonathan Rolland from the CNRS. Toulouse. France Deadline for abstract submission: 25 April 2025.

For more information and to submit your abstract, please visit: https://eseb2025.com/call-for-abstracts/ Best regards,

Dr. Thibault Latrille, Universit?? de Lausanne Dr. Carolin Kosiol, University of St Andrews Dr. Th??o Gaboriau, Universit?? de Lausanne

Th??o Gaboriau <theo.gaboriau@unil.ch>

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ESEB Barcelona ReductiveEvolution Aug17-22

Call for talks and posters for a symposium on "Letting go: reductive evolution across the tree of life" (Symposium S32) at ESEB 2025

The ESEB 2025 Congress will be held at the International Convention Centre of Barcelona (CCIB) in Barcelona, Spain, from August 17 to 22,2025.

Letting go: reductive evolution across the tree of life

Evolution has been characterized by a series of major morphological innovations, often associated with the gain of genomic novelty. Gene gains have played a fundamental role in the origins of animals and land plants, while genome duplication has driven the diversification of vertebrates and flowering plants. However, evolution does not always result in greater complexity. The role of loss in evolution, by contrast, remains relatively underexplored. Aided by sophisticated omics data and advanced analytical techniques, the prevalence and significance of reductive events in evolutionary history are being elucidated. Recent research has revealed that groups such as bryophytes, fungi, and tardigrades have undergone significant gene loss and genome simplification, shaping their evolutionary trajectories.

In this symposium, we will explore this important but overlooked evolutionary process. Our speakers will present recent studies that shed light on the role of reductive evolution across the tree of life. This symposium also provides a timely opportunity to highlight and discuss the mechanisms of reductive evolution across diverse taxonomic groups, offering new perspectives on how simplification can be as crucial to evolution as complexity.

We have two exciting invited speakers to this symposium, namely Rosa Fernï¿½ndez (Institute of Evolutionary Biology, Barcelona, Spain) and Sven Gould (Heinrich-Heine-Universitï¿½t, Dï¿½sseldorf, Germany).

Deadline for abstract submission: 25 April 2025.

For more information and to submit your abstract, please visit: https://eseb2025.com/call-for-abstracts/ We look forward to seeing you in Barcelona in August 2025.

Best wishes,

Dr. Alexander Bowles, University of Oxford (alex.bowles@biology.ox.ac.uk)

Dr. James Clark, University of Bath (jc493@bath.ac.uk)

Alex Bowles <alex.bowles@biology.ox.ac.uk>

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Hybrid Wellcome HumanEvolution Apr28-30

Human Evolution - From Fossils to Ancient and Modern Genomes (Hybrid conference) 28-30 April 2025, Wellcome Genome Campus, UK (near Cambridge)

Registration & Poster/Lightning Talk Deadline Approaching! (31 March 2025)

Join us for our 4th Conference on Human Evolutionat the beautiful Wellcome Genome Campus, where we'll explore groundbreaking archaeological discoveries and cutting-edge genetic tools shaping the field.

Topics include: -Evolutionary history -Hominin hybridization, divergence and ecologicalniches -Population structure, demography and mobility -Methodological advances in human history inference -Diseases that impacted ancient humans -Human adaptation

Speakers: María Martinon-Torres - CENIEH, Spain (keynote) Mark Stoneking - LBBE, France (keynote) María Ãvila-Arcos - National Autonomous University of Mexico (UNAM), Mexico Judith Beier - University of Tübingen, Germany Roman Garba - Academy of Sciences of the Czech Republic Amy Goldberg - Duke University, USA Ashley Hammond - American Museum of Natural History, USA Evan Irving-Pease - University of Copenhagen, Denmark Johannes Krause - Max Planck Institute for Evolutionary Anthropology, Germany Martin Kuhlwilm - University of Vienna, Austria Kateryna Makova - Pennsylvania State University, USA Alice Leplongeon - French National Centre for Scientific Research (CNRS), France Sarah Pederzani - University of Utah, USA John Rowan - University of Cambridge, UK

For more details on programme, registration and further information:

https://coursesandconferences.wellcomeconnectingscience.org/event/human-evolution-from-fossils-to-ancient-and-modern-genomes-20250428/ We have a dynamic programme that includes invited talks, short oral presentations, lightning talks and posters selected from abstracts. We hope to see you there!

Nagehan Bahadir Wellcome Connecting Science

On behalf of the Scientific Programme Committee Alice Leplongeon Marta Mirazon Lahr Lluis Quintana-Murci Carina Schlebusch

Nagehan BahadÃ½r, PhD

Programme developer - scientific meetings (She/her)

Learning and Training

Wellcome Connecting Science | Wellcome Genome Campus | Hinxton | Cambridgeshire | CB10 1RQ | UK

Wellcome Connecting Science enables everyone to explore genomic science and its impact on research, health and society.

NagehanRamazanogluBahadir@helix

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Mertola Speciation Apr5-6

Dear Colleagues,

This is the last call for registration in the first edition of the Mértola Evolution Conferences(MECs) on “Speciation: from field studies to genomics”.

Deadline: 20th of March!

Mértola Conferences aim to bring researchers and students from all over the world to discuss cutting-edge studies in biology focusing on evolution (each year a specific topic), fostering new ideas and collaborations. Mértola Conferences are promoted by EBM - Biological Station of Mértola, in collaboration with the Faculty of Sciences and CIBIO-BIOPOLIS from the University of Porto, and other national and international institutions.

Mértola is located in the Southeast Alentejo region of Portugal, near the Spanish border, crossed by the Guadiana river and in the center of the Natural Park of Guadiana Valley. It is a biodiversity hotspot - a prime Mediterranean ecosystem. The antiquity of Mértola is attested by the many archaeological remains that prove the continuous human occupation of this territory. The first traces of human presence date back to the Neolithic period, five thousand years ago, with different civilizations, like Iberians, Phoenicians, Greeks and Carthaginians represented. More information here < http://www.visitmertola.pt/mertola-vila-museu/ >.

The MEC 2025 edition, entitled “Speciation: from field studies to genomics”, is focused on speciation research, where we revisit the earliest studied systems and come back to look at new genomic data with Charles Darwin’s eyes.

MEC 2025 is pleased to announce prominent speakers in evolutionary biology: Peter Grant (Princeton University, USA); Rosemary Grant (Princeton University, USA); Leif Andersson (Uppsala University, Sweden), Joana Meier (University of Cambridge, UK), Roger Butlin (University of Sheffield, UK), Rui Faria (CIBIO/BIOPOLIS, University of Porto), Jeremy Searle (Cornell University, USA, FCUP & EBM) and Rikard Holmdahl (Karolinska Institute, Sweden), among others participants.

PROGRAM DAY 1, 5th of April Chair: Jeremy Searle 9:30-10:00 - Welcome Coffee and Cakes 10:00-10:30 - Opening Ceremony 10:30-11:45 - Rosemary Grant: “Speciation and Hybridization in Darwin’s Finches” 11:45-13:00 - Peter Grant: “Speciation: from Microcosm to Macrocosm” 13:00-14:30 - Lunch 14:30-15:30 - Leif Andersson: “Atlantic herring - an adaptive radiation with incomplete reproductive isolation” 15:30-16:00 - 2 Short contributed talks (12+3 min) 16:00-16:30 - Coffee Break 16:30-18:00 - 6 Short contributed talks (12+3 min) 19:00 - Dinner DAY 2, 6th of April Chair: Leif Andersson 09:30-10:30 - Joana Meier: “The roles of hybridisation and chromosomal rearrangements in rapid adaptive radiations” 10:30-11:00 - Coffee Break 11:00-12:00 - Rui Faria: “The role of chromosomal inversions in Littorina adaptation and speciation” 12:00-13:30 - Lunch 13:30-14:30 - Roger Butlin: “Hybrid zones and reproductive isolation” 14:30-15:00 - Jeremy Searle: “Despeciation” 15:00-15:30 - Coffee Break 15:30-16.00 - Rikard Holmdahl: “Why we became humans” 16:00-17.15 - 5 Short contributed talks 17:15 - Close of Conference 17:30-19:00 - Free time to visit Mértola

ORGANIZATION Leif Andersson, Uppsala University Miguel Carneiro < https://www.cibio.up.pt/en/-people/details/miguel-jorge-pinto-carneiro/ >, CIBIO-BIOPOLIS Rui Faria < https://www.cibio.up.pt/en/-people/details/rui-faria/ >, CIBIO-BIOPOLIS Paulo Célio Alves < https://www.cibio.up.pt/en/people/-details/paulo-celio-alves/ >, FCUP, CIBIO-BIOPOLIS & EBM Jeremy Searle, Cornell University, FCUP & EBM

Rui Faria, PhD

1. Researcher and SEAGEN Group Leader CIBIO,

Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado BIOPOLIS Program in Genomics, Biodiversity and Land Planning Campus de Vairão Rua Padre Armando Quintas, nÂº 7 4485-661, Vairão, Portugal

2. Invited Assistant Professor, Department of Biology Faculty of Sciences at the University of Porto, Rua Campo Alegre s/n 4169-007, Porto, Portugal

Webpages: Littorina Research Community < https://littorina.at.biopolis.pt/ > https://rmigueldefaria.wixsite.com/farialab-1 Rui Faria <ruifaria@cibio.up.pt>

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Newfoundland PlantEvolution Jun10-14

The Canadian Botanical Association's - Association Botanique du Canada (CBA-ABC) annual conference gathers 100-120 motivated professors, students, researchers, professionals, and naturalists to share their latest research findings. The 61st annual conference will take place at Memorial University of Newfoundland in St. John's Canada. This year's edition will be held under the theme "Botany on the rock for conservation and sustainability" and will encompass a wide range of botanical research fields, including physiology, taxonomy, phylogeny, genomics, mycology, plant development, ecology and conservation.

We have three exciting public talks

Plenary lecture: Dr. Warren Cardinal-McTeague, University of British Columbia

Weresub lecture: Dr. Yolanda Wiersma, Memorial University of Newfoundland

Flora of Newfoundland: MSc. Susan Meades, Great Lakes Forestry Centre

Main symposium speakers

Development: Dr. Danve Castroverde, Wilfrid Laurier Univ.

Ecology and Conservation: Dr. Carissa Brown, Memorial Univ.

Mycology: Dr. Az Klymiuk, Univ. Manitoba

Systematics, Evolution and Biodiversity: Dr. Edeline Gagnon, Univ. Guelph

Teaching: Dr. Laura Super, Univ. British Columbia

Three additional symposia are:

"Genomics for plant evolution, ecology and conservation"

"Fungi in Canadian forests"

"Plant ecology at the edges: ecotones and range limits"

And a teaching workshop on universal design for learning (UDL) offered by Dr. Laura Super, Univ. British Columbia

Several student and travel awards will be given. Deadline for abstract submission and early bird registration is April 1st.

For more information and to submit an abstract click here: https://harlowagency.swoogo.com/cba-abc-61stconference For more information on the Canadian Botanical Association please visit our website here: https://www.cba-abc.ca/ We are looking forward to seeing you in St John's in June 2025 and hope that you will consider our conference for sharing your research

Julissa Roncal, PhD

Associate Professor at Memorial University of Newfoundland, Canada

Canadian Botanical Association Vice-president

–

Julissa Roncal, Ph.D. (she/her)

Associate Professor and Curator of the Ayre Herbarium

Department of Biology

Memorial University of Newfoundland

45 Arctic Avenue

St. John's, NL, A1C 5S7, Canada

Office CSF4331, phone (709) 864 2241

Ayre herbarium (709) 864 6233

Mobile: (709) 351 6771

http://julissaroncal.wordpress.com/ Associate editor for the American Journal of Botany

https://bsapubs.onlinelibrary.wiley.com We acknowledge that the lands on which Memorial University's campuses are situated are in the traditional territories of diverse Indigenous groups, and we acknowledge with respect the diverse histories and cultures of the Beothuk, Mi'kmaq, Innu, and Inuit of this province.

"Roncal, Julissa" <jroncal@mun.ca>

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OnlineAndInUkraine DrosophilaExptGenetics Jun16-18

IX International Conference “Drosophilà in Experimental Genetics and Biology” 16.06.2025 - 18.06.2025 Online and in-person.

Dear colleagues!

We are glad to invite you to take part in the IX International Conference ≪Drosophila in Experimental Genetics and Biology≫, which will be held at Lesya Ukrainka Volyn National University on 16-18 June 2025.

Participants are required to fill the registration form in the link: https://forms.gle/Lrzu3qB1BYDLkFqX9 until April 1, 2023 Languages of the conference - Ukrainian and English.

Conference venue: Volyn region, Shatsk district, village of Svityaz, field research station “Hart” of Lesya Ukrainka National University, Lutsk, Ukraine. The conference will include an online school with the participation of scientists from Ukraine, Finland, Serbia, United Kingdom, France, the Netherlands, and Italy. Participants will have the opportunity to familiarize themselves with a wide range of topics in Drosophila research and take part in workshops dedicated to molecular biology methods and the basics of bioinformatics.

Please note: The Organizing Committee does not pay for travel, accommodation and meals of the participants. All questions can be send to the following email address: zinchenko.maria@vnu.edu.ua, Zinchenko Maria

The abstracts of the Conference will be published on the website of the Faculty of Biology and Forestry of Lesya Ukrainka Volyn National University.

Abstract guidelines

Abstract should not exceed one A4 page, in Microsoft Word format (doc or docx), written in Ukrainian or English. Tables and figures are not allowed. The font for the entire text is Arial, font size - 12 pt, line spacing - multiplier, 1.25.; all page margins should be 2 cm. Abstract may contain 1-4 sources of literature at the end.

Thesis structure: 1) Abstract title (bold letters, aligned to center of page, font size 14 pt). 2) Last and first name (initial) of the author/authors of the abstract. 3) Author’s (s’) affiliation: name of the institution, city, country, e-mail of the author(s). Alignment - centered, font size - 11 pt, style - italic. 4) Main text, left-aligned. The indentation of the first line of the paragraph is 1 cm. The text of the abstract should not contain hyphens and bold letters. Latin names of species and names of genes should be italicized. 5) Abstract must contain information about the author’s/authors’ own research. The text must be proof-read, and does not contain spelling and punctuation errors.

The name of the abstract file must correspond to the presenter’s name in Latin.

An example of abstract formatting

Title of work Author A., Author B., Author C. Department, Official name of the institution, Email address: autorb@gmail.com

Abstract text. The first sentence should have an indent of 1 cm. The font is Arial, the size is 12 pt. Alignment is on the left edge.

Registration fees The registration fee for onsite participants is 10 Euro and 5 Euro for online participation. The costs from the registration fees will be spent for the organization of coffee-breaks, postal costs, and so forth. Fees can be paid using paypal account qwota@ukr.net. Please indicate the purpose of the payment: Online (or in-person) participation in 9th Drosophila conference, Name Surname. Recipient - Aleksandr Zhuravlev

Please note: The Organizing Committee does not pay for travel, accommodation and meals of the participants.

With best regards, Organizing Committee of the Conference

Organizing Committee of the Conference: Oleksandr Zhuravlev - Dean of the Faculty of Biology and Forestry, Candidate of Biological Sciences, Associate Professor of Lesya Ukrainka Volyn National University, Chairman of the Organising Committee

Mariia Zinchenko - Candidate of Biological Sciences, Associate Professor, Lesya Ukrainka Volyn National University.

Iryna Kozeretska - Doctor of Biological Sciences, Associate Professor, National Antarctic Scientific Center of the Ministry of Education and Science of Ukraine, Co-Chair

Maria Bayliak - Doctor of Biological Sciences, Professor, Vasyl Stefanyk Precarpathian National University.

Dmytro Gospodaryov - Candidate of Biological Sciences, Associate Professor, Vasyl Stefanyk Precarpathian National University

Oleksandra Abrat - Candidate of Biological Sciences, Associate Professor, Vasyl Stefanyk Precarpathian National University

Oleksandr Maistrenko - PhD, PostDoc, Royal Netherlands Institute for Marine Research

Oleksandra Protsenko - Candidate of Biological Sciences, Taras Shevchenko National University of Kyiv, National Antarctic Scientific Center of the Ministry of Education and Science of Ukraine

Pirko Nadiia - Candidate of Biological Sciences, Taras Shevchenko National University of Kyiv.

Svitlana Serga - Candidate of Biological Sciences, CBGP, INRAE, Montpellier, France, National Antarctic Scientific Center of the Ministry

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.mcmaster.ca/~brian/evoldir.html

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Online ESEB InternalConflictsSTN Mar20

Dear colleagues,

We would like to invite you to the next online seminar for the “Internal Conflicts and Organismal Adaptation” Special Topic Network (STN) funded by the European Society for Evolutionary Biology, which will take place on March 20th, 22:00 UTC. Our speakers for this seminar are:

Elizabeth Ostrowski (University of Washington Bothell): Evolutionary genomics of kin recognition in the social amoeba Dictyostelium

Amy Boddy (University of California Santa Barbara): Fetal microchimerism in pregnancy and beyond

Meeting details: Link: https://georgetown.zoom.us/j/91001126475 Date: March 20th, 2025 Time: 22:00 UTC (check https://www.timeanddate.com/worldclock/converter.html for conversion)

If you would like to get on our mailing list and take part in our upcoming events, please visit our website (https://internalconflictsstn.wordpress.com/) for more information.

Sincerely, The Internal Conflicts and Organismal Adaptation STN Manus Patten, Martijn Schenkel, Arvid Ãgren, Nina Wedell, and Thomas Hitchcock

Manus Patten <mmp64@georgetown.edu>

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SMBE Barcelona SpeciesRangeMargins Aug17-22

Call for Abstracts: ESEB Symposium S14 - Evolution at Species Range Margins - August 17-22

Abstracts are invited for this symposium in the upcoming ESEB 2025 Congress in Barcelona, which will take place on 17th - 22nd August. The symposium aims to share new insights on why species have range margins and how and why marginal populations may evolve differently from others.

Background Almost all organisms have geographical distributions that are limited by range margins. But why? What prevents the evolution of local adaptation in populations at a range margin from allowing the species to expand its range into new territory? One idea is that marginal populations are small and genetically depauperate, with limited potential for local adaptation. Gene flow into such populations would then increase their adaptive potential. Another idea is that migration into range margins may bring maladaptive alleles compromising the performance of marginal populations and the species’ potential for expansion. Further questions of interest are: How do margins at high latitudes differ or resemble those at high elevations? Might the evolution of southern versus northern marginal (or leading- versus trailing-edge) populations differ? And how should we expect marginal populations to respond to changing environments or climates compared to more central populations? These are old questions, but answers remain elusive. We are keen to include in the symposium theory on species range margins and expansions and empirical work testing the theory, with research on different organisms (animals, plants and microbes) in different types of marginal habitats (latitudinal, elevational, precipitation-dependent, edaphic) and with different biological foci (ecological, population genetic).

Organizers Dr. Shengman Lyu, University of Lausanne Prof. John Pannell, University of Lausanne Prof. Sophie Karrenberg, Uppsala University

Invited Speakers Anna Hargreaves, McGill University, Montreal, Canada Lesley Lancaster, University of Aberdeen, Aberdeen, United Kingdom

Deadline for abstracts submission 25 April 2025

For more information and to submit your abstract, please visit: https://eseb2025.com/call-for-abstracts/ John Pannell <john.pannell@unil.ch>

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Spain ESEB MolEvol Aug17-22,25-28

For anyone planning to go to Spain next summer, I am advertising two conference opportunities.

At ESEB in Barcelona, I am organizing the symposium, "Gene Content Across Genomes: Models and Genomic Data" with Raquel Assis (Florida Atlantic University, USA). Keynote speakers for this symposium are Ingo Ebersberger (University of Frankfurt, Germany) and Anne-Ruxandra Carvunis (University of Pittsburgh, USA). If you want to speak in this symposium on either your modeling framework or your genomic characterization/genomic data, please do submit an abstract.https://eseb2025.com/list-of-symposia/#S25 Once you have travelled to Spain, the week after ESEB, come join us at Journal of Molecular Evolution: A European Meeting. This meeting is free, with no registration fee. There are still speaking slots and poster spaces available, so please do submit an abstract. https://www.mncn.csic.es/es/investigacion/JME2025 Please join us in both Barcelona and Madrid this August.

David Liberles

David A Liberles <daliberles@temple.edu>

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SwissAlps ArtificialSelection Aug12-15

Conference/workshop on The evolutionary consequences of unintended artificial selection on population viability in the Swiss Alps; Aug 12-15, 2025

Where: in a remote but well-equipped hotel (https://www.fafleralp.ch/) in the Jungfrau-Aletsch-Bietschhorn UNESCO World Heritage.

Invited faculty: - Shawn Narum (University of Idaho & Columbia River Inter-Tribal Fish Commission, USA) - Katja Räsänen (University of Jyväskylä, Finland) - Jérôme Goudet (University of Lausanne, Switzerland) - Yngvild Vindenes (University of Oslo, Norway) - Madhav (Maddy) Thakur (University of Bern, Switzerland) - Tamás Székely (University of Bath, UK) - Claus Wedekind (University of Lausanne, Switzerland)

The conference/workshop is open to PhD students, postgraduate students, postdocs and other academics from all universities worldwide, but the number of participants is limited.

Abstract: Wild populations are shaped by natural selection, sexual selection, and (mostly unintended) artificial selection. The latter include, for example, a decline of the mean breeding value for horn size in response to trophy hunting, or reduced individual growth rates in response to size-selective fishing. Previous research in this context has concentrated on the evolutionary responses in the specific traits under selection. The effects of unintended artificial selection on population viability are still largely unclear. For example, artificially changed selection regimes can increase the genetic load of natural populations, either by directly selecting against individuals of high breeding value for fitness (e.g., if fast growth is an indicator of low genetic load) or by relaxing natural and sexual selection and hence reducing purifying selection (e.g., in supportive breeding programs). We will discuss such problems in the context of current environmental changes and the potential of rapid evolution.

Application is open now. Participants are expected to present some of their work (talk or poster). Please send a title and abstract before July 1st, 2025.

Further information & registration: https://www.cuso.ch/activity/?p=1128&uid=7680 Claus Wedekind Department of Ecology and Evolution, Biophore, University of Lausanne, 1015 Lausanne, Switzerland. Tel. +41 21 692 42 50 https://www.unil.ch/dee/wedekind-group Claus Wedekind <claus.wedekind@unil.ch>

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YosemiteNatlPark Symbiosis Apr18-20

Registration Deadline is March 14 at midnight. Registration is FREE for graduate students and postdocs who present their work.

Dear Colleagues, The THIRTEENTH annual Yosemite Symbiosis Workshop will take place on April18-20th, 2025 at the Sierra Nevada Research Institute,Yosemite National Park.

In the previous 12 years, this meeting became a great venue for a diversity of symbiosis researchers. We hope to continue to attract a diverse group in 2025! KEYNOTE SPEAKER: Britt Koskella, UC Berkeley https://naturesmicrocosm.com/ REGISTER HERE: https://snri.ucmerced.edu/form/symbiosis-workshop-2025 LEARN EVEN MORE HERE: https://www.sachslab.com/symbiosis-2015.php *Why:* Our goal is to better integrate scientists who focus on symbiosis research, including researchers that study animal-microbe and plant-microbe systems, as well as broader topics related to microbiomes, cooperation, and mutualism. This will be our 13th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

Who: The meeting is small and intimate by design (45 participants). We typically cover a range of symbiosis topics from ecology and evolution to molecular mechanisms in different model and non-model systems.

*What: *The meeting will be made up of two half-days of talks and one poster session. Other than the keynote (˜1 hour), talks are 15 minutes long (including time for questions). Posters are flexible for size, but the ideal poster should be no larger than ˜4 feet square. When you apply for the meeting, you will provide your preference for a talk or poster.

*When: *A welcome party will occur for everyone arriving on the evening of Friday April 18th. The talks and poster sessions will be held Saturday and Sunday April 19-20, 2025.

Where: This is the best part! The meeting takes place at the Sierra Nevada Research Station, in Wawona California, within the border of Yosemite National Park!

What will it cost? We have secured funding from the Gordon and Betty Moore foundation*, allowing us to make the meeting FREE to graduate students and postdocs. *The registration will still be $300 for PIs and other types of participants (e.g. industry/foundation/journalist). The registration deadline is March 14, 2025.

*Registration *will require an abstract. Everyone who registers on time gets to present a talk or poster (your choice).

What does registration include? Registration includes lodging Friday and Saturday nights, a welcome party with light refreshments on Friday night, all meals on Saturday, and breakfast and lunch on Sunday. The cabins are rustic with shared, dorm-like rooms and bunk beds. There are no single rooms. Please don't register unless you are comfortable with the idea of staying in a rustic cabin or sharing a room. For questions about travel or lodging, please feel free to email Carolin Frank (cfrank3@ucmerced.edu).

Sorry, no guests The Yosemite field station is getting busier every year with researchers, and so must prioritize participants over guests. If you want to bring guests, we kindly ask that you make your own arrangements with the nearby Wawona hotel. If you are breastfeeding, we can try to accommodate your baby and partner, but there's no guarantee. Please email Carolin if this is your situation (cfrank3@ucmerced.edu).

Please fill out the registration form below. If you are a PI, you need to pay the registration fee in order for your registration to be complete. Payment is by credit card only. Cancellations are not allowed, but in the event that we need to cancel the workshop (e.g. due to weather), you will get a refund.

Please direct any questions to the organizers:

Joel Sachs joels@ucr.edu

A. Carolin Frank cfrank3@ucmerced.edu

Joel L. Sachs *Professor & Chair, * Evolution Ecology & Organismal Biology University of California, Riverside Chair's Office 2730 Life Sciences Building Research Office 5406 Boyce Hall Office (951) 827-6357 / Fax (951) 827-4286 / http://www.sachslab.com Zoom: http://ucr.zoom.us/my/Sachsevolution *Post address*: Sachs Lab - UC Riverside 3401 Watkins Dr., 1229 Spieth Hall, Riverside, CA 92521 joels@ucr.edu

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GradStudentPositions

Budapest SocialEvolParentalCare

The social ecology of parental care in an island bird PhD studentship based in Budapest, 2025-2029 Supervisors: Dr G.C. McDonald, Dr A. Kosztolányi & Prof. Tamás Székely University of Veterinary Medicine Budapest, Hungary (https://univet.hu/)

Parental care encompasses a diverse array of physiological and behavioural adaptations in both humans and non-human animals. Parents must defend offspring from threats and shelter them from climatic extremes. Understanding the drivers of this diversity has remained a central focus in evolutionary biology and is increasingly important given the challenges faced by wild populations as a result of climate change, predator invasions and human disturbance. Crucially, in nature individual parents are rarely independent actors and are instead embedded within complex social networks characterised by diverse social interactions. The proposed PhD project will investigate the role of the social environment in influencing patterns of parental care.

The project will focus on an individually marked natural population of ground-nesting plovers on the island of Maio, Cabo Verde. Our team has investigated the behaviour and ecology of this population since 2007. The research will combine detailed studies of parental behaviour, population monitoring and field experiments. We collaborate with a local NGO, Maio Biodiversity Foundation (FMB), and the PhD student will have the opportunity to assist conservation programmes on the island.

The student will be based within the University of Veterinary Medicine Budapest with fieldwork opportunities to study birds in their natural island habitats. Our team is carrying out cutting-edge research including GPS tracking and the PhD student will benefit from an international network of experts, with opportunities to gain international research experience.

We are seeking candidates with an MSc in a biological subject, a strong interest in fieldwork, biodiversity, animal behaviour, evolutionary biology and be willing to work in remote areas. Scholarships are available for Hungarian nationals. EU students may be eligible for funding from the Hungarian government. For several other non-EU countries, Stipendium Hungaricum offers a scholarship (https://stipendiumhungaricum.hu/). Interested candidates should get in touch by sending their

CV (max 2 pages) to grant.mcdonald@univet.hu by the 31st of March 2025.

Selected references: > Székely, T., Carmona-Isunza, M.C., Engel, N., Halimubieke, N., Jones, W., Kubelka, V., Rice, R., Tanner, C.E., Tóth, Z., Valdebenito, J.O., Wanders, K., McDonald, G.C. 2024. The causes and implications of sex role diversity in shorebird breeding systems. Ibis 166, 357-385. https://doi.org/10.1111/ibi.13277 > McDonald, G.C., Cuthill, I.C., Székely, T., Kosztolányi, A. 2023. Remating opportunities and low costs underlie maternal desertion. Evolution 77, 97-109. https://doi.org/10.1093/evolut/qpac020 > McDonald, G.C., Engel, N., Ratāo, S.S., Székely, T., Kosztolányi, A. 2020. The impact of social structure on breeding strategies in an island bird. Scientific Reports 10, 13872. https://doi.org/10.1038/s41598-020-70595-w Dr Grant C. McDonald Associate Professor

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University of Veterinary Medicine Budapest,

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CEFE-Montpellier EvolutionaryGenomicsAndTheory

DQpIZWxsbywNCg0KSSBoYXZlICp0d28qIGZ1bGx5IGZ1bmRlZCBQaEQgb3Bwb3J0dW5pdGllcyBp
biBteSBsYWIgKHRvIHN0YXJ0IE9jdCAyMDI1KSwNCndpdGggZ2Vub21pY3MgYW5kIHBvcHVsYXRp
b24gZ2VuZXRpY3MgdGhlb3J5LiBUaGlzIGlzIHBhcnQgb2YgdGhlIEVSQw0KUmVnRXZvbCBwcm9q
ZWN0IGRlZGljYXRlZCB0byBiZXR0ZXIgdW5kZXJzdGFuZCB0aGUgbXVsdGlmYWNldGVkDQpldm9s
dXRpb25hcnkgY29uc2VxdWVuY2VzIG9mIGNpcyBhbmQgdHJhbnMgcmVndWxhdG9yeSB2YXJpYXRp
b24uDQoNCk9uZSBpcyB0byB3b3JrIG9uIHNleC1hc2V4IHRyYW5zaXRpb25zIHdpdGggQ2hyaXN0
b3BoIEhhYWc7IHNlZSBwcm9qZWN0DQpkZXNjcmlwdGlvbiwgYW5kIGFwcGxpY2F0aW9uIGluc3Ry
dWN0aW9ucyBoZXJlOiBiaXQubHkvNGhwMXExQQ0KDQpPbmUgaXMgdG8gd29yayBvbiBhbGxlbGUt
c3BlY2lmaWMgZXhwcmVzc2lvbiB3aXRoIFN5bHZhaW4gR2zvv71taW47DQpzZWUgcHJvamVjdCBk
ZXNjcmlwdGlvbiwgYW5kIGFwcGxpY2F0aW9uIGluc3RydWN0aW9ucyBoZXJlOiBiaXQubHkvNGl1
S0x1UQ0KDQpUaGUgUGhEcyB3aWxsIGJlIGJhc2VkIGluIHRoZSBHRUUNCjxodHRwczovL3d3dy5j
ZWZlLmNucnMuZnIvZW4vcmVzZWFyY2gvZXZvbHV0aW9uYXJ5LWVjb2xvZ3kvZ2VuZXRpcXVlLWV0
LWVjb2xvZ2llLWV2b2x1dGl2ZS0zPg0KdGVhbSBpbiBDRUZFIGxhYiBpbiBNb250cGVsbGllciwg
YSBsYXJnZSBhbmQgaW50ZXJuYXRpb25hbCBncm91cA0Kb2YgZXZvbHV0aW9uYXJ5IGdlbmV0aWNp
c3RzIGFuZCB3aWxsIGludGVyYWN0IHdpdGggc2V2ZXJhbCBjbG9zZQ0KY29sbGFib3JhdG9ycw0K
DQpJbnRlcmVzdGVkIGNhbmRpZGF0ZXMgY2FuIGNvbnRhY3QgbWUgaW5mb3JtYWxseSBmb3IgZXh0
cmEgZGV0YWlscw0KaWYgbmVlZGVkLg0KDQpUaGFua3MgdG8gc3ByZWFkIHRoZSB3b3JkIHRvIGlu
dGVyZXN0ZWQgbWFzdGVyIHN0dWRlbnRzIQ0KDQpUaG9tYXMgTGVub3JtYW5kDQoNCg0KVGhvbWFz
IExlbm9ybWFuZA0KQ05SUyByZXNlYXJjaCBkaXJlY3Rvcg0KUEkg
czovL3d3dy5jZWZlLmNucnMuZnIvZnIvcmVjaGVyY2hlL2VlL2dlZS84
LWxlbm9ybWFuZD4NCkxhYiB3ZWJzaXRlDQo8aHR0cHM6Ly93d3cu
Q0VGRSBMYWIsIE1vbnRwZWxsaWVyIEZyYW5jZQ0KDQpUaG9tY
bGVub3JtYW5kQGNlZmUuY25ycy5mcj4NCg0KKHRvIHN1YnNjcmli
RXZvbERpciBzZW5kIG1haWwgdG8NCmdvbGRpbmdAbWNtYXN0Z
bWNtYXN0ZXIuY2E+KQ0KDQoNCg

CharlesU EvolutionGeneticCodes

PhD position - "Tracing the alternative nuclear genetic codes in non-model eukaryotes"

PhD project description: For reasons that are still unclear, ciliates serve as an evolutionary hotspot for the emergence of various genetic code aberrations. The aim of the proposed PhD project is to reconstruct the evolution of the most common variant of alternative nuclear genetic code in ciliates and eukaryotes, where UAA and UAG codons encode an amino acid instead of translation termination. In collaboration with the Laboratory of RNA Biology of Protists (Biology Centre, Czech Academy of Sciences), a student will reveal underlying mechanisms behind this major change of how information in the sequence of mRNA is translated into the protein.

What we offer: A 4-year Ph.D. position is available under the Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic. The position is funded by the Czech Science Fundation (full-time salary, attendance of scientific meetings, research) and includes also a scholarship for PhD students.

Application process: We are looking for candidates with a strong interest in microbiology, evolution, and molecular biology. They should have experience or interest in learning some basic bioinformatics. They should be fluent in English (written and spoken) with good communication and organisational skills. The successful candidate has to hold a Master's degree in Biology before they start the PhD study. To apply, please send a cover letter explaining your background, skills, and motivation for this position, your CV, and contact details of at least one academic reference willing to provide a recommendation. Please submit your application before March 31, 2025 to tomas.panek@natur.cuni.cz.

Research Interests of our lab: We combine in silico approaches with genome/transcriptome sequencing and advanced electron microscopy to characterize novel deep-branching lineages of microbial eukaryotes, their metabolism, cellular and molecular peculiarities.

OUR WEB: https://web.natur.cuni.cz/zoologie/-panek/research/ OUR PUBLICATIONS: https://-/scholar.google.com/citations?hl=cs&user=-XtWBV9MAAAAJ The PhD position starts on 1st October 2025.

We look forward to receiving your application!

TomáÂ^1 Pánek, Ph.D. Lab Head

Laboratory of Comparative Genomics of Microbial Eukaryotes Department of Zoology Faculty of Science Charles University Vinicna 7, Prague 2, 128 43 Czech Republic (Czechia)

Mgr. TomáÂ^1 Pánek, Ph.D. Tel.: +420 221 95 1072 E-mail: tomas.panek@natur.cuni.cz

Department of Zoology; Faculty of Science Charles University in Prague Faculty of Science Vinièná 7, 128 43 Praha 2 www.natur.cuni.cz/en "Mgr. TomáÂ^1 Pánek" <tomas.panek@natur.cuni.cz>

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CharlesU Prague AdaptationToPathogen

Graduate position at Charles University Prague focused on avian evolutionary immunology

The Evolutionary and Ecological Immunology (EEI) group at the Faculty of Science, Charles University, Prague, is opening a four-year funded PhD position in avian evolutionary immunology (deadline for applications: 6th April 2025).

PhD project topic: ?Immunological mechanism of host evolutionary adaptation to increasing virulence in a novel avian pathogen?

Despite their importance in predicting epidemiological trends, the molecular mechanisms of animal immunity evolution in response to infectious diseases remain mostly unknown. In the 1990s, a new strain of Mycoplasma gallisepticum (MG) caused an epidemic of mycoplasma conjunctivitis in house finches (Haemorhous mexicanus), leading to significant population declines. Recent results obtained in collaboration with our American colleagues indicate that finches have adapted to MG by increasing tolerance rather than resistance, which in coevolution promotes pathogen virulence, contributing to its transmission. Our American colleagues have access to house finch individuals from different populations, and also viable historical isolates of MG (from the 1990s as well as recent) available for infection experiments. This doctoral project aims to:

1. Analyze gene expression changes during MG infection using transcriptomics. 2. Develop a sterile immunological model to identify key regulatory genes. 3. Experimentally test the effects of knocking down key immune molecules. 4. Compare inflammation-related gene variations across finch populations. 5. Investigate immune responses to different pathogen exposures. This project is innovative in its interdisciplinary application of the modern -omics approaches and also in bridging the traditionally divided disciplines into evolutionary immunology, directing a new focus of infection biology.

Requirements: Candidates should have a strong interest in avian evolutionary biology, immunology and molecular genetics. MSc degree in biology (immunology, zoology, genetics or related fields) and good English language skills are required. For the formal requirements, please check the university web page (https://natur.cuni.cz/en/admissions/doctoral-study/-conditions-of-admission-procedure/programmes-with-commencement-in-october).

Offers: We offer a funded PhD position for four years starting from 1st October 2025. The university rules guarantee that the student will receive at least 25000 CZK/month (equivalent of ca. 1000 EUR/month). Additional salary will be negotiated based on skills and results. The PhD student will be part of a young and enthusiastic interdisciplinary team (https://-web.natur.cuni.cz/zoology/eei). Despite close collaboration with several co-workers, the project allows independent intellectual input. Collaboration with Dana Hawley's research group (https://www.biol.vt.edu/faculty/-hawley/index.html) opens the possibility of a research visit to Virginia Tech, US. We expect at least three articles to be published in the course of the study in international peer-reviewed journals. Active participation at international scientific conferences will be encouraged and supported.

Application: Applications are submitted through a Google form (https://forms.gle/-ykPMJmJ5aNPeAg1a7). Applications delivered via postal service or e-mail will not be considered.

Links: For further information see the EEI group web page (https://web.natur.cuni.cz/zoology/-eei/opportunities/), and the web of the Faculty of Science, Charles University (https://natur.cuni.cz/-en/admissions/doctoral-study/menu) or contact Prof. Michal Vinkler at michal.vinkler@natur.cuni.cz (no applications).

We look forward to receiving your online application until 6th April 2025.

Kind regards,

Michal Vinkler

doc. RNDr. Michal Vinkler, PhD

Head of the Department of Zoology Faculty of Science, Charles University Vinicna 7, CZ 128 44 Praha 2 Czech Republic, EU

Laboratory for Evolutionary and Ecological Immunology Animal Evolutionary Biology Unit

tel: +420221951845 e-mail: michal.vinkler@natur.cuni.cz

Michal Vinkler <vinkler1@natur.cuni.cz>

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CharlesU Prague BiogeographyEvolution

PhD Position in Biogeography and Evolution of Vertebrates

Research Group: Biogeography and Evolution (Antonin Machac) Department of Ecology, Charles University, Prague

https://machac.weebly.com https://natur.cuni.cz/en/biology/departments-and-work-places/department-of-ecology

Deadline: April 10, 2025

How did the diversity of life on Earth emerge? The successful candidate will address this fundamental question by analyzing the fascinating biodiversity of mammals, birds, amphibians and reptiles (approx. 30,000 species), integrating their phylogenies, maps and traits, to uncover the general principles that govern the evolution of vertebrate biodiversity. The candidate will work independently but also in close collaboration with our team and research partners internationally (ETH Switzerland, S-BiK Frankfurt, UBC Vancouver, CMEC Copenhagen). This PhD topic will be addressed using modern statistics, making the student highly qualified after graduation for work within academia and in private companies. The PhD position is funded by the Czech Science Foundation and further supplemented by the university scholarship. It builds on a large-scale vertebrate dataset and covers multiple pre-defined themes, which can be tailored to the specific interests of the PhD candidate. The collaborations, the pre-defined and the tailored themes will ensure secure dissertation research but also opportunities for high risk/high gain results.

*** PhD involves

- doctoral studies at Charles University in Prague (Department of Ecology), which belongs to the leading research institutions in the Czech Republic. The Department is situated in the historical center of Prague, one of the world's most beautiful and monumental cities - study of global vertebrate biodiversity (mammals, birds, amphibians, reptiles) - integrating molecular phylogenies, geographic maps and species traits to uncover the processes that generated biodiversity around the world and over time - addressing fundamental questions about the evolution of biodiversity, using modern statistics (regression analyses, GIS geographic information systems, phylogenetic comparative methods, implemented in R)

*** We offer

- friendly, creative and supportive environment of a large international team - membership in the diverse international PhD student community at Charles University - competitive salary (composed of 4-year PhD scholarship, doubled for 2.5 years through a research grant) sufficient to comfortably cover living costs in Prague (will be discussed at the interview) - interdisciplinary experience through national (Petr Baldrian, David Storch, Center for Theoretical Studies, IMIC) and international collaborations (ETH Zurich, Univ Copenhagen), including fully funded opportunities to attend international conferences - fully covered health insurance and contribution to the social security system - support for establishment of foreign students via the Staff Welcome Center of the University

*** We require

- strong motivation to pursue interdisciplinary research at the interface of evolution, ecology, and statistics - MSc degree in biology or related fields (in early fall 2025 at the latest) - good spoken and written English, communication at the Department is fully in English

*** Desirable but not required

- experience with quantitative methods, R programming, GIS - background in phylogeny-based research - experience with presenting and publishing research

Please submit (1) your CV, (2) one-page motivation letter, (3) contact information for one reference to Antonin Machac (A.Machac@email.cz) with “PhD Student Position 2025” in the subject line. Review of applicants will begin on April 10, 2025, and continue until the position has been filled. The first round of online interviews with pre-selected applicants will take place on April 15, 2025. The successful candidate will be assisted in submitting their PhD application to the university. The exact start date is negotiable. You can find more on the website: https://machac.weebly.com Antonin Machac <A.Machac@email.cz>

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CharlesU Prague EvolGeneticsGermlineDev

Evolutionary Genetics Group at Charles University in Prague

A PhD position is available

The fate of immortality: Understanding the mechanisms of germline-soma distinction in birds

Application deadline: March 30th, 2025 Position is for 4 years and starts in October 2025

The early specification of the immortal germline and the development of a truly disposable soma, whose main function is to carry the germline to the next generation, is a key innovation of animals with many important evolutionary consequences. However, the genetic and molecular mechanisms behind the germline-soma distinction are still poorly understood. This project aims to investigate the mechanisms of germline specification in songbirds, where germline-soma differentiation is associated with the elimination of so-called germline-restricted chromosome from somatic cells during early development. The project will combine state-of-the-art genomic and cytogenetic approaches with CRISPR/Cas9 gene editing. The PhD candidate should have experience in molecular biology, genetics and/or developmental biology. The results will have implications not only for understanding the development of the immortal animal germline, but also for studies of animal infertility and cancerogenesis, as cancers share many characteristics with immortal germ cells. The successful candidate will have the opportunity to work in an interdisciplinary team of young researchers experienced in cytogenetics, genomics and bioinformatics.

Where we are based: Our group is based at the Department of Zoology, Faculty of Science, Charles University, which belongs to the leading research institutions in the Czech Republic. The Faculty of Science is situated in the center of Prague, one of the world's most beautiful and monumental cities.

How to apply: If interested, please, send (1) CV, (2) motivation letter and (3) contact details for 2 referees to Radka Reifova (radka.reifova@natur.cuni.cz) by 30th March 2025.

Contact: Radka Reifovï¿½, Department of Zoology (radka.reifova@natur.cuni.cz).

RNDr. Radka Reifovï¿½, Ph.D. Phone: +420 221 95 1852 E-mail: radka.reifova@natur.cuni.cz, radkas@natur.cuni.cz

Web page: www.natur.cuni.cz/˜radkas/ Department of Zoology Charles University Faculty of Science Vinicnï¿½ 7, 128 44 Praha 2

Katedra zoologie Univerzita Karlova Prï¿½rodovedeckï¿½ fakulta Vinicnï¿½ 7, 128 44 Praha 2

Radka Reifovï¿½ <radka.reifova@natur.cuni.cz>

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Hamburg Germany RapidAdaptiveChange

University of Hamburg, Germany: Two Research Associate (PhD Student) positions in Rapid adaptive Change

The two PhD projects are part of a research consortium “Rapid adaptive Change” at University Hamburg. Central to all projects is a data science approach to handle and analyze large and complex data.

We aim to understand the responses of organisms to environmental change, which is critical to managing and preserving biodiversity, especially in the light of global climate change. Our approach is taxonomically and functionally broad, spanning genomic, molecular, morphological, physiological and community level analysis in animals, plants and fungi. We will apply experimental evolution, phylogenomics, network analyses as well as utilize the rich biological collections that have been capturing diversity over the past 200 years.

We are looking for PhD Students for the following subprojects:

The bog of eternal stench? The repeatability of evolutionary responses of bog communities to warming, Application deadline 26.03.2025

Find more information and apply under the following link: https://www.uni-hamburg.de/stellenangebote/ausschreibung.html?jobID=d8d9489b1e091a7456a9399ae376effe63e10616 and

Changes in population genomics of Ericaceae and their specific parasites in Northern Europe, Application deadline 31.03.2025

Find more information and apply under the following link: https://www.uni-hamburg.de/stellenangebote/ausschreibung.html?jobID=27bef96160451364faa420db0aabe5c87e2619b7 For informal inquiries please see contacts in the links or contact Kathrin Otte: kathrin.otte@uni-hamburg.de

Prof. Dr. Kathrin Otte Research Unit of Population Genomics

University of Hamburg Biology Department Institute of Cell and Systems Biology of Animals Martin-Luther-King-Pl. 3 20146 Hamburg Germany

“Otte, Prof. Dr. Kathrin” <kathrin.otte@uni-hamburg.de>

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IRBI CNRS UTours France InsectIridescence

Structural colors of insect wing scales: from materi-omic characterizations to CRISPR investigations

Application deadline: 11 April 2024

We offer a fully-funded 3-year PhD position starting in the fall (1 October 2025) co-financed by ANR and the Centre-Val de Loire Doctoral School (SSBCV) and jointly supervised by Vinodkumar SARANATHAN and Sylvain PINCEBOURDE at the Research Institute for Insect Biology (IRBI, UMR 7261, CNRS / University of Tours). The successful candidate will work in a dynamic, interdisciplinary, and international research environment interacting with world’s leading experts on biological photonics and biomimetics to the physical ecology of insects. The university strives to be an equal opportunity employer and encourages diversity. Tours is a vibrant modern city situated in heart of the UNESCO World Heritage Loire Valley, the cradle of French Renaissance, and connected by very good public transportation (buses, trams and direct high-speed trains connections: 1h to Paris).

HOW WOULD YOU LIKE TO STUDY IRIDESCENT BUGS? How complex traits such as animal coloration and patterning evolve and function is a fundamental question in biology. Many lepidopteran species serve as exemplary model systems in this field due to their simplicity and elegance. While significant progress has been made in understanding the cellular and molecular basis of lepidopteran pigment coloration, however, we have poor knowledge of the mechanisms underlying structural colors produced by photonic nanostructures within iridescent wing scales[1-4] that are often used in social and sexual communication. The PhD project will combine mechanistic, developmental and evolutionary investigations into the functional morphology of iridescent wing scale nanostructures across butterfly species in a comparative fashion. Specifically, the candidate will 1) use materi-omic approaches to create a spatio-temporally resolved map of structure-function relationships of biopolymers and membranes to understand the layer-by-layer construction of butterfly wing scale cell nanostructures during development, 2) and test the functions of key structural motifs identified and the associated genes using CRISPR. The biomimetic expertise gained from this project is in high demand and transferable to industry for sustainable manufacture.

WHO ARE WE LOOKING FOR? A scholar with a Master’s degree in biology or an equivalent (obtained by Aug. 2025) and (1) a background in molecular biology (broadly defined), evo-devo, organismal biology or a related field; (2) who is scientifically curious, creative, highly-motivated, willing to learn new skills, and able to work independently; (3) with excellent communication (English and French - language courses are provided by the University for foreign scholars) and inter-personal skills; (4) prior experience in raising insects in captivity and proficiency in programming would be advantageous, but not required.

Applications submitted via ADUM are due by 11 April 2025 (https://collegedoctoral-cvl.fr/as/ed/voirproposition.pl?site=CDCVL&matricule_prop=62591) and should include a complete CV with names and full contact details of 2-3 professional referees, a cover/motivation letter, and all transcripts (Bachelor’s and Master’s or equivalent). For informal enquiries, please write to SARANATHAN@univ-tours.fr. Online interviews will take place during the week of 14 April. Candidates shortlisted after this step will have final interviews at the doctoral school (on-site or online by request) on 21 May.

References: [1] Saranathan, V. et al. 2010. Structure, function, and self-assembly of single network gyroid (I4(1)32) photonic crystals in butterfly wing scales. PNAS 107, 11676-11681; [2] Saranathan, V. et al. 2015. Structural Diversity of Arthropod Biophotonic Nanostructures Spans Amphiphilic Phase-Space. Nano Lett. 15, 3735-42; [3] Prakash, A. et al. 2022. Antennapedia and optix regulate metallic silver wing scale development and cell shape in Bicyclus anynana butterflies. Cell Reports 40, 111052; [4] Seah, K. S. and Saranathan, V. 2023. Hierarchical morphogenesis of swallowtail butterfly wing scale nanostructures. eLife 12, 89092.

Vinod Kumar Saranathan <vinodkumar.saranathan@aya.yale.edu>

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LinkopingU Sweden MutationRates

We are looking for a PhD student in evolutionary genetics interested in contributing to a better understanding of the mechanisms that shape mutation rates.

The project: Germline mutations are the source of genetic variation and the mechanism that fuels evolutionary change. They also influence a range of evolutionary phenomena, including mutation load, extinction rates, inbreeding depression and the maintenance of outcrossing. Additionally, germline mutations are a major cause of disease. Understanding the factors that shape the germline mutation rate has therefore been a long-standing goal in evolutionary biology, but our appreciation of these factors remains limited. Mutations also occur in somatic cells. While these are not inherited across generations, they are the main cause of cancer and have been suggested to contribute to general ageing. The factors that govern the somatic mutation rate are even less understood than those that determine the germline mutation rate, and virtually nothing is known about a putative connection between these mutation rates.

Using several Drosophila melanogaster model systems, in combination with quantitative genetics, experimental evolution and direct manipulation of resource allocation patterns, this project aims to explore somatic and germline mutation rates from a life-history perspective, to determine whether they are integrated components of organisms' general life-history decisions. The work involves accumulation of mutations in different fly lines, extracting DNA and building libraries for sequencing, as well as bioinformatics analyses of sequence data.

Requirements: Competitive candidates should have a strong interest in evolutionary genetics, excellent analytical skills, and the ability to work both independently and as part of a team. Excellent written and verbal communication skills in English are essential. Candidates are further expected to have experience in processing and analyzing high-throughput genomic sequencing data and in statistical analysis. Previous experience with Drosophila melanogaster or other insect systems, DNA extraction, and library preparation is beneficial but not required.

We offer: The position is fully funded for 4 years and may be extended for up to 1 year, as students often teach 20% of their time. You can read more about employment benefits at Link?ping University at https://liu.se/en/-work-at-liu/employee-benefits Your workplace: The PhD position is placed in the research group led by Professor Urban Friberg at Link?ping University. Research in the group focuses broadly on the evolutionary genetics of aging and sex differences. You can read more about research in our group here https://liu.se/en/research/-friberg-lab. The PhD project is a collaboration with Associate professor Martin Johnsson at SLU Uppsala and Professor Matthew Webster at BMC Uppsala.

Link?ping University is a modern university, which attracts some 27 000 students from all over the world, offering an international and stimulating research environment as well as providing a multitude of opportunities for collaboration and social interactions. Link?ping is situated in central Sweden, conveniently located only a couple of hours by train/car from Stockholm and have beautiful and easily accessible surroundings.

Application procedure: All applications should be submitted through the Link?ping University application system. Read more about the position and how to apply here https://liu.se/en/work-at-liu/vacancies/26479 Please submit your application by May 5, 2025.

For informal enquiries about the position, please contact Professor Urban Friberg: urban.friberg@liu.se

urban.friberg@liu.se

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MPI-EvolBiol-Germany PolygenicAdaptation

The Max Planck Institute for Evolutionary Biology in Pl??n is an internationally oriented institution whose research focuses on the principles, mechanisms and effects of evolutionary change. Around 200 employees from more than 30 nations currently work at our institute in the departments of Theoretical Biology and Microbial Population Biology, as well as in a number of independent research groups.

We are looking for two PhD candidates in Research Group Evolution of Polygenic Traits.

The position is available from the earliest possible starting date. Contracts are awarded after an initial start-up phase (6 months; non-taxable stipend) for a period of three years (fully funded). Remuneration and social benefits are based on the German Civil Service Collective Agreement (TV??D Bund). The salary includes all mandatory social insurance contributions for health care, long-term care, unemployment, and retirement. The candidate will be part of the International Max Planck Research School for Evolutionary PhD, a well-established program with a vibrant research community and outstanding infrastructure.

Project 1 - Genetic and adaptive architecture of polygenic traits Project description: The genetic architecture of quantitative traits identified by QTL and GWA studies includes all contributing alleles and their effect sizes. However, only a subset of the underlying alleles respond to selection; these alleles constitute the adaptive architecture (1). Factors such as distance to the new trait optimum, initial allele frequencies, and pleiotropy determine which alleles are potentially adaptive. The aim of this doctoral project is to compare the genetic and adaptive architectures of a polygenic trait, female body size in Drosophila simulans. We will determine the genetic architecture of female body size using GWAS. In a parallel evolve and re-sequence (E&R) project, D. simulans populations will be experimentally evolved for larger body size. The availability of this dataset will allow comparison of the adaptive and genetic architecture of female body size, and distinguish alleles with adaptive potential from alleles with constraints. The doctoral student will have access to a large dataset of 1000 individuals for GWAS and time-series genomic, transcriptomic, and high-order phenotypic data from E&R experiments.

References: 1. Barghi N, Hermisson J, Schl??tterer C. Polygenic adaptation: a unifying framework to understand positive selection. Nat Rev Genet. 2020;21(12),769???781.

Project 2 - The genomic and phenotypic patterns of adaptation in large and small populations Project description: In quantitative genetics, adaptation of quantitative and complex traits is assumed to occur through subtle frequency changes at many loci following a shift in the trait optimum. While polygenic adaptation is likely the prevalent mode of adaptation for many quantitative and complex traits (1), we still lack a solid understanding of the selection signatures under this model. In a computer simulation study (2), we identified several distinct patterns of polygenic adaptation in populations of different sizes. Building on the results of the computer simulations, we conducted an experimental evolution in which 20 replicates of small (800 individuals) and 6 replicates of large (100,000 individuals) populations of D. simulans were adapted to a high-protein diet. The proposed project aims to test the predictions of computer simulations with empirical data. The doctoral student will have access to a large dataset consisting of time series genomic, gene expression, and fitness data for these experimentally evolved populations.

References 1. Barton NH, Etheridge AM, V??ber A. The infinitesimal model: Definition, derivation, and implications. Theor Popul Biol. 2017;118:50???73.

2. Barghi N, Schl??tterer C. Distinct patterns of selective sweep and polygenic adaptation in evolve and re-sequence studies. Genome Biol Evol. 2020;12(6):890???904

Project 3 - Evolution of gene regulatory networks Project description: Many genetic variants underlying complex traits are located in regulatory regions, and adaptation can be manifested by changes in the expression of adaptive genes (1, 2). Adaptation of complex traits may also take different evolutionary paths in replicate populations despite phenotypic convergence, i.e., genetic redundancy (3). Genetic redundancy could manifest itself as a change in the expression of genes in the same or different regulatory modules (with either similar or different functions) in different populations. The aim of this project is to understand how gene regulatory networks are modified during polygenic adaptation. Tissue-specific gene expression and genomic data from hundreds of individuals from multiple replicate populations adapting to a new trait optimum will be used to reconstruct gene regulatory networks. In addition, eQTL mapping will be performed

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Naturalis Leiden DeepSeaZooplankton

PhD student to study the diversity of deep sea zooplankton and impact of deep sea mining (4 years, fully funded)

You will combine sea-going research and laboratory analyses to study the diversity and abundance of planktonic animals from the surface ocean to the seabed.

Join the Marine Evolution & Ecology research group at Naturalis Biodiversity Center (Leiden, the Netherlands)! https://www.naturalis.nl/en/science/marine-evolution-ecology More info: https://shorturl.at/uthv7 apply by 27 April 2025

Position As PhD student you will combine sea-going research and laboratory analysis to study the diversity, abundance and community composition of planktonic animals from the surface ocean to the seabed. Zooplankton abundance and biodiversity in different size classes will be characterised using depth-stratified net tows, water column profiling with an underwater particle and plankton imaging system (UVP6), and a combination of morphological and molecular techniques (DNA metabarcoding). Focus areas are the polymetallic nodule fields in the Clarion-Clipperton Zone in the eastern tropical Pacific Ocean and hydrothermal vent fields and associated seafloor massive sulfides in the Arctic Mid Atlantic Ridge. You will be part of a “biodiversity” team at Naturalis and NIOZ, and you will work closely with another PhD student focussing on benthic biodiversity. As member of the International MiningImpact3 consortium, you will embrace an open and sharing team effort including the active exchange of data and results, regular team meetings, and integrative analyses. You will be supervised by a team of scientists from Naturalis and NIOZ, and your PhD will be awarded by the University of Amsterdam. Training and courses during the PhD trajectory will be offered by Naturalis, national graduate schools and internationally.

General requirements and skills The ideal candidate is highly motivated, ambitious, creative and has a keen interest in deep-sea biodiversity.

The successful candidate will have the following qualifications: -an MSc degree with specialisation in ecology, evolution, biological oceanography or a closely related discipline; -experience with genetic methods (DNA barcoding, metabarcoding) and/or sampling on oceanographic expeditions; -excellent command of the English language; -excellent communication and presentation skills (writing and speaking); -knowledge of statistics and computer language, like R; -the ability to work independently as well as in a team.

About us Naturalis Biodiversity Center in Leiden is the Dutch national research institute for biodiversity and systematics. With our collection of 42 million specimens, one of the world’s largest natural history collections, and our state-of-the-art research facilities we offer the (inter)national research infrastructure for species, identification and monitoring. We closely collaborate with many Dutch universities, research institutes, industry, and government. We host over 120 researchers including 15 academia embedded professors and 40 PhD students. We present the history of our planet, and the diversity of life on Earth, through permanent and temporary museum exhibitions, educational programmes, and online presence, with more than 400,000 visitors per year. All in all, a unique combination of science and culture in the Netherlands and elsewhere in the world!

The research department is organised in nine research groups comprising researchers and their postdocs and PhD-students. The current position will be in the research group Marine Evolution & Ecology, led by Katja Peijnenburg. Naturalis has a completely new lab building, including state-of-the-art molecular facilities, microCT scanners and electron microscopy.

ROYAL NIOZ NWO-NIOZ Royal Netherlands Institute for Sea Research is the Dutch national oceanographic institute and principally performs academically excellent multidisciplinary, fundamental, and frontier applied marine research addressing important scientific and societal questions pertinent to the functioning of the ocean and seas. NIOZ includes the National Marine research Facilities (NMF) department that operates a fleet of research vessels and the national pool of large seagoing equipment, and supports excellence in multidisciplinary marine research, education, and policy development.

We offer A contract (36 hours per week) for a period of one year, to be extended with three more years after a successful first year evaluation, and a monthly starting salary of euro 3,187.- gross. Additionally, the PhD candidate gets an allowance for travel expenses, holiday allowance (8%) and year-end bonus (3.4%). The starting date is preferably 1 July 2025. The successful candidate will be employed by Naturalis Biodiversity

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Poznan Poland Butterflies

Good day!

Universities in Poland offer PhD scholarships for their doctoral schools. To apply, you need to (in short):

1. Find a professor you would like to work with to guide you and support your application (optional), 2. Apply online with a research proposal and pay the application fee (~June), 3. If 2 is successful, attend an (online) interview with a short presentation (July/September) about your past and proposal, 4. If 3 is successful and you are from outside the EU, apply for a visa (not easy to get these days), and then 5. Appear at the University with original diplomas, certificates, and translations.

More details can be found, for example, at: https://amu.edu.pl/doktoranci/szkola-doktorska/rekrutacja/rekrutacja-20252026 I would be happy to support a suitable candidate who is interested in analyzing my rich data on butterfly mark-recapture and communities with some collaborators.

If you are interested and have a background in evolutionary ecology and complex data analyses, look me up online and send me a letter and CV.

Warm greetings,

Freerk Molleman

Freerk Molleman <fremol@amu.edu.pl>

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SheffieldU PlantEvolution

Horizontal gene transfer and its role in crop adaptation and evolution About the Project

Genetic variation is the substrate of evolution. Without genetic variation species are more likely to become extinct, and this is a problem for wild and crop species alike. Most genetic variation is generated through mutation. However, occasionally species can expand their gene pool through hybridisation or even horizontal gene transfer (HGT). In bacteria, HGT is common and is responsible for the spread of antibiotic resistance genes. HGT has also been recently shown to occur in plants, animals and fungi - although how this happens and the consequences of this is largely unknown.

Recently it has been shown horizontal gene transfer is also a widespread phenomenon in grasses, and this process is responsible for moving functional genes across this family into domesticated and wild species alike. Key crops such as maize, wheat and rice have dozens of horizontally acquired genes in their genomes, but how they got there and the effect they have on adaptation and agriculture is unknown. The student will investigate the mechanics of HGT in key crops using a combination of cutting edge experimental, genetic and computational approaches.

The three main fundamental biological questions are:

[1] How is this foreign DNA inserted into the genome of the recipient? Are the genes randomly inserted into the genome, or are there specific target sites that might hint at the mechanisms behind the transfers

[2] How are the transferred genes actually used by the recipient plant? Just because you have the recipe doesn't necessarily mean you know how to express it.

[3] Do LGTs in crops play a role in environmental adaptation or certain agronomic traits?

The outcomes of this project have the potential to alter our understanding of how plants can rapidly adapt to environmental change through trading genetic secrets, with potential impacts on future crop generation and climate change mitigation.

For informal enquiries about the project, please contact Dr Luke Dunning l.dunning@sheffield.ac.uk.

Deadline = March 14 2025

How to apply:

https://www.findaphd.com/phds/project/horizontal-gene-transfer-and-its-role-in-crop-adaptation-and-evolution/?p177792 *Dr Luke T. Dunning*

Senior Research Fellow Ecology and Evolutionary Biology School of Biosciences University of Sheffield @LukeTDunning < https://twitter.com/luketdunning > https://dunning-lab.sites.sheffield.ac.uk/ < https://dunning-lab.group.shef.ac.uk >

Luke Dunning <l.dunning@sheffield.ac.uk>

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SorbonneU France ComparativeGenomicTunicates

We are looking for a highly motivated candidate to apply for a competitive 3-year fellowship from the doctoral school ED515 (ï¿½cole Doctorale Complexitï¿½ du Vivant) at Sorbonne University to join the Tiozzo team (www.tiozzolab.org), based at the Institut de la Mer de Villefranche (IMEV) in Villefranche-sur-Mer, France and the Flot team at Universitï¿½ libre de Bruxelles (ULB), Belgium

Your profile

We are seeking a passionate and skilled bioinformatician with a strong academic background in both programming and biology, including proficiency in at least one programming language (Python, R, Haxe or others). The ideal candidate will have expertise in (or willingness to learn) genome assembly, comparative genomics, and comparative transcriptomics. We are looking for someone who is not just technically capable but who loves the challenge of solving complex biological problems. A master's degree (or equivalent) is required.

The project

Comparative genomics and transcriptomics of highly regenerating vs. regeneration-limited tunicates (Chordata)

Tunicates, the sister group of vertebrates, are a diverse group of marine chordates that display a remarkable range of regenerative abilities, from limited tissue and organ regeneration to whole body starting from somatic cells. This diversity in regenerative capacity is observed even among closely related species. In fact, while solitary tunicates reproduce strictly sexually and possess limited regenerative abilities, several species of colonial tunicates can regenerate their entire body, either in response to injury or as part of their asexual life cycle through various budding mechanisms. The proposed PhD project study aims to leverage in silico genomic and transcriptomic comparisons to explore the genetic and molecular basis underlying these divergent regenerative capabilities, helping to better understand the evolutionary dynamics of regeneration within this pivotal chordate group.

Solitary and colonial species are scattered throughout the tunicate phylogenetic tree, suggesting that the various forms of budding have evolved convergently. This is evidenced by the fact that each budding process involves non-homologous cells and tissues, such as epithelia or blood-like cells. However, one might hypothesize that the repeated acquisition of budding was facilitated by recurrent co-option of homologous genetic, developmental modules. To test this hypothesis of deep homology, the candidate will compare transcriptomic datasets from three distinct types of budding: peribranchial budding in Botryllus schlosseri, vasal budding in Polyandrocarpa zorritensis, and stolonial budding in Thalia democratica. The first step will involve improving the assembly and annotation of the genomes of P. zorritensis and T. democratica, taking advantage of the pipeline used to generate the existing chromosome-level genome of B. schlosseri. Following this, the candidate will analyze bulk and single-cell RNAseq data from budding tissues of the three species. They will develop a pipeline to identify orthologous genes and compare expression profiles across the different budding modes.

In order to further identify genomic features associated with budding capacity, the candidate will then compare the genomes of three tunicate species from the same family: the two colonial species B. schlosseri and P. zorritensis, and one solitary, non-budding species, Styela clava. While the genomes of B. schlosseri and S. clava have already been assembled and annotated, the P. zorritensis genome will first be scaffolded and annotated. Various comparative genomic approaches will be used, to analyze gene family expansions or contractions, presence/absence of orphan genes, gene gains and losses, and synteny block structures. Additionally, the project may provide insights into how asexual propagation affects genome evolution, particularly in relation to heritable mutations in somatic pluripotent stem cells.

How to apply

If interested, please send a CV (including the names and email addresses of two or more scholars who can serve as references) and a brief motivation letter to Stefano Tiozzo (stefano.tiozzo@imev-mer.fr) and Jean-Francois Flot (jean-francois.flot@ulb.be) by May 1st 2025. Early expressions of interest are encouraged.

Stefano Tiozzo IMEV <stefano.tiozzo@imev-mer.fr>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

UArkansas DrosophilaQuantGenetics

A PhD student position with full financial support is available in Fall 2025 in the Zhuang Lab (https://fulbright.uark.edu/departments/biology/directory/index/uid/xz036/name/Xuan+Zhuang/), Department of Biological Sciences, University of Arkansas. Research interests in the Zhuang Lab include understanding the genetic basis of complex trait variation and novel trait evolution, involving the genetic architecture of complex diseases, the origination of genetic novelty and diversity, and the underlying molecular mechanisms. Employing molecular evolution, quantitative genetics, genomics, and bioinformatics, the research group conducts studies on both model organisms and non-model organisms. We are looking for highly motivated students who are willing to tackle fundamental questions in both basic evolutionary genetics and biomedical research. We invite interested and highly qualified candidates to apply. Please contact Dr. Zhuang (xz036@uark.edu) (1) your CV; (2) a cover letter outlining research interest and experience, specifically how it is related to research focus in our lab; (3) unofficial transcripts, GRE score (if you have), and TOFEL / IELTS score (for international students).

Minimum Requirements - B.S. or M.S. in Biology or related fields. - Highly motivated individual and commitment to scientific rigorousness.

Desirable Qualifications (preferred but not required) - Basic molecular biology lab skills. - Basic knowledge of Genetics and Evolution. - Experience working with fruit fly (Drosophila). - Experience using R for data analysis. - Experience analyzing omic data sets (e.g. genome, transcriptome, metabolome, etc.).

Application Information - Department of Biological Sciences https://fulbright.uark.edu/departments/biology/prospective-students/apply-for-graduate.php - Cell and Molecular Biology Program https://cell.uark.edu/info-for- applicants/index.php

- Graduate School https://catalog.uark.edu/graduatecatalog/admissions/ - Additional fellowships are available for qualified applicants. https://graduate-and-international.uark.edu/graduate/costs-and-funding/doctoral-fellowships.php About the University Founded in 1871, the University of Arkansas is a land grant institution, classified by the Carnegie Foundation among the nation's top 2 percent of universities with the highest level of research activity (R1 University). The University of Arkansas campus is located in Fayetteville, a welcoming community ranked as one of the best places to live in the U.S. The growing region surrounding Fayetteville is home to numerous Fortune 500 companies and one of the nation's strongest economies. Northwest Arkansas is also quickly gaining a national reputation for its focus on the arts and overall quality of life. Arkansas is a natural wonder of forests, mountains and lakes framed by picturesque rivers and streams. Some of the best outdoor amenities and most spectacular hiking trails are a short drive from campus.

Xuan (Shaine) Zhuang, PhD Assistant Professor

Department of Biological Sciences

University of Arkansas

Fayetteville, AR 72701

https://zhuangxuan.wixsite.com/home Xuan Zhuang <xz036@uark.edu>

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UAuckland Two CulturalEvolution

Understanding the past and future of global cultural and linguistic diversity. (University of Auckland School of Biological Sciences)

We offer two fully funded 3-year PhD positions working with Associate Professor Simon Greenhill and Professor Quentin Atkinson to revolutionize our understanding of human linguistic and cultural diversity.

We are a cultural species - no other organism socially transmits such a diverse array of behaviour and knowledge. Worldwide, we speak more than 7000 languages, we construct our social groups and kinship systems differently, we sing, dance, and conduct diverse rituals, and the objects we use in our daily lives are as varied as the activities we undertake in those lives. This cultural information is fundamental to human identity, carries our ancestors' wisdom, documents our prehistory, and is embedded in our languages, thoughts, and societies. But most of the world's languages and the cultures they represent are not expected to survive this century. Surprisingly, we know little about how this diversity was generated or its likely future trajectory. This project will use computational models and newly available data to: 1) identify the drivers of cultural and linguistic diversity; and 2) forecast how language loss and climate change will shape the future of Indigenous languages and cultures around the globe. Our findings will inform current understanding of human diversity and make inroads to protect this precious intangible heritage before it is too late.

Potential Applicants:

Your job will be to quantify linguistic and cultural diversity around the globe, identify and test what drives this diversity, and forecast future diversity. - Excellent Master's degree in historical/typological/computational linguistics, evolutionary biology/ecology, or evolutionary/cross-cultural anthropology. - Experience with programming languages (e.g., R, Python) and computational models (Bayesian phylogenetic methods or spatial modelling). - Excellent analytical skills and attention to detail. - Effective communication and teamwork abilities.

How to apply:

To apply, please send a cover letter explaining your motivation and relevant experience, a CV/academic transcript, and contact details for two referees to simon.greenhill@auckland.ac.nz

More details:

https://www.findaphd.com/phds/project/-understanding-the-past-and-future-of-global-cultural-and-linguistic-diversity/?p183755 Simon Greenhill <simon.greenhill@auckland.ac.nz>

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UCracow SpeciationGenomics

PhD Position in Speciation Genomics

We invite applications for a PhD position within the project "Divergence and gene flow along giant newt genomes", funded by the Polish National Science Centre (NCN) OPUS grant.

About the project

Genomic gigantism has evolved independently in several eukaryotic lineages. While we understand the mechanistic basis of genome size increase, i.e. the proliferation and retention of repetitive sequences, the evolutionary mechanisms driving genome expansion have been debated for decades but are not fully understood. What remains almost completely unknown is how the sequence and structure of giant genomes evolve and what the evolutionary genomic consequences of genome gigantism are. A major gap in our knowledge is how divergence accumulates along giant genomes as populations differentiate into species, and its corollary - how introgression occurs during this process. There are at least three main reasons why divergence may accumulate qualitatively differently in giant genomes. First, the recombination rate per base par is often low, which can reduce the effectiveness of positive selection, and increase the role of linked selection over large parts of the genome. Second, due to the high proportion of repetitive sequences, a large fraction of divergence is expected to occur in repetitive parts of the genome, which can translate into presence/absence differences of many Gb even between closely related taxa. Third, giant genomes appear to be a permissive environment for transposable elements, allowing their long-term retention and providing an abundant source of variation potentially relevant to adaptation. With advances in technology, now is an opportune time to delve into these questions, particularly by comparing giant genomes with what is known about their smaller counterparts. Salamanders (Urodela) are an ancient clade characterised by genome gigantism, as the haploid genome size of all species exceeds 10 Gb. In this project, we propose to study divergence and introgression along the giant genomes in newts of the Lissotriton vulgaris species complex. The nine lineages that make up the complex form a speciation continuum that has been extensively studied at the genetic and genome-size levels, laying the foundation for the genomic work. We will integrate information on structural differences, divergence in single-copy and repetitive parts of the genome across a speciation continuum with direct assessment of introgression in replicated natural hybrid zones. We will combine the analysis of several chromosome-scale genome assemblies, obtained through a strategic partnership with the Tree of Life (ToL) programme at Wellcome Trust Sanger Institute with low coverage whole genome sequencing of hundreds of samples from our extensive DNA collection.

The successful candidate will quantify divergence and introgression in single-copy genomic regions and identify the determinants of divergence and introgression. The project will integrate genomic data from core populations of different lineages with samples from replicated transects across two natural hybrid zones. The research will involve bioinformatic, statistical, and population-genomic analyses of low-coverage whole-genome sequencing data, leveraging chromosome-scale reference genome assemblies. The PhD student will gain extensive experience in handling and interpreting large-scale genomic datasets, developing a strong skill set in bioinformatics and computational biology.

Host Institution & Location

The PhD student will be based at the Institute of Environmental Sciences, Jagiellonian University in Kraków, Poland one of the leading research institutes in Ecology and Evolution in Central Europe (www.eko.uj.edu.pl/-en_GB).

Kraków is a vibrant city with a rich cultural scene (European City of Culture 2000), hosting over 100 festivals and numerous cultural events annually. The city offers modern museums, theaters, cinemas, restaurants, and excellent access to outdoor activities such as hiking and biking. It is also well-connected to other European cities.

Funding & Salary

The position is funded for 48 months, offering a tax-free stipend of approximately 8,000 PLN (~1,900 EUR, around 130% of the average net salary in Poland). The stipend will increase by about 40% after a successful mid-term evaluation (after the second year). To estimate living costs in Kraków, applicants can use tools such as Numbeo (www.numbeo.com).

Requirements

The successful candidate must hold (or expect to obtain by July 2025) an M.Sc. degree in a relevant field. We seek applicants with: - A strong interest in Evolution, Population Genetics, and/or Genomics. - Experience with, or a keen interest in learning, Bioinformatics and Computational Biology. - Strong English language, communication, and organizational skills.

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UIC Barcelona EvolCellBiol

PhD Position in Evolutionary Cell Biology: Unravelling the Mechanisms of Multicellular Organization in Placozoans

Group description:

The Comparative Cell Biology Lab(Najle Lab), at Universitat Internacional de Catalunya (UIC), investigates the molecular underpinnings of cellular and organismal complexity from functional and evolutionary perspectives. Our research combines molecular and cell biology, biochemistry, and functional genomics, focusing on a diverse range of model systems spanning unicellular eukaryotes (protists) to simple multicellular organisms, such as early-branching animals.

Position description:

We are seeking a highly motivated PhD candidate to join our lab and explore the biology of placozoans, the simplest free-living animals. Building on foundational work by Najle et al. 2023 [DOI: 10.1016/j.cell.2023.08.027], this project aims to uncover the mechanisms governing multicellular organization in these animals with minimal structural complexity. The research will leverage cutting-edge approaches, including advanced microscopy, perturbation assays and single-cell omics technologies to unravel the functional role of placozoa-specific cell types. This position provides an exciting opportunity to make meaningful contributions to the field of evolutionary cell biology.

In addition to research, the position involves participation in teaching activities, offering valuable experience in academic development and instruction.

The position will be fully-funded for four years and is expected to start in September 2025.

Requirements:

A Master's degree (or equivalent) in Biology, Biomedicine, Genetics, Biotechnology or a related field. A strong interest in advancing research in non-conventional model systems and developing innovative tools. Experience in basic molecular biology is essential. Familiarity with confocal microscopy is highly desirable, and basic bioinformatics skills (e.g., R, python) will be a plus. Motivation to engage in teaching activities, as the position includes teaching responsibilities. Fluency in English, strong organizational skills, and a proactive, enthusiastic, and curious mindset.

What we offer:

A supportive research environment with personalized mentorship and guidance. Opportunities to collaborate across disciplines within a focused academic setting. Access to advanced tools and techniques. Professional development opportunities, including teaching experience.

Application process:

To apply, please submit a single PDFcontaining:

A cover letter, explaining your background and, importantly, your motivation to join the project. Your CV, including the contact details of 2-3 references.

Send your application before April 30th, 2025 to Dr Sebastián R. Najle at najlelab@gmail.com

Thank you very much.

Kind regards,

Sebastián R. Najle, PhD Single-cell Genomics and Evolution Lab Systems Biology Programme Centre for Genomic Regulation (CRG) Barcelona Biomedical Research Park (PRBB) Dr. Aiguader 88, 08003 Barcelona, Spain

sebastian.najle@crg.eu

Sebastian Rodrigo Najle <sebastian.najle@crg.eu>

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UJagiellonianCracow QuiescentCellVariability

PhD position in Quiescent cell Variability

We invite applications for a PhD position within the project "The influence of ecological factors on the quiescent state: from the characteristics of individual eukaryotic cells to population dynamics", funded by the Polish National Science Centre (NCN) OPUS grant.

—About the Project Background information:— Quiescence is a fundamental, but poorly understood cellular state crucial for survival for all eukaryotes. Yeast (Saccharomyces cerevisiae) serves as a model organism to study quiescence, providing insights into cellular aging, stress resistance, and microbial population dynamics. Understanding the genetic and ecological determinants of quiescent cell evolvability has broad implications for medicine, biotechnology, and science of ageing. Whitin a project we focus on— questions that remain unanswered: How do environmental factors (e.g., nutrient availability, exometabolome presence, and population density) influence quiescent cells phenotype heterogeneity in yeast populations? What are the genetic underpinnings of quiescence variability, and how do mutations shape adaptation to long-term starvation? How do evolutionary trade-offs affect the survival and regrowth dynamics of variable quiescent populations? How does quiescence influence antifungal resistance, and can different quiescence cell types exhibit bet-hedging strategies?

About the Position —The successful candidate will perform experimental evolution of yeast populations under controlled starvation regimes and identify mutations driving quiescence-related adaptations using whole genome sequencing (WGS). The project will involve phenotypic characterization of quiescent cells through flow cytometry, fluorescence microscopy, and microfluidics techniques, alongside analyses of population-level survival, regrowth dynamics, and evolutionary trade-offs. There will be opportunities to apply mathematical modeling to investigate density-dependent effects on quiescent populations and to collaborate with international research groups for advanced microscopy and microfluidics training. The PhD student will gain extensive experience in experimental evolution, microbial phenotyping, and genomic analysis, developing a strong skill set in microbiology, evolutionary biology, and quantitative data analysis.

Host Institution & Location The PhD student will be based at the Institute of Environmental Sciences, Faculty of Biology of the Jagiellonian University in Kraków, Poland - one of the leading research institutes in Ecology and Evolution in Central Europe (www.eko.uj.edu.pl/-en_GB). Kraków is a vibrant city with a rich cultural scene (European City of Culture 2000), hosting over 100 festivals and numerous cultural events annually. The city offers modern museums, theaters, cinemas, restaurants, and excellent access to outdoor activities such as hiking and biking. It is also well-connected to other European cities.

Founding & Salary The position is funded for 48 months, offering a tax-free stipend of approximately 8,000 PLN (~1,900 EUR, around 130% of the average net salary in Poland). The stipend will increase by about 40% after a successful mid-term evaluation (after the second year). To estimate living costs in Kraków, applicants can use tools such as Numbeo (www.numbeo.com).

Requirements The successful candidate will hold (or expect to hold by July 2025) a Master's degree in Microbiology, Molecular Biology, Biotechnology, Genetics, Evolutionary Biology or a related field. We are looking for candidates with: -——— A strong interest in microbiology, evolution and molecular biology -——— Experience or interest in learning to work with microbial systems and culture techniques, and basic bioinformatics and molecular techniques -——— Good analytical skills -——— Fluency in English (written and spoken), good communication and organisational skills -——— Open to international collaboration and research visits abroad

Application Process To apply, please send: -———— A cover letter explaining your background, skills, and motivation for this position -———— A CV -———— Contact details of at least one academic reference willing to provide a recommendation.

Applications and informal inquiries should be sent to dr hab. Dominika WÂ³och-Salamon, Prof. UJ (dominika.wloch-salamon@uj.edu.pl).

Deadline & Selection Process

Review of applications is ongoing. To ensure full consideration, please apply by 28th April 2025. The selected candidate will receive assistance with the formal application to the PhD school at Jagiellonian University, with entrance exams scheduled for early July 2025.

The PhD position starts on 1st October 2025.

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ULille France SpeciationInSilene

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UppsalaU MolecularEvolution

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USalzburg Austria Ten GeoBioInteractions

The University of Salzburg (Austria) invites applications for

*10 PhD positions within the interdisciplinary research training program "Alpine geo- and biodiversity during environmental changes (AlpsChange)".

We are looking for students interested in bridging disciplinary gaps between geo- and biosciences and in establishing links to social sciences - skills that are essential to address the challenges caused by the ongoing climate and biodiversity crises. The students will be based in the FWF-funded doctoral program AlpsChange, which is integrated into the Doctoral School "Dynamic Mountain Environments and Society" at the Paris-Lodron University of Salzburg and offers an interdisciplinary research and training agenda.

The students will be part of an active and interdisciplinary consortium, conduct research at the interface between geo- and biosciences and apply state-of-the-art approaches and methods of both disciplines and of history (e.g. remote sensing, field and laboratory experiments and analyses, numerical and analogue modelling), benefitting from the wide range of expertise available in the AlpsChange consortium. Each student will be supervised by an interdisciplinary team of researchers. The University of Salzburg offers excellent research facilities, and a very pleasant working and living environment in a beautiful landscape with numerous lakes and mountains.

Applications for one or more of the 10 projects (see below) are welcome. Please indicate your preference if you are applying for more than one of the projects. A successful applicant will be highly motivated, proficient in spoken and written English, and willing to work in an interdisciplinary context. A Master-level degree or equivalent in a relevant discipline, preferably in the field of bio- or geosciences, is required.

Please send your application stating your project preference and including a letter of motivation, CV, certificates and contact details of two potential referees in electronic form as a single pdf file latest by April 13th 2025 to AlpsChange@plus.ac.at. Please contact AlpsChange@plus.ac.at in case you have any questions. Start dates are flexible between October 2025 and January 2026. All projects will be fully funded for 3.5 years and students will receive a monthly salary based on currently euro 2786 before tax.

Further information and details of the single projects can be found at https://www.plus.ac.at/doctorate-school-plus/doctorate-school-plus-2/kollegs-der-doctorate-school-plus-2022-2025/dynamic-mountain-environments-society-vol-2/doc-funds/ . Overview of the projects: *Project 1: Edaphic properties as drivers of plant diversification with feedbacks on soil chemistry

*Project 2: The impact of metallophyte vegetation on weathering rates and soil formation

*Project 3: Hydrogeological patterns and alpine spring metacommunities

*Project 4: Shelter under Shards - habitat changes quantify growth of dilatant rock fracture networks in mountain belts

*Project 5: Significance of cool scree slopes for biodiversity in a warming climate

*Project 6: Landscape response to a changing climate in the Eastern Alps: Analysing Big Data for past, present, and future conditions

*Project 7: Climate change effects on habitat distribution and plant-animal interactions

*Project 8: Effects of rapid climate and land-use change on species diversity across a mountain front

*Project 9: Past and future warming induced community dynamics of Alpine vegetation

*Project 10: The Return of the Trees - post disturbance landscape stabilisation due to a changing energy economy from wood to fossil fuels

"anja.hoerger@plus.ac.at" <anja.hoerger@plus.ac.at>

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UStockholm YeastEvolutionaryGenomics

PhD position in Yeast Evolutionary Genomics, University of Stockholm, Sweden

The Stelkens Lab is hiring a highly motivated person for a 4-year fully funded PhD position. Research topics include but are not limited to: 1) Parallel evolution of climate adaptation in Europe and South America, 2) The genetic architecture of temperature adaptation, 3) The evolution of pathogenicity as a by-product of thermotolerance.

The selected candidate will use the powerful microbial model system budding yeast (Saccharomyces spp.), experimental evolution, and cutting-edge genomic tools to study evolutionary processes. We are looking for candidates with a strong interest in evolutionary biology, ideally with some experience in experimental evolution and/or molecular, population, and quantitative genetics. Prior training in yeast cultivation, statistics, and programming (e.g. R, Python) is a plus. Applicants should be independent thinkers, well-organized, good communicators, and happy to work in an international team. Applicants are required to hold a MSc degree (or equivalent qualification) in biology.

Training will be provided in molecular genetics, whole genome sequencing, statistics, bioinformatics, yeast cultivation, and microbiology. The work will mostly be lab-based but may include some fieldwork. There is flexibility within the project for the student to develop their own interests with guidance and support from the supervisor and collaborators. The position can be combined with teaching (maximum 20%), which prolongs the employment. The successful candidate will receive a salary and full social benefits.

Work environment: Stockholm University is located four metro stops from the centre of Stockholm, one of the most beautiful and dynamic capital cities of Europe. SU is home to a vibrant scientific community, including the Science for Life Laboratory and the Swedish Museum of Natural History. Sweden is a free and open society, and strives to be one of the world's most innovative and research-intensive nations. We enjoy a respected system of democracy and individual rights, free health care, freedom of speech, a free press, the right to scrutinize those in power, and access to beautiful nature. Most Swedes speak English.

It is strongly recommended that you read relevant literature and tailor your cover letter and application according to the position. Applications without this will not be considered.

Application: Use the official Stockholm University job portal. Please send formal application, including a statement of motivation, relevant expertise, your CV, and the contact details of at least two references. Link to application portal with more details: https://su.varbi.com/en/what:job/jobID:798314/ Start date: negotiable, but in 2025 Application deadline: 22. April 2025

Informal enquiries to Rike Stelkens: rike.stelkens@zoologi.su.se

Rike Stelkens Associate Professor Yeast Evolutionary Genomics Department of Zoology Stockholm University, Sweden

email: rike.stelkens@zoologi.su.se tel: +46 (0) 816 4223 lab website: stelkenslab.com

Rike Stelkens <rike.stelkens@zoologi.su.se>

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UZurich EvolutionCochlearSystem

"Open PhD position on Biomechanics and Anatomy of the Ape and Hominin Organ of Hearing

We invite applications for a PhD position at the Evolutionary Morphology and Palaeobiology of Vertebrates group (www.msanchezlab.net) in the Department of Paleontology of the University of Zurich. The PhD candidate will work in the context of an Ambizione Swiss National Science Foundation, a project led by Dr. Alessandro Urciuoli.

The PhD candidate will explore the evolutionary trajectory of the organ of hearing in extant and extinct hominids from a morphological and functional perspective. The project will involve the anatomical description of the cochlear system in ape species, the adaptation of human-based computational simulations (finite element models) of the organ of hearing to that of extant apes, and the reconstruction of the hearing sensitivity to sound frequencies in fossil hominins. The candidate will rely on digital images of the cochlear membranous system of apes and humans obtained with the most advanced synchrotron-based computed tomography technology and housed at the Comparative Ear Bank digital repository. The PhD student will be part of an international network devoted to the holistic analysis of inner ear structures and will have the opportunity to perform research stays at European institutions.

We are looking for a highly motivated student of Life, Biomedical, or Engineering Sciences with a background in bioengineering, paleoanthropology, or otorhinolaryngology. Proficient English writing skills are essential. Due to the multidisciplinary nature of the project, knowledge in one or more of the following fields is desirable: finite element modelling and theory, fluid dynamics, auditory physiology, biomechanics, and/or ear anatomy. Skills in Python and MATLAB programming, CAD software, and/or digital image handling and processing will also be positively evaluated. The prospective student is expected to have received a master's degree or equivalent by the start of the PhD and will hopefully have published or are preparing to publish on her/his Masters. The student is to enroll in the evolutionary biology graduate program (www.evobio.uzh.ch/en.html).

The University of Zurich is one of the top research institutions in Europe and offers an exceptional academic environment for research and study. The Department of Paleontology has state-of-the-art research facilities in an international and stimulating academic environment. The ongoing collaborations with the Evolutionary Anthropology Department, the Institute of Evolutionary Medicine, and the Department of Otorhinolaryngology, Head and Neck Surgery will provide a unique opportunity for knowledge interchange and development. The Natural History Museum of the University is closely tied to our department, offering opportunities to participate in and develop skills in scientific outreach activities. The city of Zurich, in close proximity to the Alps, with a lake and river in which to swim in the summer, offers conditions for an excellent quality of life. We offer a vibrant, collaborative work environment and high-quality supervision. All former PhD students of the SÃÂnchez-Villagra group graduated with excellent publication records and almost all have consecutively moved on to postdoc positions at renowned academic institutions. Our group represents an international environment and has been hosting PhD students from many countries across the world.

To apply, please send a letter of motivation including information on previous scientific work and publications if available (maximum of 2 pages), a CV, and contact details of two referees. Please ensure that all those parts are combined into a single PDF-file. Together with an electronic copy of the Masters-thesis, please send your application to Alexandra Wegmann (alexandra.wegmann@uzh.ch).

The deadline for applications is 20th of April 2025. Applications received after the deadline may be considered if the position is not yet filled. Applicants should be prepared to be interviewed in the first half of May 2025 and ideally start on September 1st of 2025 (starting date may be discussed). The planned duration for the PhD project is four years and compensation follows the standards set by the University of Zurich's salary guidelines. If you have further questions, do not hesitate to contact us (alessandro.urciuoli@pim.uzh.ch)."

Kind regards

Alexandra

Alexandra Wegmann <alexandra.wegmann@uzh.ch>

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Jobs

ArkansasStateU BiologicalCollections

Position Summary:

The Arkansas Center for Biodiversity Collections (ACBC), housed in the Department of Biological Sciences at Arkansas State University, invites applications for a multi-year, non-tenure track, 9-month, Visiting Assistant Professor of Biological Collections position to begin in August 2025. Up to 2.5 months of summer funding can be supplemented through successful grant funding.

Duties & Responsibilities:

The successful candidate will primarily be expected to support the ACBC through grants, management and curation of the United States Fish & Wildlife Service Red Wolf collection at A-State, and ACBC database management of aquatic macroinvertebrates, insects, bivalves, fishes, amphibians, reptiles, birds, mammals, diatoms, and plants. The successful candidate will be expected to teach up to 1 course per year based on expertise (e.g., Mammalogy; Collections Curation and Research Design; Plant Systematics). Finally, the successful candidate will be expected to integrate undergraduates into daily operations, including undergraduate students in the Natural History Collections Curation Club (NHC3).

Knowledge/Skills/Abilities:

Ideal applicants would possess a PhD in an area relevant to biological collections and demonstrate a history, or the potential, of external funding relevant to biological collections. Collection- and curation-scientists working in the areas of mammalogy are especially encouraged to apply, however, other areas of taxonomic expertise will also be considered.

General Days/Hours:

Monday - Friday 8:00 a.m. - 5:00 p.m. Additional hours as requested or needed Regular and reliable attendance

Other:

Please note: all position postings close at 12:00 A.M. CDT on the position closing date; in other words, make sure your application is submitted by 11:59pm the day before the closing date.

ABOUT THE DEPARTMENT: The Department of Biological Sciences at Arkansas State University is a growing department with 550 undergraduate students and approximately 11 MS students. It houses the Arkansas State University Museum of Zoology (ASUMZ) and the Arkansas State University Herbarium (STAR). Through research initiatives, the Department addresses local and global biological issues including multiple levels of biological organization. A great deal of research is approached from an interdisciplinary perspective, therefore in addition to master programs within the Biological Sciences department, many faculty members also participate in the Environmental Sciences and Molecular Biosciences graduate programs, which have a combined 40 MS and 40 PhD students. Faculty members also have strong collaborations with ABI, where medical research and agricultural initiatives help to improve the health of Arkansans.

ABOUT THE COLLEGE: The Beck College of Sciences & Mathematics is comprised of faculty from the Departments of Biological Sciences, Chemistry and Physics, and Mathematics and Statistics. It offers a wide range of both undergraduate (B.S., B.A., and B.S.E.) and graduate degrees (M.S., M.A., and Ph.D.) in both traditional and interdisciplinary areas. The College is physically housed in over 150,000 square feet in the Lab Sciences Complex and maintains a wealth of research equipment and facilities for use by faculty and students.

ABOUT THE UNIVERSITY: Founded in 1909, Arkansas State University (ASU) is one of the premier institutions of higher education in the state. With technologically advanced facilities and a population of more than16,000 students (including those at the sister campuses), the university is a major education force in the state. The Jonesboro campus, which is located on 900 acres, has a student population of more than 14,000. Students come from nearly all 50 states and territories and 68 countries. ASU is a state-assisted university located in northeast Arkansas, 70 miles (1 hr.) from Memphis, Tennessee. The university offers a wide variety of majors to students from diverse backgrounds and ethnicities. Jonesboro is a quiet, safe community of about 80,000 inhabitants. People are friendly and very helpful. Recreational opportunities abound in the Ozark foothills to the west.

HOW TO APPLY: Applicants should apply on-line: http://jobs.astate.edu (position P00701). Please submit a cover letter, curriculum vitae, a statement of research experience and plans, teaching philosophy, a statement of commitment to increasing diversity within the field of biology and contact information for at least three references.

QUESTIONS regarding this position should be sent to: Dr. Kyle Gustafson, Search Committee Chair, kgustafson@astate.edu.

APPLICANT REVIEW: To take full advantage of this opportunity, applications should be submitted immediately, but no later than April 18, 2025.

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AuburnU Alabama MNH GIS Analyst

We are reopening our position for GIS Analyst at the Alabama Natural Heritage Program. Being a small program, we hope to add to our taxonomic expertise with this position. If anyone has questions, they can direct them to me at armbrjw@auburn.edu.

Jon Armbruster Director, Auburn University Museum of Natural History

Analyst, Geographical Information Systems Alabama Natural Heritage Program Auburn University Museum of Natural History

The Alabama Natural Heritage Program (ALNHP) of the Auburn University Museum of Natural History (AUMNH) is seeking an expert in Geographical Information Systems (GIS) as they apply to natural history surveys and collections. The successful candidate will have experience in building and using habitat suitability models, the use of GIS to develop maps in the development and successful outcome of ALNHP and AUMNH projects, and have experience in conservation, ecology, or a related discipline on plants, animals, or other organisms related to the mission of ALNHP. The candidate will be responsible for the upkeep and addition of species records to the ALNHP monitored species list in the program Biotics (https://www.natureserve.org/products/biotics-5), serve as the ALNHP point of contact with NatureServe, and to interact with students on GIS-related projects. The candidate will be expected to contribute to AUMNH outreach and education efforts. The successful candidate may have the opportunity to contribute to classes or workshops in using GIS in Natural History. A bachelor's degree in biology or a related environmental field with a specialization in GIS is required, but a master's or Ph.D. in these fields is preferred. For more information on the AUMNH, please visit: http://www.aumnh.auburn.edu . Evaluation of applications will begin 11 April 2025. Submit a CV, a cover letter describing relevant experience (GIS experience including habitat suitability modeling, natural history experience, and experience with the Natural Heritage Program Network or similar organizations), and names and contact information of three references. For more information, contact Dr. Jonathan W. Armbruster, Director AUMNH, Department of Biological Sciences, 101 Life Sciences, Auburn University, AL 36849, Armbrjw@auburn.edu. See aumnh.auburn.edu for more information on the museum and natural heritage program. Auburn University is an equal opportunity/affirmative action employer and actively seeks applications from qualified women and minority candidates.

Minimum Qualifications: Level I - Bachelor's Degree in Biology, Environmental Sciences, or closely related field with no relevant experience. Level II - Bachelor's Degree in Biology, Environmental Sciences, or closely related field with 2 years of experience with GIS. Level III - Bachelor's Degree in Biology, Environmental Sciences, or closely related field with 4 years of experience in GIS.

Desired Qualifications: A Master's or PhD in Biology, Environmental Sciences, or closely related field with 2 or more years experience in GIS.

Salary Range: $43,600 - $81,160

To apply: Visit https://www.auemployment.com/postings/51671 Jonathan W. Armbruster Director and Curator of Fishes, Auburn University Museum of Natural History Professor, Department of Biological Sciences 101 Life Sciences Building Auburn, AL 36849 334-844-9261

Office: 131 Biodiversity Learning Center (M. White

Smith)

Jonathan Armbruster <armbrjw@auburn.edu>

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CNRS Guyane CoordinationNouraguesSciStation

Hello everyone, Here's a fantastic opportunity within our unit! For ambitious scientists! Here's an offer for a Scientific Coordination Officer at the Nouragues Station: - 1-year fixed-term contract - Application deadline: Wednesday, March 26, 2025, 11:59:00 PM Paris time - Work location: CAYENNE - Here is the job description: https://emploi.cnrs.fr/Offres/CDD/UAR3456-MARMIC-010/Default.aspx Here the description of the Nouragues research station https://cnrs-nouragues.fr/en/ Mathieu Chouteau Chargé de recherche CNRS USR MIXTE 3456 LEEISA Centre de Recherche de Montabo 275 Route de Montabo 97300 Cayenne CEDEX Guyane Française 0694 40 39 61 (5h de moins que la France Métropolitaine) https://mathieuchouteau.weebl#.com/ Remplacer le '#' par 'y' car le mail cnrs filtre.

CHOUTEAU Mathieu <mathieu.chouteau@cnrs.fr>

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Gainesville Florida ArthropodsCollectionsManager

Collections manager position open at Florida State Collection of Arthropods

We are happy to announce that the position of collections manager at the Florida State Collection of Arthropods has been posted! A comprehensive arthropod collection is essential for supporting our mission to protect natural habitats and agriculture in Florida, and a dedicated manager is a vital part of our team. Please reach out with any questions.

COLLECTIONS MANAGER (BIOLOGICAL SCIENTIST IV) - 42001238, assigned to ENTOMOLOGY and headquartered in Gainesville, Florida. This announcement is for ALL QUALIFIED CANDIDATES and will close on Thursday, March 20, 2025. Questions may be directed to Dr. Patrick Gorring by calling (352) 395-4725 or emailing Patrick.Gorring@FDACS.gov; or to Dr. Paul Skelley by calling (352) 395-4678 or emailing Paul.Skelley@FDACS.gov.

Apply here: 42001238

"Gorring, Patrick" <Patrick.Gorring@fdacs.gov>

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HongKongU EcolBiodiversity

Tenure-Track Professor/Associate Professor/Assistant Professor

Applications are invited for appointment as Tenure-Track Professor/Associate Professor/Assistant Professor in the broad area of Ecology and Biodiversity in the School of Biological Sciences (Ref.: 531611), to commence as soon as possible, on a three-year fixed-term basis, with the possibility of renewal and consideration for tenure before the expiry of a second three-year fixed-term contract. Direct tenure may be offered to outstanding and qualified Professor/Associate Professor candidates subject to University approval.

The Faculty of Science provides a supportive and friendly environment and has been undertaking programme of recruitment to invest in areas of acknowledged strength and internationally competitive activity. Information about the Faculty can be obtained from https://www.scifac.hku.hk/ and https://www.cpao.hku.hk/firstandforemost/rankings . The Area of Ecology and Biodiversity (AoEB) is one of the two research areas in the School of Biological Sciences. AoEB oversees a range of projects on fundamental research in ecology and evolution, as well as applied work on environmental change, ecological restoration, and wildlife forensics and conservation. It has strengths in ecology, evolutionary and environmental biology, marine sciences, as well as in global change and conservation biology. Hong Kong has a diverse array of tropical ecosystems that are rich in biodiversity, where there are ample opportunities to research the ecological effects of anthropogenic change on terrestrial and aquatic biota, including both endemic and globally threatened species. For more information on AoEB, please visit: https://www.biosch.hku.hk/-

research/EB-research-areas/ . Applicants should possess a Ph.D. degree in fields relevant to the positions, strong academic track records and a high level of scholarly accomplishments. The appointees will have the freedom to choose their research directions within the broad area of ecology and biodiversity, including conservation biology and ecological genetics. Candidates whose research and expertise reside in the field of plant ecology are particularly encouraged to apply. The appointees are expected to build up strong research environments, supervise Ph.D. and M.Sc. students, and apply for research funding through the various funding instruments available in Hong Kong. Enquiries about the posts should be sent to biosch@hku.hk.

A highly competitive salary commensurate with qualifications and experience will be offered, in addition to annual leave and medical benefits. At current rates, salaries tax does not exceed 15% of gross income. The appointments will attract a contract-end gratuity and University contribution to a retirement benefits scheme, totalling up to 15% of basic salary. Housing benefits will also be provided as applicable.

The University only accepts online application for the above posts. Applicants should apply online and upload an up-to-date C.V. with the contact details of 3 referees who are able to provide written reference, a publication list, a letter of intent explaining why they would like to be considered for the positions, a teaching statement and expression of their research interests in PDF format. Review of applications will commence as soon as possible and continue until June 30, 2025, or until the posts are filled, whichever is earlier.

Juha Kari Kristian Merilae <merila@hku.hk>

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MichiganStateU GrassEvolution

Position Summary The Department of Plant, Soil and Microbial Sciences (PSM) at Michigan State University (MSU) invites applications for a full-time, 12-month, fixed-term Assistant Professor position with assigned duties of 35% research, 50% teaching, and 15% advising. The positionÂÂs start date is anticipated to be May 16, with an appointment for two years.

The selected candidate will play a key role in (a) conducting research related to turfgrass management, (b) teaching undergraduate turfgrass management courses, and (c) advising and recruiting students in the Institute of Agricultural Technology (IAT) Golf and Sports and Commercial Turf Management Certificate Programs. Experience and interest in sports turfgrass management research is required. There is funding for the successful candidate to conduct field studies providing data for the Fédération Internationale de Football Association (FIFA) for the 2026 World Cup games. The successful candidate will have access to field, greenhouse, and laboratory facilities. MSUÂÂs Hancock Turfgrass Research Center is a 56-acre field research facility adjacent to campus with state-of-the-art equipment and an attached laboratory.

Teaching Responsibilities: - CSS 232: Introduction to Turfgrass Management: Turfgrass utilization, identification, establishment, and management principles. Responses to various cultural practices. (4 credits; 2 credits starting Fall 2026) - CSS 262: Turfgrass Management Seminar: Presentations by turf students and industry professionals. Topics include internship experiences, technical expertise, and keys to successful career pathways. (1 credit) - CSS 267: Performance Turf Design and Instruction: Performance turfgrass design, construction, renovation and establishment principles. (2 credits) - CSS 269: Turfgrass Strategies: Issues in turfgrass management including employee relations, cultural, and environmental problems. Offered the first ten weeks of spring semester. (2 credits) - AT 293: Professional Internship in Ag Tech: (3 credits) summer semester

Advising Responsibilities: - Professional advising for ˜40 IAT students annually, including admissions, orientation, and academic, career, and internship planning - Internship visits for the IAT students as well as coordinating visits for the students in the turfgrass concentration - Advisor of MSU Turfgrass Club, a registered student organization (RSO)

The PSM department includes over 70 faculty members and strong graduate and undergraduate programs. The IAT includes over 25 appointed faculty and staff with substantial student enrollment. MSU, PSM, and IAT are committed to fostering accessibility and an inclusive community that enriches our learning environment and innovative research and seek colleagues driven by the same motivation.

Commitment to Creating a Sense of Belonging: Michigan State University occupies the ancestral, traditional, and contemporary Lands of the Anishinaabeg ÂC Three Fires Confederacy of Ojibwe, Odawa and Potawatomi people. The University resides on Land ceded in the 1819 Treaty of Saginaw. Michigan State University is dedicated to achieving excellence by fostering an environment that welcomes a broad range of perspectives and experiences, ensuring that all individuals have the opportunity to contribute and thrive. We are an equal opportunity / affirmative action employer. The College of Agriculture and Natural Resources (CANR) is particularly interested in candidates of all backgrounds who are committed to the principle that academic excellence is achieved through open access and proactive inclusion. Candidates are invited to view PSM community norms.

Location: The position will be based at Michigan State University in East Lansing, MI, USA. Michigan State University is one of the top research universities in the world and home to nationally ranked and recognized academic, residential college, and service-learning programs. MSU is a diverse community of dedicated students and scholars, athletes and artists, and scientists that provide regional, national, and international leadership in basic and applied research and excellence in teaching. In addition, consistent with its Land Grant origins, the MSU community pursues international engagement and provides strong extension programs that partner with diverse stakeholders to provide much needed research in the areas of food, energy, water and the environment. MSU enjoys a parkÂ©\like campus with outlying research facilities and natural areas. The campus is located in the city of East Lansing, adjacent to the capital city of Lansing. The Lansing metropolitan area has a diverse population of >500,000. Local communities have excellent school systems

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.mcmaster.ca/~brian/evoldir.html

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PrincetonU MosquitoeEvolNeuroBehavior

The McBride Lab at Princeton University (http://mcbridelab.princeton.edu) is looking for a lab technician to support research on mosquito behavior, genetics, and evolution starting in mid/late summer 2025. The technician will devote ~70% of their time to a specific research project and the remaining ~30% time to general maintenance and lab support. The technician will be welcomed as a full lab member, attending journal clubs and lab meetings and contributing to a dynamic and interactive lab atmosphere. This is an opportunity to become deeply involved in exciting research at the interface of evolution, genetics, and neuroscience and is well-suited for a recent college graduate looking for more experience/focus before graduate school.

Research project activities may include:

- Mosquito breeding and behavioral experiments - Generation of transgenic strains using CRISPR/Cas9 - Molecular biology studies including DNA/RNA extraction, PCR, cloning

Essential Qualifications:

The interested candidate should have a bachelor's degree in biology or related field and previous experience in a research laboratory (beyond lab classes). Previous experience rearing insects, studying behavior, and/or carrying out molecular biology protocols in a research setting is strongly preferred. A demonstrated interest in evolution, neuroscience, genomics and/or behavior is also preferred. It is essential that candidates be highly organized, detail-oriented, and demonstrate enthusiasm for working and communicating with others in a collaborative lab setting.

Princeton University is an Equal Opportunity Employer and all qualified applicants will receive consideration for employment without regard to age, race, color, religion, sex, sexual orientation, gender identity or expression, national origin, disability status, protected veteran status, or any other characteristic protected by law.

Contact Lindy McBride at csm7@princeton.edu with questions or email a cover letter/resume to apply.

Lindy McBride <csm7@princeton.edu>

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SmithC VisistProf Genetics

Visiting Assistant Professor of Biological Sciences

The Department of Biological Sciences at Smith College invites applications for a one-year, benefits eligible position at the rank of Visiting Assistant Professor to begin July 1, 2025, with the possibility of renewal for a second year. Teaching responsibilities will include: the introductory course in Biodiversity, Ecology, and Conservation with discussion sections and a lab section, an intermediate course in Genetics or Evolution, and an upper-level course in the candidate's area of expertise to complete a 3:2 teaching load over the course of the academic year. Candidates with expertise in organismal biology, ecology and/or evolutionary genetics are encouraged to apply. Successful candidates should be prepared to engage actively with undergraduates of diverse backgrounds. A Ph.D. in biology or a relevant field is expected by the time of appointment. Prior teaching experience at the undergraduate level is preferred. Candidates from groups underrepresented in science are encouraged to apply.

Located in Northampton, MA, Smith College is the largest women's college in the country and is dedicated to excellence in teaching and research across the liberal arts. Exceptional resources at Smith College include the College's MacLeish Field Station, BSL-2 plant growth room, research greenhouse, a Botanic Garden and Herbarium; facilities to support research and teaching also include a spatial analysis and GIS lab, and staffed centers of microscopy, molecular biology, proteomics, and aqueous biogeochemistry. Programs in Biochemistry, Environmental Science and Policy, Neuroscience, and Landscape Studies facilitate interdisciplinary collaboration. Smith College is a member of The Five College Consortium, which also includes Amherst College, Mount Holyoke College, Hampshire College and the University of Massachusetts, Amherst. This Consortium provides faculty with opportunities for collaborative research and further enhances the rich intellectual and cultural life of the Pioneer Valley for both faculty and students. Smith College offers a variety of initiatives meant to foster the success of faculty at every stage of their careers.

Submit application at http://apply.interfolio.com/164123 with a cover letter, curriculum vitae, diversity/inclusion statement, statement of teaching philosophy and the contact information for three confidential references. Finalists may be asked for additional materials. Review of applications will begin on March 24, 2025.

As set forth in our mission and values, Smith College is committed to promoting a culture of equity and inclusion among students, staff and faculty. The College will not discriminate in employment on the basis of age, race, color, ethnicity, national origin, creed, religion, sex, sexual orientation, gender identity, gender expression, pregnancy, genetic information, age, veteran status, physical or mental disability, or any other classification protected by law. Smith College is an equal opportunity employer and complies with all state and federal laws that prohibit discrimination.

Please email Laura Katz (lkatz@smith.edu) with questions

Laura Katz <lkatz@smith.edu>

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UExeter:FieldAssist InsectSociality

We seek multiple field assistants to help research how helping may have evolved in social insects. The assistants will be working alongside a Postdoctoral researcher at a nature reserve just outside of Guildford, Surrey, UK. The fieldwork will be for ~2 months from the start of June until mid-end August 2025. Applicants must be available for at least 1 month during this time, and preference will be given to candidates available for the entire duration of the field work.

A. pubescens is a solitary wasp (doesn't sting humans) and lays each egg in a separate burrow, provisioning several paralysed caterpillars for each egg. This system allows us to manipulate egg-laying and provisioning behaviour to test how helping may have evolved in Hymenoptera. The fieldwork involves: observing and manipulating provisioning and egg-laying behaviour, recording nests with video cameras and data recording/entry. The work will involve long days in the field (~10 hours) and weekend work.

Experience of fieldwork and a degree/working towards a degree in a Behaviour/Evolution/Ecology-related topic are desired. Flexibility around the start and end date of the assistant position is required. The successful applicants must have enthusiasm for fieldwork, and will obtain excellent experience of cutting-edge research. Because the work involves recording colour marks on individuals, the job would not be suitable for someone who is colour-blind.

See our research group website for more information about the kind of work we do (http://biosciences.exeter.ac.uk/staff/index.php?web_id=Jeremy_Field). A couple of our previous papers on this system are: (1) Field & Brace (2004). Pre-social benefits of extended parental care. Nature 428: 650-652; (2) Field et al. (2023).ÂBrood parasites that care: alternative nesting tactics in a subsocial wasp. American Naturalist 202(5): 655-666.

Accommodation will be provided, but assistants are required to pay for their own food/personal expenses.

Assistants receive pounds 125 per week to help cover personal costs.

To apply, please send a CV to Lucy Winder l.winder2@exeter.ac.uk. Applicants must have the right to work in the UK. Informal enquiries are welcome. The positions will remain open until suitable candidates are found so early application is recommended.

Dr Lucy Winder (she/her)

Postdoctoral Research Fellow University of Exeter www.exeter.ac.uk Stella Turk Building, Treliever Road, Penryn, Cornwall TR10 9FE

“Winder, Lucy” <L.Winder2@exeter.ac.uk>

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UManchester EvolutionaryBiol

University of Manchester - Senior Lecturer or Professor in Zoology/Biology (Academic Teaching and Research)

We seek an outstanding candidate for an Academic Teaching and Research Senior Lecturer or Professor position in the research area of Zoology/Organismal Biology. You will be expected to have a well-established record of obtaining research funding, producing high quality research outputs and leading an active research group in your area of research. You will contribute to the delivery of the Undergraduate and Postgraduate curriculum by preparing and giving lectures, seminars, tutorials, workshops and/or field courses as well as undertaking any associated management and administrative duties. The role will include developing and marking assessments to accurately measure students’ performance and providing advice and guidance to students to support academic and personal progress.

Job reference:BMH-028286 Salary:Senior Lecturer - Grade 8 59,139 - 70,579 OR Professor -Grade 9E Professorial Scale

For further details see The University of Manchester - Job Information | Apply for Senior Lecturer or Professor in Zoology/Biology (Academic Teaching and Research)

Or contact Prof Ray O’Keefe rokeefe@manchester.ac.uk

Best regards, Reinmar Hager

Dr Reinmar Hager Senior Lecturer in Biology Senior Postgraduate Tutor, Division of Evolution, Infection and Genomics Chair of the School Board, School of Biological Sciences

School of Biological Sciences | Faculty of Biology, Medicine and Health | Michael Smith Building

The University of Manchester | Manchester M13 9PT, UK Tel. ++44 (0)161-275-1550 | Research Profile

Reinmar Hager <Reinmar.Hager@manchester.ac.uk>

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UOttawa ComparativeEvolPhysiology

uOttawa is hiring a tenure-track position in comparative physiology and the search explicitly includes candidates who work ***at the interface of ecology and evolution***. Note language requirements below.

Summary below; full posting here: https://uottawa.wd3.myworkdayjobs.com/en-US/uOttawa_External_Career_Site/details/Assistant-Professor-in-Comparative-Physiology_JR20485?workerSubType=f04d695cd5b5100e684a3af2049c0000 The Department of Biology at the University of Ottawa invites applications for a tenure-track position at the rank of Assistant Professor. The successful candidate will demonstrate the potential to build an internationally recognized and externally funded research program that fully engages trainees at all levels, building collaborations within and beyond our collegial, research-intensive department. Candidates must be able to teach in both French and English at the time of hiring at undergraduate and graduate levels. The starting date is July 1, 2025.

For this position in comparative physiology, we are seeking candidates interested in physiological mechanisms using integrative approaches linking the cell to the whole animal or at the interface with the fields of ecology and evolution. Although our interests are broad, we are particularly interested in candidates researching the physiology of invertebrates in changing environments, one of the established and growing areas of expertise in the Department. The successful candidate will join an established group of comparative physiologists working on diverse research areas using invertebrate and vertebrate models.

The successful candidate will join a research-intensive, growing Department of 40 researchers working in a wide range of fields, including cell and molecular biology, physiology, ecotoxicology, neuroscience, developmental biology, ecology and conservation, evolutionary biology, bioinformatics, and science education. The Department maintains close collaborations with researchers at the Ottawa Hospital Research Institute, the University of Ottawa Brain and Mind Research Institute, the Ottawa Heart Institute, Carleton University, federal science departments and agencies, and the Canadian Museum of Nature. The Faculty of Science provides access to core facilities for molecular biology, genomics, chemistry, microscopy and aquatic animal care to all its members.

Required qualifications: PhD in Biology or a related discipline. Postdoctoral experience is expected. A demonstrated track record of research excellence must be clearly presented, along with commitment and strategies for teaching and graduate training. The candidate must be able to teach in both French and English, the two official languages of the University, at the time of hiring.

Review of applications will begin March 15, 2025.

Howard Rundle <hrundle@uottawa.ca>

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UppsalaU EvolutionaryGenomics

A position as senior research engineer in Leif Andersson's research group at the Department of Medical Biochemistry and Microbiology, Uppsala University (https://www.scilifelab.se/researchers/leif-andersson/). We are looking for someone with a passionate interest in evolutionary biology and with a strong competence in functional genomics who wants to participate in a research project where we use molecular biological methods to elucidate molecular mechanisms important for the adaptation of wild species to their environment. Our flagship project concerns the hundreds of genes we have identified as important for genetic adaptation in Atlantic and Baltic herring. We also conduct research on a wide range of other species, such as the Darwin's finches on the Galapagos Islands. The work involves performing various molecular genetics and biochemical analyses.

Qualification Requirements. PhD in molecular genetics or equivalent. Extensive experience in molecular genetic work, particularly expression analysis, DNA sequencing, protein chemistry, single-cell sequencing, transfection experiments, and/or chromatin analysis. As the candidate will be involved in several large-scale projects with many samples, excellent analytical and organizational skills, flexibility, and the ability to handle potentially stressful situations are required. The candidate is expected to work independently, take their own initiatives, but also collaborate with other members of the group as well as national and international partners. Excellent oral and written skills in English are required. Great emphasis is placed on personal qualities such as good communication, collaboration, and organizational skills, as well as the ability to solve problems independently.

About the employment. The employment is a permanent position (probationary period may be applied). Scope of employment 100%. Starting date as agreed. Placement: Uppsala

For further information about the position: please contact professor Leif Andersson, leif.andersson@imbim.uu.se

Please submit your written application no later than April 22, 2025, UFV-PA 2025/669,

https://www.uu.se/en/about-uu/join-us/jobs-and-vacancies/job-details?query=804992 Leif Andersson <leif.andersson@imbim.uu.se>

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Vienna PartTimeAdmin PolygenicAdaptation

Open position: Part time administrative coordinator (20-30 hours/week), special research program (SFB) on polygenic adaptation (Univ. of Veterinary Medicine, Vienna)

We are searching for a communicative and independent person, who has very strong management skills, and enjoys working in an international environment. The SFB (https://www.vetmeduni.ac.at/sfb-polygenic-adaptation) is a joint research program with 8 faculties from 4 participating institutions: Vetmeduni, Gregor Mendel Institute, ISTA, and University of Vienna. The coordinator is responsible for the internal and external communications of the SFB. The coordinator position is based at the Institute of Population Genetics at Vetmeduni (https://www.vetmeduni.ac.at/en/population-genetics) and embedded in the evolutionary research community in Vienna (http://www.evolvienna.at).

Requirements:

- Fluent in German and English.

- PhD in one of the following disciplines: Life sciences, statistics, informatics; previous experience with population genetics is a bonus.

Duties:

- Coordinate recruitment of postdocs and PhD students.

- Provide administrative support to the SFB faculty and early-stage researchers including postdocs and PhD students (visa and residence permits, local registration in Vienna and registration in PhD programs, housing, relocation support, health related issues), in particular for non-German speakers.

- Plan and coordinate the training activities, workshops and meetings including bimonthly meetings, weekly journal clubs, and the visits of invited seminar speakers and scientific advisory board (SAB).

- Organize social events for the members of the SFB.

- Manage interaction with the administration of the participating institutions.

- Maintain and update the SFB website.

- Provide help in the financial management of the SFB, writing annual reports, and securing further funding.

- Manage the international networking with other institutions operating similar training programs.

- Organizing the outreach program (to the general public and to the scientific community) and public relations activities including press releases about publications of the SFB.

What we offer:

The successful applicant will receive a postdoctoral salary (gross euro 4,932 for 40h contracts including health benefits, contribution to pension funds etc.) according to the FWF rules (https://www.fwf.ac.at/en/research-funding/personnel-costs/#c6541).

The position is available from 1.5.2025. The initial contract is for one year, but can be extended up to 6 years.

How to apply:

Your application should contain a one-page cover letter, a one-page motivation letter, CV, and the names and contact details of 3 references, in one single PDF file. Applications should be sent to Christian Schloetterer: christian.schloetterer@vetmeduni.ac.at <neda.barghi@vetmeduni.ac.at>

The deadline for application is 14.3.2025 and the search continues until the position is filled.

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe

Zoom: https://bokuvienna.zoom.us/j/99886139039?pwd=dnZXUHZlK2dkWVBxU1NXQ2NCRXhwUT09 phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://www.vetmeduni.ac.at/en/population-genetics/ Vienna Graduate School of Population Genetics http://www.popgen-vienna.at Christian Schlötterer <schlotc@gmail.com>

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WSL Switzerland HeadBiodiversity-ConservationBiology

The Swiss Federal Institute for Forest, Snow and Landscape Research WSL is part of the ETH Domain. Approximately 600 people work on the sustainable use and protection of the environment and on the handling of natural hazards. The research unit Biodiversity and Conservation Biology investigates the diversity of life in its various forms, from genetic diversity to the diversity of species and ecosystems and their interactions, and provides the basis for evidence-based nature conservation. The directorate of WSL wishes in order of succession planning to fill in by November 1st, 2025, or by agreement the position of a

HEAD OF RESEARCH UNIT BIODIVERSITY AND CONSERVATION BIOLOGY 90'100% (f/m/d)

As a researcher with an international reputation, you will manage the research unit with more than 100 collaborators. The coordination and support of the 7 different research groups and the management of your own projects are part of your diverse area of responsibility. You acquire third-party funding, maintain the interface to other research fields and further develop the topic of biodiversity within the frame of the WSL strategy in the environment of the ETH Domain. You are committed to cooperate with public authorities and expert organisations at national and international levels and promote the important outreach activities of this unit at the interface between research and practice.

You are at an advanced stage of your scientific career and have experience in leading research groups and managing larger research projects. You have a strong track record in the development and funding of research projects, an excellent publication list and an established international network. Candidates with a sound expertise in organismic biodiversity at the interface of basic and applied research and experience in the application of research results in biodiversity conservation are particularly encouraged to apply. Proven knowledge in the biodiversity of forest ecosystems, mountain and/or cultural landscapes is an advantage. You are an initiative, integrative and committed personality with good negotiating skills and a well-structured way of working. You are also motivated to develop the research unit scientifically, have convincing communication skills and are fluent in English and at least in one Swiss national language.

Please send your complete application to Susanne Jost, Head of Human Resources WSL, by uploading the requested documents through our webpage. Applications via email will not be considered. Prof. Dr. Rolf Holderegger, Director WSL, Tel. +41 (044) 739 24 55, will be happy to answer any questions or to offer further information. WSL is committed to diversity and inclusion as core values. We actively promote gender equality and foster an open, inclusive work environment.

The add can also be found online at https://apply.refline.ch/273855/1714/pub/2/index.html (EN) and https://apply.refline.ch/273855/1714/pub/1/index.html (DE)

Please consider a delayed response owing to my part-time employment.

Felix Gugerli Kuenzle, PhD/Senior Scientist Swiss Federal Research Institute WSL Research Unit Biodiversity & Conservation Biology; Ecological Genetics Zuercherstrasse 111 CH-8903 Birmensdorf

SWITZERLAND

phone: +41-(0)44-739-2590 https://www.wsl.ch/en/employees/gugerli.html Felix Gugerli Künzle <felix.gugerli@wsl.ch>

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Other

Chicago Intern LichenGenomics

Undergraduate/Graduate Internship: Genomic Study of Lichens

Department:

Negaunee Integrative Research Ctr

Location:

Chicago, IL

Bioinformatics Internship: Genomic study of the bipolar lichen species Stereocaulon

The Field Museum is pleased to announce one 2025 Bioinformatic study on the bipolar lichen species Stereocaulon in the Grainger Bioinformatic Center Internship. The internship will offer the intern experience and knowledge of fundamental bioinformatics principles, which will be applied to processing genetic data, specifically processing RADseq with ipyrad to study the genetic differentiation of the bipolar lichen species Stereocaulon alpinum. This is a paid full-time internship (35 hours per week) for 12 weeks. The salary is $17.50/hr for undergraduates or $18/hr for masterï¿½s students and recent graduates. Start and end dates are negotiable, but the internship must take place within the period from April 1 to Sept 30.

The intern will work under the supervision of Alejandrina Barcenas (GBC Postdoctoral Researcher) to process RADseq data. This data will be used to investigate population genetics, including genetic differentiation, gene flow, and phylogenetic relationships between populations of the bipolar lichen Stereocaulon alpinum. We will use programs such as RAxML, fineRADstructure, PCA, and DAPC.

Pay is $17.50/hour for undergraduate and $18.00/hour for graduate and recent grads.

Qualifications The internship is open to advanced undergraduates, recent graduates (six months or less), or graduate students currently studying biological sciences, computer science, or a related field. Previous experience in the following areas will be a plus: knowledge of Linux-related operating systems.

Application Instructions Interested candidates should submit the following documents in their online application:

A cover letter explaining what you would bring to the project and how your previous experience makes you a good candidate for the internship. Please indicate your availability within the time frame of the internship.

Resume Transcript (unofficial transcripts are acceptable) Letter of recommendation

Application deadine date is 3/31/25. Applicants chosen for intervews will be contacted by 4/07/25. Desired start date of May 5th, 2025.

Applicants must apply through the Field Museum website atwww.fieldmuseum.org/careers . Applications through other websites will not be considered.

Alejandrina Barcenas <abarcenas@fieldmuseum.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>) golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

IntlMolluscOfTheYear VoteNow

Dear friends,

It's that time of year again! Voting is opens today for international Mollusc of the Year There are five finalists, the winner is decided by a popular vote - We have five amazing molluscs who are all deserving winners for 2025

Arctica islandica - a.k.a. world's oldest mollusc Cellana exarata - 'opihi makaiauli / Hawaiian black-foot limpet Glaucus atlanticus - the blue dragon Muusoctopus sp. - the Dorado Octopus Xenophora conchyliophora - a mollusc who is itself a shell collector

YOU decide the champion, and we sequence its genome. Vote now, and tell your friends and family! (and also any journalists you happen to know!)

Read more and vote here: https://moty.senckenberg.science Voting ends 31 March

Cheers,

Julia Sigwart & Carola Greve

Prof. Dr. Julia Sigwart Head of Section, Malacology Senckenberg Research Institute and Museum, Frankfurt, Germany julia.sigwart@senckenberg.de

You couldÂ Watch how species get named - https://www.youtube.com/watch?v=yn7kUDRVcVM Subscribe to the Senckenberg Ocean Species Alliance - http://sosa.senckenberg.de Join the Molluscalist community - https://www.listserv.dfn.de/sympa/subscribe/molluscalist Download my book "What Species Mean" - http://bit.ly/whatspeciesmean bit.ly/SMFMalacology | @sigwartae

Julia Sigwart <j.sigwart@qub.ac.uk>

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LinneSysGrant DeadlineMar10

Dear all,

This year's edition of the LinneSys is open.

You can apply for up to 15000GBP for sytematics and/or taxonomy projects.

The only requirement is that you are a member of The Systematics Association < https://systass.org/-membership/ > or the Linnean Society of London < https://www.linnean.org/our-fellows >.

Applications close 23:59 GMT+0 Monday, March 10th (10 days!)

More details: https://systass.org/linnesys/ On behalf of the Systematics Association Council,

Ana Serra Silva Communications Officer for the Systematics Association

Communications SystAss <communications@systass.org>

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LinneSys Scheme DeadlineMar10

Dear all,

This year's edition of the LinneSys is open.

You can apply for up to *1500GBP* for sytematics and/or taxonomy projects.

The only requirement is that you are a member of The Systematics Association < https://systass.org/-membership/ > or the Linnean Society of London < https://www.linnean.org/our-fellows >.

Applications close 23:59 GMT+0 Monday, March 10th (10 days!)

More details: https://systass.org/linnesys/ On behalf of the Systematics Association Council,

Ana Serra Silva Communications Officer for the Systematics Association

Communications SystAss <communications@systass.org>

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NaturalHistoryCollection BasedPHDResearchers Award

Dears,

we are CETAF, the Consortium of European Taxonomic Facilities. We are promoting the 6th edition of the CETAF E-SCoRe Award, a prize dedicated to Researchers who are basing their work on Natural History Collections. This 2025 edition is for PHD only.

The prize is 1.000 euros + 1.500 for visiting and researching in the facilities of a member institution.

Deadline 30.03.25. Here are all the details and the link to the application form: https://cetaf.org/template-activities/cetaf-initiatives/escore/ We would appreciate it if you can circulate it in the community, Best regards, AM

Alessandro Marchi

Communications Officer

CETAF - CONSORTIUM OF EUROPEAN TAXONOMIC FACILITIES

c/o Royal Belgian Institute of Natural Sciences

rue Vautier, 29 1000, Brussels. Belgium

www.cetaf.org Alessandro Marchi <amarchi@naturalsciences.be>

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OmennPrize BestArticleOnEvolAndMedicine NominationDeadline

Please forward to all who share an interest in evolution, medicine and public health

Nominations for the $5000 Gilbert S. Omenn Prize are open now. The Prize is awarded by the International Society for Evolution, Medicine, and Public Health https://isemph.org for the best article published in the previous calendar year on a topic related to evolution in the context of medicine and public health. The first author is invited, expenses paid, to present a plenary talk at the Society's annual meeting. This year's meeting will be July 8-10 at Vanderbilt University, Nashville, Tennessee. Abstracts for the meeting are welcome and due Feb 3. https://isemph.org The deadline for nominations for the Omenn Prize is March 31, 2025, but sooner is better. The easy to complete nomination form is at the link. < https://airtable.com/appcSXUCdP41Bi8Zi/shryvTewHhBZGt5qC >

?¿'??"Details below and at https://isemph.org/Omenn-Prize ?¿'

Nominations are open until March 31, 2025 for the best article in any peer-reviewed journal on a topic related to evolution in the context of medicine and public health with a final publication date in 2024. The winning article is announced in May and the prize is awarded to the first author of the article at the ISEMPH annual meeting. The prize includes travel, lodging, and an invitation to present at talk at the ISEMPH annual meeting. All peer-reviewed articles that use evolutionary principles to advance understanding of a disease or disease process are eligible. The prize committee will give priority to articles with implications for human health, but many basic science or theoretical articles have such implications. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome.

The prize is made possible by a generous donation by Gilbert Omenn, M.D., PhD. Director of the Center for Computational Medicine and Bioinformatics at the University of Michigan where he is a Professor of Internal Medicine, Human Genetics, and Public Health. Dr. Omenn served as Executive Vice President for Medical Affairs as Chief Executive Officer of the University of Michigan Health System from 1997-2002. He is a past president of the American Association for the Advancement of Science and a member of the Institute of Medicine of the National Academy of Sciences. Reply-Forward Add reaction

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SmithsonianNatlZoo ContractTechn

The Center for Conservation Genomics is looking to contract a laboratory technician for one year. The independent contractor will extract DNA and produce and sequence DNA libraries from historic bear samples in the Ancient DNA Laboratory at the Center for Conservation Genomics (Smithsonian's National Zoological Park and Conservation Biology Institute). The contracted technician must be a US citizen or permanent resident and have at least a Bachelor's degree in a relevant field. Prior experience in ancient DNA research is preferred. If interested, please send a CV and a statement of interest (including dates of availability) to:

Michael Campana campanam@si.edu

"Campana, Michael" <CampanaM@si.edu>

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Survey ComparativeHistoneData

Subject: Your help is needed: Please Give us Input on Comparative Histone Modification Data and Analysis

Dear Evolutionary Colleagues,

What do you think are important tools and reagents needed for investigating histone biology across species and populations? We're eager to gather your insights. Our team has developed a 10-question survey to understand how the chromatin community can benefit from new technologies to advance our understanding of histone and histone modification landscapes. We intend to use this data to help us write a NIH grant that aims to bring new technologies (e.g., automatic CUT&RUN) to the wider research field, including capabilities for non-model or emerging model systems. Your input would be extremely valuable, and they would help us to determine what the community needs. The survey should take less than 8 minutes to complete. A few additional details are below

Link to Survey: https://unc.az1.qualtrics.com/jfe/form/SV_ewYvikjQ2gHtzHE Best regards, UNC AIxB

Histone Biology Group (Brian, Sam, Bob, and Corbin)

PS. Want to learn more about histone biology at UNC? https://www.med.unc.edu/epigenetics/ As there is a link to a survey, please see below if you want to participate in the survey.

Important Details Voluntary Participation Your participation in this study is entirely voluntary. Deciding not to participate will not affect your relationship with the University of North Carolina at Chapel Hill (UNC), whether as a student, employee, or community member.

Privacy and Confidentiality To protect your identity as a research subject, the research team will implement measures to ensure that your personal information is kept confidential. Any data collected during the study will be stored securely and only accessible to the research team. No identifying information will be included in published findings or reports.

Risks There are minimal risks associated with this study. All reasonable measures will be taken to protect your data.

Conflict of Interest Disclosure Who is sponsoring this study?

This research is supported by the University of North Carolina at Chapel Hill (the sponsor). This means that the research team is being compensated by the sponsor for conducting the study. Additionally, Dr. Samantha Pattenden, a co-investigator on this study, has an inventorship interest in an epigenetic technology that could be enhanced by the outcomes of this research. If the approach proves beneficial, Dr. Pattenden may receive financial benefits in the future.

If you would like more information about the study or its potential implications, please contact cdjones@unc.edu or kkenmogn@unc.edu. Thank you for considering this opportunity to contribute to our understanding of histone modifications. We look forward to your participation!

Cheers, Corbin Jones UNC Biology University of North Carolina at Chapel Hill cdjones@email.unc.edu

"Jones, Corbin D" <cdjones@email.unc.edu>

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PostDocs

BASEInst Chile eDNA

The Institute of Biodiversity of Antarctic and Subantarctic Ecosystems (https://www.institutobase.cl/en/) calls for a postdoctoral position in environmental DNA, metabarcoding and metagenomics.

Bases and information regarding this competition are available at this link as of January 2025. https://institutobase.cl/wp-content/uploads/2025/01/20241217_Postdoc-Metabarcoding-de-DNA-ambiental-EN.docx.pdf The submission of background information must be made through the e-mail administracion@institutobase.cl and the deadline is March 31, 2025. The final decision regarding the award of the postdoctoral positions will be made by the Council of Principal Investigators of the ICN2021_002 project, during April 2025.

Applications will be open until February 28, 2023 Feel free to distribute this announcement widely.

Dr. Elie POULIN

Laboratorio de Ecologï¿½a Molecular (LEM) Instituto Milenio Ecosistemas Antï¿½rticos y Subantï¿½rticos (BASE) Instituto de Ecologï¿½a y Biodiversidad (IEB) Departamento de Ciencias Ecolï¿½gicas Facultad de Ciencias, Universidad de Chile Las Palmeras 3425 CP 7800003, ï¿½uï¿½oa, Santiago, Chile https://www.institutobase.cl/ https://www.researchgate.net/profile/Elie_Poulin Phone:(56)-2-29787298 E-mail:epoulin@uchile.cl

Elie Albert Poulin <epoulin@uchile.cl>

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BostonU InsectBiodiversityGenomics

Postdoctoral Research Associate - Evolutionary Genomics & Insect Biodiversity

The Strickland Lab seeks a highly motivated postdoctoral researcher with an interest in integrative evolutionary biology to join our team. Our lab investigates the molecular mechanisms that drive biological diversity and adaptation in insects, combining high throughput -omics approaches with ecology, natural history, and behavioral studies. The postdoctoral researcher will be expected to carry out projects consisting of differential gene expression studies with RNA-sequencing data, genome assembly and annotation for two new insect genomes, and population genomics studies using RAD-sequencing. Learn more about our research at lynettestrickland.weebly.com.

Applicants with expertise in one or more of the listed areas are encouraged to apply:

* Genomics, including transcriptomics, genome assembly and annotation * Population genetics/genomics, including RAD-sequencing, Pool- Sequencing, etc * Bioinformatics or computational experience

Minimum qualifications include:

* A PhD in Biology, Entomology, Evolutionary Biology, or a related discipline * Research experience in one or more of the following fields: evolutionary biology, computational biology, population genetics, insect ecology/biology, molecular ecology * Evidence of scientific productivity in the form of publications in peer-reviewed journals * Strong science writing and communication skills * Ability to work independently as well as collaboratively as part of team * Mentoring experience

The postdoc will be expected to carry out projects related to the description above and will have the opportunity to develop studies within their specific areas of interest as they relate to insect evolution. This position includes potential collaborations with other postdocs and faculty in the BU Biology Department, including Ecology, Evolution, and Behavior, Cell and Molecular Biology, and Neurobiology. Pay rate starts at $67,500/year, start date is flexible, and appointment is initially for one year with the possibility to extend for an additional 1-2 years provided acceptable progress.

Application Process To apply, please submit the following to lynettes@bu.edu with the subject line “Strickland Lab Postdoc.”

* a one-page cover letter detailing your research interests and relevant experience, * a current CV * contact information for three references

Lynette R. Strickland, PhD she/hers Assistant Professor Department of Biology Boston University https://lynettestrickland.weebly.com/ I do not expect you to respond outside of your normal work hours.

“Strickland, Lynette” <lynettes@bu.edu>

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ColoradoStateU HostPathogenCoevolution

Postdoctoral Position: Population and Landscape Genomics to Inform Host-Pathogen Co-evolution and Conservation Management

A postdoctoral position focused on population and landscape genomics to inform host-pathogen co-evolution of wild cervids and chronic wasting disease (CWD) is available in the Funk Lab of Conservation Genomics and Evolutionary Ecology at Colorado State University. Funded by the USDA National Wildlife Research Center, the postdoctoral scientist will harness whole-genome sequence (WGS) data collected from mule deer to test the landscape factors that influence connectivity and CWD transmission, understand the roles of gene flow and pathogen-mediated selection in the ecology and epidemiology of CWD, and investigate fitness consequences of polymorphisms in the prion protein gene that influence the incubation period of CWD, among other research question. In addition to publishing their results in peer-reviewed scientific journals, the postdoctoral scientist will communicate their results at scientific conferences and with federal and state scientists and decision makers to improve conservation management of wild cervid populations. The postdoctoral scientist will be part of a collaborative team from the USDA NWRC (Dr. Jenn Malmberg) and Utah State University (Dr. Kezia Manlove).

Required qualifications:

-â€â€â€â€â.D. by the time of start date in evolutionary biology, population genetics, integrative biology, disease ecology and evolution, or some equivalent.

-â€â€â€â€âcommunication (verbal and written) and organizational skills.

-â€â€â€â€âattitude and desire to work as part of a dynamic, multi-disciplinary team.

-â€â€â€â€âexpertise in bioinformatics, genomics, and the application of genomics to evolutionary and conservation questions.

-â€â€â€â€âgenerating, analyzing, and/or integrating large datasets - whole genome sequencing, RAD sequencing, and/or transcriptome sequencing.

Preferred qualifications:

-â€â€â€â€âin Python or Perl, and R.

-â€â€â€â€âin disease ecology.

The successful candidate will work under the supervision of Professor Dr. Chris Funk at Colorado State University, and in collaboration with other team members.

The appointment can be extended up to three years, pending satisfactory performance. The salary will be commensurate with experience. Preferred start date is approximately June 1, 2025.

To apply: E-mail a single PDF including a cover letter, a CV, and the names and contact information of three references to the Funk Laboratory Manager, Mackenzie Woods (Mackenzie.Woods@colostate.edu), with the subject line as “Postdoctoral application your name”. Review of applications will begin April 7, 2025, and continue until a suitable candidate is identified. Informal inquiries prior to application are welcome and can be directed to Chris Funk (Chris.Funk@colostate.edu).

“Funk,Chris” <Chris.Funk@colostate.edu>

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DenmarkTU Aqua PopulationGenomics

Dear colleagues, We are offering a postdoc opportunity at DTU Aqua:

If you are embarking on a career as a researcher and seeking the best foundation to achieve your dreams and ambitions, look no further. At DTU Aqua, you will pioneer new advancements at the cutting edge of what is possible.

Responsibilities and qualifications: Your overall focus will be to strengthen the department’s competences within computational analysis of genomic data of marine fish species. You will work with nearby colleagues, and with both academic and industrial partners in Denmark as well as abroad. Your primary tasks will be to:

- Analyse genomic data from several externally funded projects related to fisheries genomics - Perform bioinformatics analysis on low-coverage and high-coverage whole-genome sequencing data. Previous experience with such data and familiarity with genomic tools like ANGSD is a plus. - Conduct genomic analysis of archived marine fish material to describe and understand historical genetic changes. Experience with ancient DNA genomic analysis is a plus. - Conduct field and experimental work ("wetlab") to collect samples and metadata for projects. An interest in these tasks is advantageous. - Collaborate with interdisciplinary teams to integrate findings and advance our understanding of fisheries genomics. - Prepare and present research findings in scientific publications. - Contribute to the teaching of MSc courses at the department

As a formal qualification, you must hold a PhD degree (or equivalent).

We offer: DTU is a leading technical university globally recognized for the excellence of its research, education, innovation and scientific advice. We offer a rewarding and challenging job in an international environment. We strive for academic excellence in an environment characterized by collegial respect and academic freedom tempered by responsibility.

Salary and terms of employment: The appointment will be based on the collective agreement with the Danish Confederation of Professional Associations. The allowance will be agreed upon with the relevant union.

The position is a full-time position. The period of employment is 2 years. The starting time is negotiable, but preferably May-June 2025.

The fellow will be employed at DTU AquasÂs location in Silkeborg, Jutland, which besides the Population Genetics group also hosts the section for Freshwater Fisheries and Ecology (FFE).

You can read more about career paths at DTU here.

Further information: Further information may be obtained from Dorte Bekkevold (db@aqua.dtu.dk) and Belén Jiménez-Mena (bmen@aqua.dtu.dk).

You can read more about the department at https://www.aqua.dtu.dk/ and https://www.aqua.dtu.dk/forskning/forskningsomraader/populationsgenetik If you are applying from abroad, you may find useful information on working in Denmark and at DTU at DTU - Moving to Denmark.

Application procedure: Your complete online application must be submitted no later than 3 April 2025 (23:59 Danish time).

Applications must be submitted as one PDF file containing all materials to be given consideration. To apply, please open the link "Apply now" at the main website where the post has been announced fill out the online application form, and attach all your materials in English in one PDF file. The file must include: - Application (cover letter) - CV - Academic Diplomas (MSc/PhD - in English) - List of publications - Two names of references who can be contacted - Other material that you would like to include to support your application

Applications received after the deadline will not be considered.

All interested candidates irrespective of age, gender, disability, race, religion or ethnic background are encouraged to apply. As the position involves research in critical technology, which is subject to special rules for security and export control, among other things, open-source background checks will be conducted on qualified candidates for the position.

Technology for people DTU develops technology for people. With our international elite research and study programmes, we are helping to create a better world and to solve the global challenges formulated in the UN's 17 Sustainable Development Goals. Hans Christian Ãrsted founded DTU in 1829 with a clear mission to develop and create value using science and engineering to benefit society. That mission lives on today. DTU has 13,500 students and 6,000 employees. We work in an international atmosphere and have an inclusive, evolving, and informal working environment. DTU has campuses in all parts of Denmark and in Greenland, and we collaborate with the best universities around the world.

LINK TO APPLY:

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EdinburghU GenomicsMetagenomicsPopDecline 2

This is re-advertisement of a 3-year NERC-funded postdoc position in Genomics and Metagenomics of Population Declines

We are looking for an experienced and enthusiastic scientist to work on a project that studies the interactions of host and microbiome during population declines. The post holder will focus on the analyses of temporal host genomic data from museum specimens of several mammalian species.

One of the greatest hallmarks of recent human-driven effects on the environment is biodiversity loss, including rapid population declines and associated loss of genetic diversity. Host-associated microbiomes are central to host survival and are themselves impacted by host genetics. Recognising this intimate connection between the hosts and their microbiomes, we aim to answer a central question: How did human-driven population declines during the last two centuries impact host-associated microbiomes and what consequences does it have for the hosts? We will integrate host genomic data and microbial fossils preserved in the form of the calcified oral biofilm - dental calculus - to study host-microbiome co-evolution during periods of unprecedented population declines.

The project is based at the University of Edinburgh, Institute of Ecology and Evolution, in the group of Dr. Katerina Guschanski. It is based on analyses of genomic and metagenomic data derived from museum-preserved specimens of several mammalian species and their microbiomes to study their joint effects in declining populations. The paired host-microbiome samples span from before population declines, during the bottleneck, and following (potential) population recovery, depending on the species.

Your task You will be using population genomics framework to understand the effects of population size reduction on the host, and multi-omics/hologenomics approaches to study the interactions between hosts and the microbiomes. Even though the main focus is on data analyses, you will have the chance to participate in sampling in various natural history museums and contribute to data generation in the newly established ancient DNA lab. You will be assisted by a postdoc with expertise in metagenomics and a research technician (for data generation), and will be closely interacting with PhD and Honours students.

Requirements A PhD degree in population genomics, evolutionary genomics, conservation genomics or a related field. Strong knowledge of population genetics theory and extensive previous experience in population genomics analyses, particularly of low-quality, low-coverage whole genome datasets (e.g. ancient DNA), ideally in wild, non-model organisms. Proven ability to use and develop code for large-scale genomics data analyses and strong skills working with large-scale datasets. You will be collaborating closely with a postdoctoral researcher who is an expert in metagenomics, so we are looking for a curious, highly collaborative, and cross-disciplinary mindset and a broad interest in biodiversity conservation. Experience with wet lab analyses of ancient DNA or molecular lab work would be an asset, as well as experience with multi-omics statistics.

What we offer We are a highly international research group working on various questions of evolution, speciation, adaptation, and conservation genomics, with particular focus on how human actions affect the environment. As part of the Institute of Ecology and Evolution, the post is located in a world-class, dynamic scientific environment with over 40 research groups working on all aspects of evolutionary ecology, population genetics, behaviour and more. It is a highly collaborative and welcoming place, which provides the resources to advance your own career along your desired path through mentorship, professional development opportunities, and opportunities to develop collaborations that extend beyond the core group.

Application More information on the post and the link to the application portal is here: https://elxw.fa.em3.oraclecloud.com/hcmUI/-CandidateExperience/en/sites/CX_1001/job/12170 Application deadline: March 27th, 2025 Expected interview dates: Early-mid April Expected starting date: July 1st, 2025 or soon thereafter

Contact: Please reach out to Katerina.guschanski@ed.ac.uk for more information and informal inquiries about the post.

The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336. Is e buidheann carthannais a th' ann an Oilthigh DhÃ¹n Ãideann, clàraichte an Alba, àireamh clàraidh SC005336.

Katerina Guschanski <Katerina.Guschanski@ed.ac.uk>

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Helsinki AncientDNALab

Postdoctoral position in the field of paleogenomics / ancient DNA Professor Antti Sajantila's research group at the University of Helsinki Faculty of Medicine in Helsinki, Finland, is looking for a postdoctoral researcher to work with us in our newly established ancient DNA facilities.

We are an enthusiastic team composed of the PI, three postdocs, one PhD student, and two BSc students. Our focus is on the analysis of human and pathogen genomes (viruses) from samples derived from archaeological sites in North Europe and South America. Our projects are multidisciplinary integrating several methodological approaches.

The Project: The successful candidate will work with human and pathogen DNA data obtained from the Levänluhta archaeological site in Finland. Levänluhta is one of Northern Europe's most intriguing Iron Age mysteries: a water burial dated to the 5th to the 8th centuries, contrasting starkly with the typical burial customs of the time. This waterlogged environment hosted remarkably preserved remains of around 100 individuals, making it one of Finland's oldest known burial sites with well-preserved human bones. We are interested in uncovering the genetic make-up and relationships of these people as well as the pathogens they carried. To date, genetic data have been published from only a few individuals showing an interesting affinity to modern-day Saami in northern Fennoscandia (see https://www.nature.com/articles/s41467-018-07483-5 and https://www.nature.com/articles/s41586-019-1279-z).

Qualifications: Applicants should have a PhD in bioinformatics, biology, evolutionary biology, genetics, medicine, or a similar field, and a strong understanding of working with ancient DNA. Experience in using bioinformatic tools and population genetic software suited to aDNA analysis is a necessity.

Postdoc Period: Minimum of two years.

Salary: To be discussed during the interview.

Application: Please submit the following materials: 1. A one-page cover letter detailing your interest in the position. 2. A CV with up to 10 of your most relevant publications. 3. Contact information for at least two professional references. Send your application to antti.sajantila@helsinki.fi.

Deadline: The position will be filled as soon as a suitable candidate is found.

More about us: Professor Antti Sajantila: www.helsinki.fi/en/about-us/people/people-finder/-antti-sajantila-9010014 Research group (PaleOmics lab): https://www.helsinki.fi/en/researchgroups/sajalab sajaLab | University of Helsinki sajalab - Department of Forensic Medicine. The PaleOmics lab is located in the Department of Forensic Medicine, University of Helsinki and led by Professor Antti Sajantila.The general interest of the group is to understand disease and molecular evolution, human population diversity and migrations of past populations. www.helsinki.fi
"Sajantila, Antti J" <antti.sajantila@helsinki.fi>

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IGB-Berlin EcoEvoModeling

The research group 'Eco-Evolutionary Dynamics' at the Department of Evolutionary and Integrative Ecology of IGB invites applications for a 2-year postdoctoral position in modeling of eco-evolutionary community dynamics starting as soon as possible. The research group is located in Berlin-Friedrichshagen at Lake Müggelsee. We are seeking a highly motivated person who has a keen interest in theoretical questions about eco-evolutionary dynamics and has a passion for science.

The postdoctoral position is part of a DFG project and centres around addressing questions on eco-evolutionary dynamics of multi-species communities using theoretical modeling approaches. The candidate will focus on developing a mathematical model (e.g., preferably individual-based models) from basic equations to investigate questions at the interface of community ecology and evolutionary biology. The project's main objective will be to test how interactions between specific processes of community ecology (species sorting, ecological drift and dispersal) and evolutionary biology (selection, genetic drift and gene flow) shape eco-evolutionary community dynamics.

Your role

* Develop a theoretical model (e.g., individual-based, analytical differential equations) to tackle novel questions on eco- evolutionary dynamics in future scenarios of environmental change. * Report results in scientific publication(s) and conference(s).

Your profile

* Completed PhD degree in mathematical modeling preferably in the field of evolutionary ecology. * Experience with developing mathematical models preferably in the field of evolutionary ecology (e.g., individual-based models). * Experience with modeling trait evolution is desirable. * Experience with building a mathematical model from basic equations is a benefit. * Demonstration of leading scientific publications. * The working language of the group is English, and suitable reading, writing (including scientific writing) and speaking skills are required. * Engaged person with a team-spirit.

Our offer We offer an interesting position in an international and dynamic scientific environment. We foster flat hierarchies and active participation. We allow maximum individual freedom, enabling everyone to develop and use their creativity to the best of their abilities. The position is for 2 years with a starting date as soon as possible. Salary is paid according to the German salary scheme for the public sector (TVöD Bund E13). It is an 80-100% position with up to 39 working hours per week.

We foster your career development < https://www.igb-berlin.de/karriere > by providing qualification and training opportunities. We actively support the reconciliation of work and family life < https://-www.igb-berlin.de/en/equal-opportunities >. Given our commitment to diversity < https://www.igb-berlin.de/sites/default/files/media-files/download-files/FVB_Diversity_and_Inclusion_Strategy.pdf >, we welcome all applications, regardless of gender and gender identity, origin, nationality, religion, belief, health and physical disabilities, age or sexual orientation. IGB is committed to increasing the number of women in this field, therefore applications from women are particularly welcome. Various measures are in place at IGB to support gender equality < https://www.igb-berlin.de/sites/default/files/media-files/download-files/GEP_IGB_2021.pdf >. Applicants with a disability < https://www.igb-berlin.de/en/-colleagues-with-disabilities > will be given preference if they are equally qualified.

Are you interested? We look forward to receiving your application by 20.04.2025 with the usual documents (1-page cover letter, CV, certificates/ references/letters of recommendation). Please state the job reference number 08/2025 and apply exclusively via our recruitment platform at www.igb-berlin.de/en/jobs. Questions can be directed to Dr. Lynn Govaert by e-mail (lynn.govaert@igb-berlin.de).

Dr. Lynn Govaert Group Leader (IGB)

Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB)

Evolutionary and Integrative Ecology Müggelseedamm 301 12587 Berlin, Germany

phone: +49 30 64181-713

email: lynn.govaert@igb-berlin.de

www.igb-berlin.de/en/profile/lynn-govaert www.igb-berlin.de/en/govaert

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Jena Germany KillifishPopQuantGenetics

I work at the Leibniz Institute on Aging as a group leader, and my group studies the evolution of life history trait combining quantitative genetics, population genetics, and experimental work in the lab.

Lab website: https://valenzano-lab.github.io/labsite/ . We are looking for a postdoctoral candidate working on population genetics, comparative genomics, bioinformatics in annual killifish.

The project explores the role of hybridization, selection and population size oscillation in life history trait evolution in killifish. The candidate will have the opportunity to work in the lab in Germany, and do field research in Zimbabwe in our recently established molecular field laboratory and station.

Here is the official post: https://jobs.leibniz-fli.de/f78ok . Dario Riccardo Valenzano,PhD Scientific Director Leibniz Institute on Aging - Fritz-Lipmann Institute Professor of Evolutionary Biology / Host-Microbiome Interactions in Aging Excellence Cluster "Balance of theMicroverse" Friedrich Schiller University Beutenbergstrasse 11, 07745 Jena, Germany

Dario.Valenzano@leibniz-fli.de https://valenzano-lab.github.io/labsite/ Dario Valenzano <Dario.Valenzano@leibniz-fli.de>

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LinkopingU Sweden AvianBrainSizeEvol

Sweden_Linkoping_QuantativeGenetics/Phylogenetics (LiU.se)

Two-year postdoc position at Linköping University, Sweden, on avian brain size evolution using quantitative genetic data and phylogenetic comparative methods. This is a Carl Tryggers-funded project to study the genomic basis of avian brain size evolution, with a specific focus on the size of the cerebrum (forebrain) and cerebellum (hindbrain).

Project description This project aims to firstly identify causative genes underlying cerebellum size and cerebrum size variation using the large expansion (both absolute and in proportion to the whole brain) of these two regions that occurred during domestication in chickens. Secondly, using phylogenetic comparative methods to test which of these candidate genes have undergone the strongest positive co-evolution with cerebellum and cerebrum size, and thereby which genes have had the strongest impact on these regions' size evolution.

This is part of a collaboration between the Henriksen lab (Linköping University - Department of Physics, Chemistry and Biology) and the Krzysztof lab (Linköping University - Department of Computer and Information Science), and the postdoc will be part of both research groups.

Requirements - A Ph.D. in a related field. - Experience with phylogenetic comparative analysis - Experience with R programming, data management, and statistical analysis

Valuable skills/knowledge §A strong basis in population quantitative genetics and phylogenetics, ideally with prior experience of combining these. §Knowledge of brain size evolution §Strong computational and coding skills

If interested, please send an email to Rie Henriksen (rie.henriksen@liu.se) before the 15th ofApril 2025, including a motivation letter (1 page) and a short CV (5 pages) with one or two contacts for reference. If you have doubts/questions, please do get in touch in the same email.

Rie Henrâ, Associateprofessor IFM Biology Linköping University 58183 Linköping SWEDEN

email: rie.henriksen@liu.se Phone: +46 (0) 70 089 50 84 https://www.researchgate.net/profile/Rie_Henriksen https://liu.se/en/research/henriksen-group Rie Henriksen <rie.henriksen@liu.se>

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MNH Sweden BalticRingedSealGenomicMonitoring

One postdoc position in genomic monitoring of Baltic ringed seal is available in the group of Nicolas Dussex at the Swedish Museum of Natural History, Stockholm.

Please apply here: https://recruit.visma.com/spa/public/apply?guidAssignment=e26f2a76-eb6e-434c-94b7-91dc3c319d67&publishCode=AMS&TK=7a68f9f1-355b-4e0e-89e7-bfcaf49b4935 For more information, please email: nicolas.dussex@gmail.com

https://nicolasdussex.wixsite.com/ndevol Nicolas Dussex <nicolas.dussex@gmail.com>

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RuhrU Germany PlantGenomics

Postdoctoral Researcher (TV-L E14, 3 years) Evolutionary and Comparative Computational Plant Genomics

At the Chair of Molecular Genetics and Physiology of Plants, we pursue genome-enabled computational approaches as well as experimental molecular functional analyses to develop an integrated understanding of plant evolutionary adaptations to rapid environmental change. Our goal is to decipher the underlying molecular mechanisms and evolutionary processes (e.g. recent and ongoing projects ERC-Advanced Grant "LEAP-EXTREME", Transregio TRR 341 "Plant Ecological Genetics", Research Priority Programme SPP 1819 "Rapid Evolutionary Adaptation"). Team members take advantage of large existing datasets from genome resequencing (ca. 1000 edaphically and ionomically indexed individuals), methylome sequencing, high-quality de novo genome assemblies (ca. 50) and extensive transcriptome datasets (tissue-based and single-cell) of the Zn/Cd-hyperaccumulating extremophile Arabidopsis halleri. A. halleri is a diploid stoloniferous perennial and obligate outcrosser with exceptionally large genetic and phenotypic diversity, well-suited for comparisons with closely related species including Arabidopsis thaliana.

Project: You will answer biological questions by employing computer-based analyses of nucleotide sequence data, partly together with environmental and/or phenotypic parameters, population genomics (e.g. demographic analyses and simulations, population genetic studies based on individual genes or gene groups, genome-wide selection scans), possibly also genome analyses (e.g. assembly, annotation, analysis of structural variation), or analysis of regulatory/co-expression networks based on transcriptome data, in Arabidopsis halleri and closely related plant species. Additional experimental components are possible.

Additional tasks: Publications and presentations; teaching and supervision of students (4th semester undergraduates to doctoral students); organization and management of computational resources; working in interdisciplinary teams, acquisition of third-party funding.

Your profile: PhD degree in population genetics, evolutionary/comparative genomics, genome analysis, bioinformatics, or related; programming skills and experience in R, Python and/or Perl, as well as in the computational analysis and the management of large nucleic acid sequence data sets ("short read" and "long read"); excellent oral and written communication skills (either at least C1 equivalent in both German and English, or alternatively C2 equivalent in English); first or senior authorship on at least one published (or accepted) peer-reviewed original scientific publication; outstanding ability and motivation for scientific work and excellence; creative, analytical, independent, well-structured and well-documented working style; excellent background in (population) genetics.

We offer: Team-oriented supportive cutting-edge distinguished international research group in a campus University setting (35,000 students) that includes a large Botanical Garden; city (~ 300,000 people) located within a metropolitan region (5 mio. people) in northwestern Germany; several large Universities and research centers within 1 h travel; 45 min from Düsseldorf airport; adjacent to the Ruhr river valley bordering rural mountain/forest region; contract extension possible (depending on success).

Please address your application including a cover letter (describing your current research interests, how you envisage to contribute, and your career goals), CV, list of publications, and scans of academic degree certificates to Professor Dr. Ute Krämer (mgpp@rub.de), Molecular Genetics and Physiology of Plants, Ruhr University Bochum, Universitätsstraße 150, Box 44, ND 3/30, D-44801 Bochum, Germany. We will begin to evaluate applications immediately (closing date: 7 April 2025, starting: between May and September 2025).

Professor Dr. Ute Kraemer Molecular Genetics and Physiology of Plants Ruhr University Bochum Universitätsstraße 150, ND 3/30, Box 44 D-44801 Bochum, Germany

Contact: Mrs. Frauke Gesell, Tel. +49-(0)234-32-28004, FAX +49-(0)234-32-14187, E-mail: MGPP@rub.de

Web: https://mgpp.rub.de Ute Kraemer <Ute.Kraemer@ruhr-uni-bochum.de>

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SanDiego NHM MammalianPaleontology

Applications are invited for a Postdoctoral Fellowship position in the Department of Paleontology at the San Diego Natural History Museum (SDNHM). The James R. Colclough Paleontology Postdoctoral Fellowship supports research in Cenozoic mammalian paleontology and taphonomy. The Fellowship was created to honor the memory of James R. Colclough, longtime volunteer in the Department of Paleontology, and is funded by the James R. Colclough Paleontology Endowment.

OBJECTIVE: The Fellowship is designed to advance the academic and professional training of the next generation of vertebrate paleontologists and taphonomists by providing them with the funding and facilities to pursue specific, time-limited research projects in association with Museum scientists and utilizing vertebrate fossil specimens and data housed in the SDNHM Department of Paleontology.

RESPONSIBILITIES: Duties will include conducting original research in Cenozoic mammalian paleontology and/or taphonomy, providing research assistance to the Curator of Paleontology, and introducing new technologies and analytical methods into the Museum setting. Postdoctoral Fellows are expected to be in residence at SDNHM full time and actively engaged in the SDNHM community. The position will include opportunities for interactions with colleagues at nearby San Diego State University, University of California-San Diego, and University of San Diego.

QUALIFICATIONS: To be considered for this position, applicants must have received a PhD degree within the past six (6) years. Soon-to-graduate PhDs may apply, but all formal requirements for a PhD must be completed before the start of the appointment.

This is a full-time, position with benefits such as health insurance, vacation, 15 paid holidays, reciprocal free admission to all of Balboa Park's museums, as well as to the San Diego Zoo and Safari Park.

COMPENSATION: Annual compensation is $68,640. Supplemental research funds also may be available. Appointments will typically be made for two years contingent on satisfactory progress in year one.

STARTING DATE: On or after August 1, 2025.

TO APPLY: Applicants should submit a cover letter (1-2 pages), a succinct statement (˜700 words) detailing current work and research interests, an up to date curriculum vitae, a list of any publications, and the names and contact information for two professional references.

Please submit materials to tdemere@sdnhm.org by May 16,2025.

Tom Demï¿½rï¿½, Ph.D.

Curator, Department of Paleontology Director, Department of PaleoServices

If we seem busy, it's because we have millions of years of work to do. Find out what we're up to.

P 619.255.0232 C 619.540.1870 F 619.232.0187 E tdemere@sdnhm.org

Mailing address: P.O. Box 121390, San Diego, CA 92112-1390 Street address: 1788 El Prado, San Diego, CA 92101

Tom Demere <tdemere@sdnhm.org>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

SGN Frankfurt TerrestrialBiodiversity

Job announcement Ref. #04-25003

For over 200 years the Senckenberg Gesellschaft für Naturforschung (SGN) has represented one of the most relevant institutions investigating nature and its diversity. Currently, scientists from more than 40 countries across 12 locations in Germany conduct research in the fields of biodiversity, Earth system analysis and climate change.

Following its mission to "analyze and document biodiversity in Earth system dynamics - to serve science and society" Senckenberg stands for curiosity-driven and application-oriented collections-based research.

The Department of River Ecology and Conservation at Senckenberg Gelnhausen invites applications for a

Postdoctoral Researcher in terrestrial ecology (m/f/d) (full time or part time)

We are looking for enthusiastic ecologists (m/f/d) with a background in biodiversity research, specifically species and community ecology, macro-ecology, conservation, and assessments.

The position is part of a larger project which aims at developing a global biodiversity footprint index to simultaneously assess global biodiversity and human impact on ecosystems. The project will be done in close collaboration with remote sensing experts from the University of Marburg, Germany.

Your potential tasks:

Reviewing local, regional and global biodiversity assessment methods Developing a comprehensive and robust biodiversity footprint index which - simultaneously allows for assessing human impact in space and time and - provides a global perspective on biodiversity status and change Developing an automatization of the biodiversity footprint index Data analysis, preparation of manuscripts and reports

Your profile:

PhD in Ecology or a related field Solid background in biodiversity research, species and community ecology, conservation, biodiversity assessments Advanced skills in GIS and statistical analyses, preferably using R Strong track record of international publications Excellent written and oral communication and project presentation skills

Salary and benefits are according to a public service position in Germany (TV-H E13). The contract is full-time or part-time (at least 75 %). It should ideally begin as soon as possible and will initially be limited to 2 years with a possible extension.

Senckenberg is committed to diversity. We benefit from the different expertise, perspectives and personalities of our staff and welcome every application from qualified candidates, irrespective of age, gender, ethnic or cultural origin, religion and ideology, sexual orientation and identity or disability. Women are particularly encouraged to apply, as they are underrepresented in the field of this position; in the case of equal qualifications and suitability they will be given preference. Applicants with a severe disability will be given special consideration in case of equal suitability. Senckenberg actively supports the compatibility of work and family and places great emphasis on an equal and inclusive work culture.

Please send your application until March 23rd, 2025 preferably by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref. #04-25003) and include

a letter outlining your suitability for the post,a detailed CV,contact details of 2 references,a list of publications and acquired funding to: Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt

E-Mail: recruiting@senckenberg.de

Applications can also be submitted via our online application tool: https://www.senckenberg.de/de/karriere/-bewerbung/ For scientific enquiries please get in contact with Prof. Dr. Peter Haase.

E-Mail: peter.haase@senckenberg.de

Mit freundlichen Grüßen / Yours sincerely Maria di Biase Referentin Recruiting/HR Department & Personalmarketing Besucheradresse: Mertonstraße 17-21, 60325 Frankfurt am Main (1. OG) Telefon/Phone: 0049 (0)69 / 7542 - Stellv. Leiterin Personal/Human Resources-1458 Loke, Uta Recruiting/HR Department & Personalmarketing - 1478 Gajcevic, Isabel - 1309 Heinrichsohn, Sabine - 1564 di Biase, Maria -1566 John, Alexandra Fax: 0049 (0)69 / 7542-1445 Mail: recruiting@senckenberg.de

Senckenberg Gesellschaft für Naturforschung Rechtsfähiger Verein gemäß ç 22 BGB

Mitglied der Leibniz-Gemeinschaft

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Vernetzen Sie sich mit uns:www.senckenberg.de/-socialmedia Maria Di Biase <recruiting@senckenberg.de>

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SmithC Massachusetts ExtremophileMicroeukaryotes

Postdoctoral Position: Biodiversity of microbial eukaryotes in extreme environments

The Department of Biological Sciences at Smith College invites applications for a benefits eligible postdoctoral fellow, focusing on genome evolution in microeukaryotes (aka protists), to begin on or after June 1, 2025.

The bulk of the work will focus on bioinformatic analyses of data generated in the lab from diverse amoebae, including species sampled from extreme (e.g. high temperature) environments.

The initial appointment is for one year, with the possibility of extending for additional years.

The position will be housed in Professor Laura Katz's laboratory in the Department of Biological Sciences; questions should be directed to lkatz@smith.edu.

The goals of this research include characterizing genome architecture in poorly-studied clades and reconstructing the evolutionary history of both genes and species (i.e. species delimitation).

The ideal candidate will: 1) be a productive researcher with interests in both biodiversity and phylogenomics of microorganisms; 2) have experience identifying and isolating diverse microbes; 3) have knowledge of bioinformatic and/or phylogenetic tools; 3) have excellent communication and interpersonal skills; and 4) be interested in collaborating with graduate and undergraduate students in the laboratory.

Located in Northampton, MA, Smith College is the largest women's college in the US and is dedicated to excellence in teaching and research. The College is a member of the Five College Consortium with Amherst, Hampshire and Mt. Holyoke Colleges, and the University of Massachusetts Amherst.

Submit application through Smith's employment website with a cover letter, curriculum vitae, sample publications and the contact information for three confidential references. Finalists may be asked for additional materials. https://tinyurl.com/bde3aruy Laura Katz <lkatz@smith.edu>

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StockholmU VirulenceEvolution

I am looking for a postdoc for my new lab at Stockholm University to work on the project"Dynamic interactions between host social behavior and parasite virulence".

This position is part of a larger research project that aims to provide integrated theoretical and empirical tests of the dynamic interactions between host social behavior, parasite transmission, and virulence evolution. Using a small fish - the guppy - and its parasites, we have run experimental epidemics in host populations that differ in their social behavior. Phenotypic and genomic data from this large-scale experiment, along with mathematical models, will generate refined theoretical predictions that we will test in natural Trinidadian stream communities. Using our experiment, model, and field sampling, we will test how host social behavior: 1) shapes the size and structure of parasite populations; 2) drives parasite virulence evolution; 3) responds to an outbreak to slow its spread. Such an integrative approach is essential and will identify and evaluate general ecological and evolutionary mechanisms by which host social behavior and parasite virulence interact across systems: it has substantial relevance for infectious disease management across species including humans.

The postdoc will work collaboratively with other members of the project team who will be based primarily at the University of Pittsburgh, the University of Texas at El Paso, and the University of California, Berkeley.

Initially, the post doc will work on analysis of existing data from experimental epidemics of the parasiteGyrodactylus turnbulliin groups of Trinidadian guppiesPoecilia reticulata. These data include time series of parasite counts and social interactions from individually identified fish throughout the course of epidemics. Other data types include microbiome samples, female reproductive status, and male ornamentation. There is scope to develop independent research questions within the broader project, and potentially to run additional experimental epidemics, experimental infections, mathematical modelling, and/or fieldwork to test questions emerging from the analysis.

More details and application instructions are here: https://su.varbi.com/en/what:job/jobID:798807/-where:4/ Please contact me for more information!

Jessica Stephenson Tenured Researcher (starting 1st July 2025), Department of Zoology, Stockholm University, Stockholm, Sweden jfrstephenson@gmail.com

jfstephenson.com

Jessica Stephenson <jfrstephenson@gmail.com>

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Taipei Taiwan VirusesOfMicrobes

*Three-year postdoc positions (with possible extension) in evolutionary biology of viruses of microbes *Application open until May 31, 2025 or until positions are filled

Postdoc positions are available in the Ku Lab at the Institute of Plant and Microbial Biology, Taipei, Taiwan. The two potential research areas are: 1. Giant viruses: evolution of viral gigantism, genome regulation, and virus-host interactions Giant viruses are DNA viruses with extraordinary genomes that are associated with a wide range of eukaryotic hosts, including animals, fungi, amoebae, algae, and many other microeukaryotes. 2. Phages: evolution of phage resistance and susceptibility and dynamic phage-bacteria interactions We focus on phages that infect antibiotic- resistant bacteria to study what determines the outcome of phage infection and to apply this knowledge to develop broad-range phages.

Our institute is part of Academia Sinica, the Taiwanese academy of sciences. The working language in our lab and institute is English. Knowledge in Mandarin or other Taiwanese languages is not required, but foreign researchers are encouraged to take Mandarin classes if they want. More details can be found on our lab and institute websites.

Application requirements: 1. A PhD degree in biology, informatics, natural sciences or related fields 2. English writing and speaking skills 3. Ability to work both independently and as part of a team 4. Experience and knowledge in genomics, bioinformatics, evolutionary biology or microbial ecology

To apply, please send an email with the subject IPMB_application_Postdoc_YourName directly to Chuan Ku, briefly describing your research interests, experience, skills, future plan, and contact details of at least two referees. A single PDF should be attached that includes your CV and relevant documents. Shortlisted candidates will be invited for an interview. If an onsite interview is possible, we will cover the costs for flight and accommodation.

Inquiries are also welcome.

Dr. Chuan Ku (associate professor & EMBO Global Investigator) email: chuanku@gate.sinica.edu.tw Twitter/X: @chuanku_ Bluesky: @chuanku.bsky.social Lab website: https://chuanku-lab.github.io/kulab/ Institute website: https://ipmb.sinica.edu.tw/en chuanku <chuanku@gate.sinica.edu.tw>

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TrentU DeerEpigenetics

Postdoctoral Fellow Position - Deer Epigenetics

We are recruiting a fully-funded PDF to study the epigenomics of white-tailed deer and mule deer. The PDF will take advantage of hundreds of mule deer samples to build epigenetic clocks and study variation in mule deer aging. Disease status and phenotypic data are also available for 100s of white-tailed deer and mule deer. The PDF will have the flexibility to adapt the project to their interests and the opportunity to collaborate and work with our partners in Wyoming.

Location:

The PDF will join the lab group of Aaron Shafer at Trent University in Peterborough, ON, and will have access to networking and training opportunities through both Trent and the project leads with the Wyoming Fish and Game Department.

Qualifications and Eligibility:

The successful candidate must have PhD in Biology or a related discipline. The ideal candidate will have experience with genomic data, bioinformatics, or data-analytics. Applicants should have strong written and oral communication skills, and experience using R to analyse data. Experience using high performance computing would be considered an asset.

Salary:

The applicant will receive 60K CAD per year + vacation + non-discretional benefits. One year of funding is guaranteed plus one year renewal upon satisfactory progress. A third year of funding can be discussed.

To Apply:

Please send the following to Prof. Aaron Shafer (aaronshafer [at] trentu.ca): A statement outlining research interests, career goals, and how your previous experience and training relates to this project.

1. Your c.v.

2. Contact information for two references

Deadline to apply: April 1st or until filled

Applications will be reviewed as they are received.

Start Date: Summer / Fall 2025 (flexible)

Aaron B.A. Shafer Associate Professor Trent University Peterborough, Ontario Canada, K9J 7B8 http://www.aaronshafer.ca (He / him; learn more < https://www.glsen.org/activity/pronouns-guide-glsen >)

Department of Forensic Science - Chair Environmental & Life Sciences Graduate Program Applied Modelling & Quantitative Methods Graduate Program

Aaron Shafer <aaronshafer@trentu.ca>

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UBristol EvolNutritionImmunityPregnancy

2-year postdoc position available in Nutrition and Immunity in Pregnancy

Deadline: 11 March

We are seeking an experienced postdoc to work on our UKRI Future Leaders Fellowship project 'Nutrition and immunity in pregnancy: maternal responses and consequences for offspring'. Broadly, this project seeks to take an evolutionary perspective on how pregnant mothers respond to the dual challenges of nutritional and immune stressors, and the immediate and long-term consequences for their offspring. We use a combination of evolutionary models, experiments on viviparous insects (tsetse and Pacific beetle-mimic cockroaches) and analyses of health studies in human populations across contrasting geographic contexts.

The postdoc will play a critical role in implementing experiments on nutrition and infection in pregnant insects. They will also have the opportunity to be involved in human cohort data analysis, with particular focus on data which overlap with the insect experiments (including the metabolic and epigenomic data). They will work under mentorship of Sinead English, in collaboration with a research technician and project partners at the Universities of Cincinnati (US), Stellenbosch (South Africa), Macquarie (Australia), on the insect studies; and with collaborators in Exeter and King's College London, for the human studies.

The role will suit someone with expertise in conducting laboratory experiments on insect models, in the extraction and processing of samples for molecular analysis, and excellent data processing and handling skills. In addition, expertise in, or enthusiasm for, comparative transcriptomic and epigenomic analyses will be desirable. Finally, an enthusiasm for linking evolutionary insights to topics of public health importance is required for this post.

The successful candidate will join the Evolution and Vector Ecology lab in the School of Biological Sciences, University of Bristol. This is a dynamic and inclusive environment which provides career development support for early career researchers. Bristol is a vibrant city, which is also well connected, and close to beautiful green space.

For informal queries about the role please contact: Dr Sinead English - sinead.english@bristol.ac.uk

Contract type: Fixed funding for 2 years

To apply, please follow link at: https://www.jobs.ac.uk/job/DLV631/research-associate-senior-research-associate-in-nutrition-and-immunity-in-pregnancy Interviews will be held on 24 or 25 March 2025.

Dr Sinead English Associate Professor in Evolution & Public Health UKRI Future Leaders Fellow

School of Biological Sciences, University of Bristol Website: www.evelab.org Bluesky: @englishse.bsky.social

Please note I work part-time: my office days are Mon/Wed/Thurs

Sinead English <sinead.english@bristol.ac.uk>

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UCalifornia Berkeley HumanEvolGenetics

Post-doctoral position ??? University of California, Berkeley ??? Human Evolutionary Genetics.

Description: The Moorjani Lab (https://moorjanilab.org/) at the University of California, Berkeley develops and applies statistical methods to genetic data from present-day and ancient individuals to learn about human demographic history and its impact on disease and adaptation. We are interesting in learning about human germline mutation rate, demographic inference and archaic ancestry. Some ongoing projects include:(1) uncovering the determinants of human germline mutation rate, (2) characterizing major population events in human evolution, such as gene flow, bottlenecks and expansions, and (3) identifying genetic variants linked to environmental adaptations and human diseases. The research in the lab involves both development of new methods and large-scale genomic data analysis.

Responsibilities: A successful candidate will develop and apply computational approaches to large genomic datasets to characterize patterns of population history and evolution. The main responsibilities include conducting research, attending regular lab meetings and journal clubs, and preparing research results for publication and presentations at scientific meetings. Opportunities may also exist for mentoring graduate and undergraduate students.

Required qualifications: Ph.D. or equivalent in genetics, genomics, computational biology or related fields and demonstrated record of productivity and publications. Experience with programming (e.g. C/C++, Python/Perl, R or other programming languages), genomic data analysis and methods development.

Please contact Priya with your CV and a brief overview of research questions you are interested in pursuing. Please also request three recommenders to send a letter of reference on your behalf.

Salary: This is a multi-year postdoctoral position (initial appointment is for 12 months and renewable annually up to three more years). Salary is commensurate with qualifications and experience.

Contact: Priya Moorjani Assistant Professor Department of Molecular and Cell Biology Center for Computational Biology https://moorjanilab.org/ Email: moorjani@berkeley.edu

Priya G Moorjani <moorjani@berkeley.edu>

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UJagiellonianCracow EvolutionQuiescentState

Postdoc Position in Quiescent cell Variability

We invite applications for a postdoc position within the project “The influence of ecological factors on the quiescent state: from the characteristics of individual eukaryotic cells to population dynamics”, funded by the

Polish National Science Centre (NCN) OPUS grant.

About the Project Background information:— Quiescence (Q) is a fundamental survival state in eukaryotic cells, allowing organisms to persist under starvation conditions. The project aims to explore the cellular and molecular mechanisms underlying quiescent state variability and its impact on adaptation, antifungal resistance, and population dynamics. The project investigates how individual quiescent cells reorganize their internal structures and how these changes influence population-level survival, stress tolerance, and adaptation. Main questions are:— What structural and metabolic changes occur in single quiescent cells over time, and how do they impact survival and regrowth? How do different quiescent phenotypes respond to antifungal treatments, and what are the mechanisms of resistance? How does population density affect quiescence-related survival strategies, and how the Allee Effect influence quiescent cell fitness? What evolutionary trade-offs exist between quiescence depth, regrowth potential, and stress resistance? About the Position The Postdoctoral researcher will focus on developing and applying advanced microscopy, microfluidics, and single-cell analysis techniques to investigate quiescence at both individual and population levels. The candidate will: -——— Develop and apply fluorescence microscopy and microfluidics techniques for single-cell quiescence analysis. -——— Characterize cytoskeletal, mitochondrial, and metabolic changes in quiescent cells. -——— Conduct live-cell imaging experiments to monitor quiescent cell aging and reactivation dynamics. -——— Investigate antifungal resistance mechanisms in quiescent yeast populations. -——— Collaborate with international partners to integrate advanced imaging and microfluidic technologies into the research workflow. -——— Contribute to mathematical modelling efforts linking single-cell characteristics to population-level dynamics. Host Institution & Location The PhD student will be based at the Institute of Environmental Sciences, Faculty of Biology of the Jagiellonian University in Kraków, Poland - one of the leading research institutes in Ecology and Evolution in Central Europe (www.eko.uj.edu.pl/-en_GB). Kraków is a vibrant city with a rich cultural scene (European City of Culture 2000), hosting over 100 festivals and numerous cultural events annually. The city offers modern museums, theaters, cinemas, restaurants, and excellent access to outdoor activities such as hiking and biking. It is also well-connected to other European cities.

Founding & Salary The position is for 4 years (after successful probation) and the salary is 140k PLN/year before tax. To estimate living costs in Kraków, applicants can use tools such as Numbeo (www.numbeo.com).

Requirements The successful candidate will have a Ph.D. in a relevant field by June 2025 (or obtained no more than 7 years ago, possible extension due to e.g. parental leave). We are looking for candidates with: -——— Possess experience in fluorescence microscopy, image analysis, and/or preferably microfluidic single-cell analysis and techniques. -——— Be familiar with yeast biology -——— Proficiency in image analysis -——— Have strong analytical skills and the ability to work independently while coordinating with a multidisciplinary team -——— Fluency in English (written and spoken), good communication and organisational skills -——— Be willing to collaborate with international research groups and conduct short research stays abroad. -——— Strong track record of scientific publications in peer-reviewed journals. -——— Willingness to mentor PhD and Master's students in the lab.

Deadline & Selection Process If interested, please send a cover letter explaining your background, skills, and interest in the project, CV, and contact information of two academics willing to provide references to— dr hab. Dominika WÂ^{3}och-Salamon, Prof. UJ (dominika.wloch-salamon@uj.edu.pl). Review of applications is ongoing; apply by 28th April, 2025 to ensure full consideration. The start date of the position is 01.09.2025 (but may be negotiable!).

We look forward to receiving your application!

dr hab. Dominika WÂ^{3}och-Salamon Prof. UJ Instytut Nauk o Ârodowisku/ Institute of Environmental Sciences Uniwersytet Jagiellon̄ski/ Jagiellonian University + 48 12 664-51-35

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.mcmaster.ca/~brian/evoldir.html

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ULausanne PDF PhD Bioinformatics

Fully funded bioinformatician position at the University of Lausanne

The Engel Lab (https://engelbeelab.com/) at the University of Lausanne is looking for a bioinformatician to join the team. The successful candidate whether a postdoc or a PhD graduate will lead and support research projects within the NCCR Microbiomes, a Swiss consortium focused on the ecology and evolution of microbial communities (https://nccr-microbiomes.ch/). Start date: To be discussed, preferably between July-September 2025. More details: https://shorturl.at/-mC46o Having been part of the Engel Lab for 1.5 years, I can confidently say it offers a supportive and constructive work environment.

Fully funded Phd and Postdoc position at the University of Lausanne

I am excited to share that I will be starting a lab at the University of Lausanne this summer, focusing on the evolution of gut microbiota in mammals. We have two fully funded positions available (start date flexible, but preferably between October-December 2025):

PhD Position(bioinformatics or experimental focus) - Details and application:https://tinyurl.com/43ucs3zf Postdoc Position(bioinformatics or experimental focus) - Details and application:https://tinyurl.com/mu2945n6 I would greatly appreciate it if you could share this information with anyone who might be interested.

Thank you! Florent

Florent Mazel Research Manager Dpt. of Fundamental Microbiology Univ. of Lausanne & NCCR Microbiomes Biophore Building CH-1015 Lausanne Switzerland

https://microbiota-evolution.weebly.com https://nccr-microbiomes.ch/ Florent Mazel <florent.mazel@unil.ch>

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ULausanne PDF PhD EvolutionGutMicrobiota

Dear Colleague,

Ievoldir@evol.biology.mcmaster.ce am excited to share that I will be starting a lab at the University of Lausanne this summer, focusing on the evolution of gut microbiota in mammals. We have two fully funded positions available (start date flexible, but preferably between October-December 2025):

PhD Position (bioinformatics or experimental focus) - Details and application: https://tinyurl.com/43ucs3zf Postdoc Position (bioinformatics or experimental focus) - Details and application: https://tinyurl.com/mu2945n6 I would greatly appreciate it if you could share this information with anyone who might be interested.

Thank you! Florent

Florent Mazel Research Manager Dpt. of Fundamental Microbiology Univ. of Lausanne & NCCR Microbiomes Biophore Building CH-1015 Lausanne Switzerland

https://microbiota-evolution.weebly.com https://nccr-microbiomes.ch/ Florent Mazel <florent.mazel@unil.ch>

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UMontpellier BiodiversityMonitoringEcolNetworks

We are seeking a postdoctoral researcher for a two-year position as part of a collaborative project between the University of Montpellier (France) and CIBIO (Portugal). The researcher will analyse a pre-existing metabarcoding/metagenomic dataset comprising multi-trophic interactions among plants, insects, and bats, along with their associated fungal and viral pathogens.

The full project description and how to apply is available here: https://euraxess.ec.europa.eu/jobs/324850#job-information Deadline for application: 12 Apr 2025 - 23:59 (Europe/Paris) Documents needed: a detailed CV + a cover letter.

Sï¿½bastien Puechmaille <s.puechmaille@gmail.com>

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UNorthernBritishColumbia Two ConservationGenomics

2 Postdoctoral Positions in Population Viability Modelling and Conservation Genomics

Posting Date: March 2, 2025

We invite applications for TWO Postdoctoral Fellows in the Department of Ecosystem Science and Management at the University of Northern British Columbia, Canada with a start date in Summer 2025. One position will focus on Population Growth and Viability Modelling and the other on Conservation Genomics. Both positions are full-time for a term of 2 years with the possibility of extension to 3 years. The Postdocs will work in partnership with the Marmot Recovery Foundation (MRF), a charitable organization whose mission is to recover the wild population of the endemic and critically endangered Vancouver Island marmot (Marmota vancouverensis). MRF has been collecting population data for over 25 years and has DNA samples from ~1,000 individuals.

We seek candidates who will contribute novel applied research to advance marmot conservation by studying historical population trends, building population viability models to directly guide in-the-wild recovery efforts, sequencing genomes to estimate diversity/inbreeding/relatedness, and developing the first genotype-informed conservation breeding program in Canada. The successful candidates will play integral roles in shaping ongoing conservation actions and be part of a multidisciplinary team composed of academics, veterinarians, managers, and conservation biologists from UNBC, Vancouver Island University, MRF, Wilder Institute/Calgary Zoo, and Provincial and Federal Governments.

Applicants must have completed a Ph.D., within the previous four years or will be awarded within three months of beginning the Fellowship, in biology or a closely related discipline and have demonstrated experience with population modelling or population/conservation genomics. The successful candidates will have fluency in written and verbal English and a growing record of scholarly activity related to their field, while evidence of collaborating with partners and implementing applied management solutions resulting from research would be an asset.

Postdoctoral Fellows will receive annual salaries of $60,000, 4% vacation pay, competitive health benefits, and be based at the Prince George campus with opportunities for summer fieldwork on Vancouver Island. For more information, including separate job descriptions for each Postdoctoral Fellow position, please visit the Marmot Recovery Foundationï¿½s website at: https://marmots.org/recovery-efforts/about-the-foundation/careers/ Applications received by April 11, 2025 will receive full consideration.

Jamie Gorrell <Jamie.Gorrell@unbc.ca>

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UOslo GalapagosPlantStructuralVariants

Link with all info https://www.jobbnorge.no/en/available-jobs/job/277333/postdoctoral-research-fellow-in-evolutionary-and-comparative-genomics
Contact info jose.cerca@ibv.uio.no

What Postdoctoral Research Fellow in Evolutionary and Comparative Genomics

*Context *Some of the most diverse lineages on our planet (e.g. Darwin's Finches and Hawaiian Silverswords), are found in oceanic archipelagos. Paradoxically, species in these regions often have small population sizes, frequently experience bottlenecks and founder events, and are prone to inbreeding all factors typically detrimental to genetic diversity. How, then, can these remotely located lineages, subject to such genetic constraints, maintain enough diversity to radiate and evolve? This project aims to explore this fascinating paradox.

This Postdoc project will incorporate ecology, genomics, and evolutionary biology to investigate the evolution of genetic variation on three lineages within the Asteraceae family in the Galápagos: Scalesia, Lecocarpus, and Darwiniothamnus. There may be opportunities for fieldwork in the Galápagos, and research visits abroad (Australia, Canada, Ecuador) as part of this research project.

We will focus on: *The impact of structural variants in local adaptation* *Pangenome approaches to detect variation in gene content across individuals;*

Where The position provides an exciting opportunity to join a friendly, diverse and very active research group with a focus on close mentorship, skills and career development, at the University of Oslo. The group is situated with the Centre for Ecological and Evolutionary Synthesis (CEES) which is a vibrant interdisciplinary research cluster with an active and welcoming research culture. There will be possibilities for supervision of PhD and MSc students. The main purpose of a postdoctoral fellowship is to provide the candidates with enhanced skills to pursue a scientific top position within or beyond academia. To promote a strategic career path, all postdoctoral research fellows are required to submit a professional development plan no later than one month after commencement of the postdoctoral period.

Qualification requirements - Applicants must hold a degree equivalent to a Norwegian doctoral degree in biology, bioinformatics, genomics, ecology, evolutionary biology, or alike. Doctoral dissertation must be submitted for evaluation by the closing date. Only applicants with an approved doctoral thesis and public defense are eligible for appointment. - Fluent oral and written communication skills in English

Desired qualifications: - Experience with whole genome data and computational biology or bioinformatics (genome assembly and annotation, pangenome graphs, population genomics) using Nanopore, PacBio and/or Illumina data - Strong interest in biodiversity genomics

We offer - Attractive welfare schemes and a generous pension agreement - Professionally stimulating working environment - Vibrant international academic environment - Postdoctoral development programmes - Opportunity of up to 1.5 hours a week of exercise during working hours. - A workplace with good development and career opportunities. - Membership in the Statens Pensjonskasse, which is one of Norway's best pension schemes with beneficial mortgages and good insurance schemes. - Salary in position as Postdoctoral Fellow, position code 1352 in salary range NOK from 579 700 to 657 300, depending on competence and experience.

>From the salary, 2 percent is deducted in statutory contributions to the State Pension Fund.

Application Your application should include:

- A well-justified cover letter including a statement of interest, briefly summarizing your scientific work and interests, and a personal assessment focusing on how you fit the description of the person we seek. - Documentation of English proficiency, if applicable - CV (summarizing education, positions, pedagogical experience, administrative experience and other qualifying activity) - Copies of educational certificates, academic transcript of records - A complete list of publications and up to 5 academic works that the applicant wishes to be considered by the evaluation committee (PDFs should be attached in the application) - Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number) - [Optional, but beneficial] A 1-2 page research proposal outlining research questions, and an experimental design focusing on structural variants, pangenomes and Galápagos plants. - [Optional, but beneficial] A previously submitted grant application (e.g. MSCA or any other grant) by the candidate, so the committee assesses interests and merits

islandevolution.github.io [group website]

jcerca.github.io [personal website]

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UOulu Finland RemoteSensing

We are now looking for

a Postdoctoral Researcher in Ecosystem Monitoring With Remote Sensing

to join us as part of the Profi8 interdisciplinary research program "SAFIRE: Safeguarding Biodiversity through Interdisciplinary Research on Habitat Restoration" at the University of Oulu, Oulu, Finland.

The University has recently launched a new strategic research programme, SAFIRE, which brings together the faculties of natural sciences, humanities, and engineering. SAFIRE's focus is the production of scientifically excellent and actionable knowledge on habitat restoration, especially in the Arctic regions. SAFIRE aims to develop transdisciplinary processes to improve habitat restoration through basic and applied science, engaging and co-producing knowledge and solutions with societal actors, and the integration of advanced modelling approaches, both at the level of individual projects, and at an institutional level within Oulu University. SAFIRE will also advance research and discussion concerning the multiple environmental and societal contributors to ecosystem restoration and will strengthen the collaborative role of the natural sciences, social sciences, humanities, and engineering, in current political and scientific debates about the environment, especially but not limited to the Arctic. Through three linked tenure track appointments, and significant investment in transdisciplinary collaboration between research disciplines and with societal actors, SAFIRE will promote inter- and transdisciplinary and citizen-engaged studies of the environment and raise the University's profile as an international leader in restoring inter-related ecological and social systems.

SAFIRE is part of a wider Profi8 program at the University of Oulu, funded by the Research Council Finland, and it is co-led by the Faculties of Science and Humanities at the University of Oulu.

About the job

We are looking for a remote sensing specialist to work on different tasks related to monitoring of the status and functioning of various managed, degraded, restored, and pristine ecosystems. We are mainly focusing on terrestrial ecosystems (e.g., forests, peatlands) but there can be also tasks related to freshwater and marine habitats. The remote sensing datasets will be connected to a wide range of field monitoring datasets (e.g., vegetation, environmental dna). You will primarily work with long-term monitoring utilizing satellite imagery (e.g., Landsat, Sentinel) but there are also possibilities for utilizing drone and other high spatial resolution data.

You should have a proven track record in high-quality scientific publishing as well as processing and analyzing satellite imagery e.g., through cloud-based geospatial analysis platforms such as Google Earth Engine. We are looking for a team player who has a strong motivation and capability to work with ecologists as well as researchers from various backgrounds and disciplines. You are expected to have expertise in different statistical and machine learning methods, coding languages and processing environments (e.g., R, Python). You are expected to participate in external funding calls.

What we offer?

* The support of an experienced and enthusiastic team where you can share your expertise and grow as an expert.

* Wellness benefit ePassi covering sport, culture and well-being. Read more about other staff benefits here. < https://www.oulu.fi/en/university/careers/staff-benefits >

* Our Buddy Programme < https://www.oulu.fi/en/university/careers/university-oulu-buddy-programme > and Spouse Network < https://www.oulu.fi/en/university/careers/university-oulu-spouse-network > support you and close ones in settling into Oulu.

* Development and career options of the big organization.

* We have an HR Excellence in Research < https://www.oulu.fi/en/university/careers/hr-excellence-research > -quality label which is a recognition awarded by the European Commission for the development of researchers' working conditions and careers.

* Work that matters and a workplace that promotes flexibility and work-life balance. Read more about working with us. < https://www.oulu.fi/en/university/careers >

* Finland is one of the most livable countries in the world, with a high quality of life, safety, an excellent education system, and a competitive economy. Read more about living in Oulu < https://www.oulu.fi/en/university/careers/living-oulu >.

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UOulu Finland Two EnvironmentalDNA

We are looking for a Postdoctoral Researcher in Environmental DNA based Biodiversity Monitoring to join us in the Ecology and Genetics Research Unit at the Faculty of Sciences at the University of Oulu as part of the European Union Interreg Aurora project NORTHDIVeRSITY.

NORTHDIVeRSITY (https://www.luke.fi/en/projects/northdiversity) is an international collaboration between the University of Oulu in Finland, the Natural Resources Institute Finland (LUKE) and the UmeÃ¥ University in Sweden to establish environmental DNA (eDNA) based biodiversity monitoring as an efficient tool for routine biodiversity monitoring.

In the last decades massive global changes have been recorded, resulting in altered ecosystems and large-scale biodiversity loss. These changes have been shown to be especially pronounced in Northern regions. However, biodiversity is essential for the functioning of ecosystems and human well-being. To reverse this trend and ensure sustainable livelihoods, regional, national and international agreements demand actions. These include the identification, protection and restoration of low biodiversity habitats. However, identifying these using traditional methods is costly and time demanding. To streamline this process in the North, the project uses, validates and develops efficient environmental DNA (eDNA) based monitoring tools and approaches, specifically tailored to Northern habitats. The approaches will be developed in close collaboration with national and international stakeholders.

About the job

As a postdoctoral researcher you will:

* establish and validate molecular approaches for biodiversity monitoring (especially of terrestrial and freshwater habitats) * work in an international research team

* work with national and international stakeholders * support Master's and PhD students * be involved in Master's and PhD level teaching * will be part of a multidisciplinary research group * participate in external funding calls.

What we offer?

* The support of an experienced and enthusiastic team where you can share your expertise and grow as an expert.

* Wellness benefit ePassi covering sport, culture and well-being. Read more about other staff benefits here. < https://www.oulu.fi/en/university/careers/staff-benefits >

* Our Buddy Programme < https://www.oulu.fi/en/university/careers/university-oulu-buddy-programme > and Spouse Network < https://www.oulu.fi/en/university/careers/university-oulu-spouse-network > support you and close ones in settling into Oulu.

* Development and career options of the big organization.

* We have an HR Excellence in Research < https://www.oulu.fi/en/university/careers/hr-excellence-research > -quality label which is a recognition awarded by the European Commission for the development of researchers' working conditions and careers.

* Work that matters and a workplace that promotes flexibility and work-life balance. Read more about working with us. < https://www.oulu.fi/en/university/careers >

* Finland is one of the most livable countries in the world, with a high quality of life, safety, an excellent education system, and a competitive economy. Read more about living in Oulu < https://www.oulu.fi/en/university/careers/living-oulu >.

Who are you? In order to succeed and enjoy the position, we expect from you:

* Doctoral degree in the field of Molecular Biology or Genetics, Zoology, Ecology or other related fields. The degree must be obtained no more than 10 years ago. * Proven experience working with environmental DNA, both in the laboratory as well as on the analyses of large-scale eDNA data. * Ability for independent and creative scientific work. * Fluent in written and spoken English. * Ability to conceive, execute and complete research projects * Being a team player.

We also appreciate

* Experience working with stakeholders. * Experience with method development or standardizations.

Salary The position is fixed-term for from the 01.06.2025 or as soon as possible thereafter until the 31.11.2027. The salary will be based on levels 5-6 of the demand level chart for teaching and research staff of Finnish universities. In addition, a salary component based on personal work performance will be paid (a maximum of 50 % of the job-specific

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Uppsala PhylogeneticMethods

A postdoc/researcher position is available in Mariana Braga's group at the Swedish University of Agricultural Sciences (SLU) in Uppsala, Sweden. Research in the Evolving Networks lab (evonetslab.github.io) centers around understanding how species interactions change over time and space, with a focus on butterfly caterpillar-plant interactions and development of phylogenetic methods. The EvonetsLab is supported by a Starting Grant from the European Research Council and a DDLS Fellowship from the SciLifeLab and Wallenberg Swedish program for data-driven life science.

We are looking for a highly motivated and independent yet collaborative candidate with documented experience with phylogenetic comparative methods and R-package development. The successful candidate will be working within the development team of TreePPL (www.treeppl.org), a universal probabilistic programming language and new software for phylogenetics. The successful candidate will be responsible for the user-interface aspects of the project, through development of the R package treepplr (www.github.com/treeppl/treepplr). The work will include development and implementation of methods to test model adequacy, inference diagnostics, model comparison, and visualization of outputs from various models, including host repertoire evolution, tree inference, and diversification.

All interested candidates irrespective of age, nationality, gender, disability, religion or ethnic background are encouraged to apply. The team's common language is English so fluency in English is essential. To successfully carry out the various tasks, the candidate should take initiative, work independently and demonstrate that they are solution-oriented and can adapt and come up with creative solutions to technical problems. We put strong emphasis on personal qualifications such as collaborative skills. Since the applicant will be working closely with other group members, excellent communication, good will and reliability are required.

Due to Swedish regulation for employment of postdocs, there are two application alternatives:

If you have a PhD degree for less than 3 years, excluding deductible time such as sick or parental leave (until May 11th), follow this link https://www.slu.se/en/about-slu/work-at-slu/jobs-vacancies/?rmpage=job&rmjob=12612&rmlang=UK If your PhD degree is older than 3 years, follow this link https://www.slu.se/en/about-slu/work-at-slu/jobs-vacancies/?rmpage=job&rmjob=12616&rmlang=UK You will find more information about the positions and how to apply in those links.

Application deadline May 11 2025.

Mariana P. Braga, Ph.D.

Associate Senior Lecturer Data-Driven Life Sciences Fellow

Department of Ecology Swedish University of Agricultural Sciences SciLifeLab Uppsala - Sweden

The Evolving Networks Lab < http://evonetslab.github.io/ > Google Scholar profile < https://scholar.google.com/citations?user=jhRKaPAAAAAJ&hl=en >

Mariana P Braga <mpiresbr@gmail.com>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

UPuertoRico ButterflyEvoDevo

TITLE: POST-DOCTORAL position in Butterfly Evolutionary Developmental Biology: Omics, Computational Science, and AI

TYPE OF CONTRACT: Special Appointment

BASIC SALARY: $50K - $65K annually

TYPE OF WORK: FULL TIME (37.5 hrs./week)

DATE OF PUBLICATION: March 10, 2025

APPLICATION PERIOD: April 3 0 , 2025

STARTING DATE: June, 2025

WHO QUALIFIES TO APPLY: ALL CANDIDATES THAT REUNITE ALL SPECIAL REQUISITES FOR THE POSITION

JOBDESCRIPTION

This is a unique opportunity to join a large team and international network of scientists to work on a multi-year project that embraces the most important questions in development and evolution utilizing state of the art technologies. We are seeking a highly motivated Post-Doctoral Fellows to join our research team focusing on developmental evolutionary questions. We are recruiting 4 post-doctoral fellows. We use butterflies as a study system and omics, computational biology and AI as tools to determine fundamental molecular rules in the making of life.

Project Team

The team Principal Investigator, Riccardo Papa, is an expert in genomics, evolution, and development. The project is composed by a large team of researchers with diverse skills that will enrich the learning capability of the applicants and future job opportunities. Our team is composed of biologists, chemists, computer scientists, chemical engineers, educators, and finance advisors. Our team members are experts in the fields of evolution, genomics, functional genetics, epigenetics, proteomics, metabolomics, computer science, chemical engineer, social sciences and business. We also have partners from the private, non-profit and entrepreneur sectors. Finally, we have a large network of national (USA) and international collaborators that will participate in the development of this project and will represent an added value for personal growth.

Professional development

This proposal will offer an opportunity for professional development with activities and workshops that cover omics data generation, computational data analysis, AI, entrepreneurship and science communication. All together these workshops will provide a stronger foundation for mentoring and greater opportunity for personal growth and future job applications.

Project Description

This project aims to develop transformative science in Puerto Rico by tackling a fundamental problem of developmental biology and evolution, using two butterfly model systems. The project will integrate a diverse set of omics, developmental, and artificial intelligence (AI) techniques to illuminate the genome-tophenome pathway of a complex trait at a cellular level. The project aspires to create a detailed map of molecular processes for evolutionary comparisons. It brings together a multidisciplinary team of researchers spread across seven academic institutions within the University of Puerto Rico system and international collaborators. The project will address a scientifically important topic: the mechanistic underpinnings that instruct cells to undergo fates and acquire diverse functions to build homologous tissues, organs, and traits over the course of development and evolution. The project's ambition is to decode the genomic architecture and molecular logic of the differentiation and function of cells and organs during the entire developmental trajectory of an organism. The proposed research involves four Aims, including understanding the constraints and freedoms in organismal development (genomics focus), deciphering the molecular toolkit for building a butterfly (molecular architecture focus), understanding a butterfly wing's cell differentiation and the development of wing scales with unique colors (cellular fate focus), and building cyberinfrastructure to find patterns across omics data (focus on scalability, data integration, and artificial intelligence (AI) predictability).

Link to NSF award

https://www.nsf.gov/awardsearch/showAward?AWD_ID=2435987&HistoricalAwards=false Principal Investigator Google Scholar profile

https://scholar.google.com/citations?user=Ah6lS28AAAAJ&hl=en Position Overview

We are looking for an enthusiastic, highly motivated, and skilled researcher to contribute to our ongoing studies on butterfly evolution and development. The ideal candidate will demonstrate a strong desire to grow both professionally and scientifically. This position offers an excellent opportunity for a passionate scientist to work on cutting-edge projects investigating the molecular mechanisms underlying butterfly organismal development and evolution. We seek individuals who are not only technically proficient but also bring energy, curiosity, ambition, and a commitment to advancing their expertise in the field. By joining

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UStockholm YeastEvolutionaryGenomics

Postdoctoral position in Yeast Evolutionary Genomics at the University of Stockholm, Sweden

The Stelkens Lab is hiring a highly motivated person for a 2-year fully funded postdoc position. Research topics include but are not limited to: 1) Parallel evolution of climate adaptation in Europe and South America, 2) The genetic architecture of temperature adaptation, 3) The evolution of pathogenicity as a by-product of thermotolerance.

The selected candidate will use the powerful microbial model system budding yeast (Saccharomyces spp.), experimental evolution, and cutting-edge genomic tools to study evolutionary processes. We are looking for candidates with a strong interest in evolutionary biology, ideally with some experience in experimental evolution and/or molecular, population, and quantitative genetics. Prior training in yeast cultivation, statistics, and programming (e.g. R, Python) is a plus. Applicants should be independent thinkers, well-organized, good communicators, and happy to work in an international team.

Applicants are required to hold a PhD degree. The degree must have been completed at latest before the employment decision is made, but no more than three years before the closing date. An older degree may be acceptable under special circumstances.

The work will mostly be lab-based but may include some fieldwork. There is flexibility within the project for the postdoc to develop their own projects. The successful candidate will receive a salary and full social benefits.

Work environment: Stockholm University is located four metro stops from the centre of Stockholm, one of the most beautiful and dynamic capital cities of Europe. SU is home to a vibrant scientific community, including the Science for Life Laboratory and the Swedish Museum of Natural History. Sweden is a free and open society, and strives to be one of the worlds most innovative and research-intensive nations. We enjoy a respected system of democracy and individual rights, free health care, freedom of speech, a free press, the right to scrutinize those in power, and access to beautiful nature. Most Swedes speak English.

We highly recommend reading relevant literature to prepare your application (e.g. doi.org/10.1093/molbev/msac242, doi.org/10.1371/journal.pgen.1011154, doi.org/10.1093/evolinnean/kzae023).

Application: Use the official Stockholm University job portal. Please send formal application, including a statement of motivation, relevant expertise, your CV, and the contact details of at least two references. Link to application portal with more details: https://su.varbi.com/en/what:job/jobID:807371/where:4/ Start date: Start date August 2025 or as per agreement. Application deadline: 30. April 2025

Informal enquiries to Rike Stelkens: rike.stelkens@zoologi.su.se

Rike Stelkens Associate Professor Yeast Evolutionary Genomics Department of Zoology Stockholm University, Sweden

email:rike.stelkens@zoologi.su.se tel: +46 (0) 816 4223 lab website:stelkenslab.com

Rike Stelkens <rike.stelkens@zoologi.su.se>

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USussex InsectBehaviourEvolution

Post title: Postdoctoral Research Fellow in Insect Ecology and Behaviour (Ref. 40298)

School/department: University of Sussex, Life Sciences, Ecology and Evolution Hours: full time or part time hours considered up to a maximum of 1 FTE/37.5 hours per week. Requests for flexible working options will be considered (subject to business need) but a minimum of 0.8 FTE is required for the role.

Location: Brighton, United Kingdom Contract Type: fixed term until 28 February 2027 Reference: 40298 Grade and Salary: Grade 7 starting at £ 37,999 to £ 45,163 per annum, pro rata if part time. Closing date: March 31, 2025, 11:59 PM. Applications must be received by midnight of the closing date. Expected Interview date: To be confirmed. Interviews will be conducted via Zoom. Expected start date: 1 July 2025

About the role

We wish to appoint a postdoctoral research fellow to work on the NERC-funded project Living at the edge: causes and consequences of individual variation in a changing world“.

The project studies the effects of landscape fragmentation on behaviour, physiology, morphology, life history and related traits (and their covariation) in a forest-living ground beetle species using individuals living at an edge of a habitat and those at a core. The project combines both experimental and correlative approaches and applies a wide range of methods in the field and laboratory. These range from enclosure experiments, translocations, radio-telemetry, and behavioural and physiological assays.

You will plan and execute fieldwork and lab-experiments, manage and analyse project data, write up manuscripts and present results at conferences and to the wider audience. You will be supervised by Dr Wiebke Schuett (Project Lead) and Prof Jeremy Niven (both School of Life Sciences) and will work closely with other research team members, including a research technician and a PhD student.

About you

You have a PhD in animal behaviour, ecology or an allied biological science. You are a highly motivated, talented, well-organised and meticulous person with strong skills in quantitative analysis, experience in behavioural observations and/or experimental design and excellent team-working ability. You have a background and demonstrable interest in one or more of behavioural ecology, insect physiology, evolution and/or ecology. It is advantageous if you have previous experience in collecting data in the field, physiological and/or parentage analyses, advanced statistical modelling using R, working with insects and/or on animal personality, and handling large data sets. Holding a driving license is desirable.

About our School

In the School of Life Sciences we strive to understand the mechanisms that drive biological and chemical processes and to develop innovative and diverse approaches to enhance human health, technology and the environment. We undertake multidisciplinary research, teaching and engagement across a wide range of subjects, from Chemistry through Cellular and Molecular Biosciences to Conservation Biology.

The School comprises five Departments: Biochemistry & Biomedicine, Genome Damage and Stability Centre, Neuroscience, Ecology & Evolution and Chemistry. We also house the Sussex Drug Discovery Centre which works to deliver the bench- to-bedside translation of our discoveries. The breadth and depth of our cutting-edge research and innovative teaching practice is delivered by a diverse community who work across boundaries to deliver excellence, engage with real world problems and produce impact.

We pride ourselves on our world-leading research and have a strong research economy, with approximately 50% of our income stemming from research and an active grant portfolio of over £50 million. We host or form part of three University Centres of Excellence: the Genome Damage and Stability Centre, Sussex Neuroscience and Sussex Sustainability Research Programme. In the 2021 Research Excellence Framework, 90.6 % of our Biological Sciences outputs and 84.8% of our Chemistry outputs were rated as world-leading or internationally excellent. We are proud that in both areas, 100% of our Impact cases were rated as world-leading or internationally excellent.

The School is committed to the Universitys core values of kindness, integrity, inclusion, collaboration and courage. We believe that equality, diversity and inclusion is everyones responsibility and aim to provide a friendly and supportive environment for all who work, study and visit the School of Life Sciences. Please find further information regarding the School of Life Sciences on our website. The School of Life Sciences is proud to hold a Silver Athena Swan Award.

Why work here

Our university is situated off the A27, next to the beautiful South Downs where you will enjoy everything that our 150-acre campus has to offer. We are accessible by public transport; Falmer train station is

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UTennessee Knoxville EvolutionAnimalBehavior

We are now looking for a Postdoctoral Researcher to join us as part of our Collaborator for Animal Behavior (CoLAB) research group at the University of Tennessee, Knoxville.

The Collaborative for Animal Behavior Center (CoLAB) at the University of Tennessee invites applications for a post-doctoral research associate position starting August 1, 2025. This position offers recent Ph.D. graduates the opportunity to conduct independent, cutting-edge research in animal behavior and evolution while collaborating with faculty and students in a dynamic academic environment. CoLAB is a newly funded Center at the University of Tennessee whose goal is to understand how animals perceive and respond to environmental changes driven by natural and anthropogenic forces. By addressing critical challenges across three interconnected themes behavioral responses to environmental change, information transfer in human-altered environments, and the development of quantitative methods to uncover the principles underlying behavior the Center aims to make fundamental advances in understanding how animals collectively respond to a rapidly changing world. Scholars will develop their own research projects, engage in mentorship and outreach, and have access to state-of-the-art facilities to explore how animals respond to environmental change.

Scholars may study behaviors of any organism and at any level (genes, hormones, whole organisms). Scholars are expected to be independent and propose their own research projects. Applicants should identify two to three faculty from The University of Tennessee's Collaborative for Animal Behavior Center (colab.utk.edu), who will serve as sponsors and provide lab space and resources to the scholar. Applicants are also encouraged to discuss their planned educational and community engagement activities with their proposed sponsors. Scholars will have opportunities to engage broadly and foster collaboration with faculty, postdoctoral researchers, and graduate students as members of CoLAB and the University of Tennessee.Join us at CoLAB to explore the fascinating world of animal behavior and make significant contributions to this exciting field!

Job responsibilities

- Conduct independent, cutting-edge research in the field of animal behavior - Collaborate with faculty and students across CoLAB - Mentor undergraduate and graduate students in their independent research projects - Participate in opportunities to engage with the broader university community and contribute to outreach programs - Required Qualifications

- Education:Applicants must have completed their Ph.D. by the start date of the position (August 1st, 2025) - Experience:Applicants must have a strong track record of research excellence in animal behavior or related fields. - Knowledge, Skills, and Abilities:Applicants must have the ability to write clearly and scientifically and have a strong publication record. Applicants who are not currently US citizens must be eligible for J-1 Scholar or H-1B visa status.

Work Location

University of Tennessee, Knoxville, Tennessee

Compensation and Benefits

Anticipated hiring range: $60,000 per year plus health benefits (+ $10,000 annual research stipend and funds to cover attendance at one academic conference per year)

How to apply?

For best consideration, applicants should submit the below materials before May 1st 2025 (this deadline has been extended from April 1st).

Link to the position:

https://fa-ewlq-saasfaprod1.fa.ocs.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1/job/1992/?utm_medium=jobshare&utm_source=External+Job+Share Contact information

If you have further questions, please get in touch with Liz Derryberry (ederryb1@utk.edu) or Claire Hemingway (chemingw@utk.edu).

All the best,

Claire.

"Hemingway, Claire" <chemingw@utk.edu>

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UToronto EcolEvolBiol

The Department of Ecology and Evolutionary Biology at the St. George campus of the University of Toronto invites applications for a Departmental Postdoctoral Fellowship. We encourage applications from highly motivated postdoctoral fellows with broad interests in ecology and evolutionary biology.

Salary: $70,000 per year. Expected start date: As early as July 1, 2025 and no later than December 1, 2025. Term: 12 months; renewable for another 12 months subject to suitable research progress. Location: Toronto, Ontario, Canada.

Application deadline: April 25, 2025

See full details below and application instructions at https://eeb.utoronto.ca/employment-2/ DEPARTMENT OF ECOLOGY AND EVOLUTIONARY BIOLOGY Faculty of Arts and Science University of Toronto

JOB POSTING - The EEB Postdoctoral Fellowship

The Department of Ecology and Evolutionary Biology at the St. George campus of the University of Toronto invites applications for a Departmental Postdoctoral Fellowship.

Area of Research: Ecology and/or Evolution

Description of duties: We encourage applications from highly motivated postdoctoral fellows with broad interests in ecology and evolutionary biology. The Fellow may collaborate with a single or multiple advisors on research in ecology and evolution. We seek candidates who propose innovative and independent research programs. Given this independence, there will be access to a small research supplement to support the successful candidate's research. To facilitate interactions within the department, the Fellow will organize a workshop on a topic related to the Fellow's interest for graduate students, postdocs and faculty. Prior to applying, we encourage candidates to contact faculty members with shared interests about potential research collaborations.

The Fellow will be a fully participating member in the Department of Ecology and Evolutionary Biology (EEB) at the University of Toronto's St. George campus, which offers leading-edge facilities (see below). The University of Toronto is a family friendly employer that has won awards as one of Canada's Top Family-Friendly employers for seven consecutive years. Employment as a Postdoctoral Fellow at the University of Toronto is covered by the terms of the CUPE 3902 Unit 5 Collective Agreement, which provides a Child Care benefit to eligible Postdoctoral Fellows. This is in addition to numerous other benefits that help support department members and their families.

Salary: $70,000 per year

Required qualifications:

Applicants must have a PhD in ecology and/or evolution or a related area of study, and field-specific qualifications as set by the faculty advisor(s).

Application instructions

Applicants must submit a cover letter indicating the date that they will be available to begin the position, a curriculum vitae, copies of 2 publications or preprints, and a short description (2-3 pages) of past research accomplishments and future research plans. Applicants should include names and e-mail addresses for two potential referees.

EEB values equity, diversity, and inclusivity (EDI) and candidates should provide a short (maximum one page) statement about how they contribute to enhancing EDI. This could include past activities and training, lived experience that has informed your approaches to EDI work, or planned future contributions addressing academic inequities in relation to race, gender, sexual orientation, disability, economic justice and the like.

All application materials must be submitted as a PDF(s) in a single email to: Adriana Milani, Assistant to the Chair, at chairsec.eeb@utoronto.ca by the closing date.

Closing date: April 25, 2025 This position will remain open until filled, however we will begin to review complete applications after April 25, 2025.

Supervisor: Chair, Department of Ecology and Evolution, University of Toronto

Expected start date: As early as July 1, 2025 and no later than December 1, 2025

Term: 12 months; renewable for another 12 months subject to suitable research progress.

FTE: 100%

The University of Toronto is a leading academic institution in Canada with over 60 faculty members specializing in ecology and evolution. Strong links exist between the Department of Ecology and Evolutionary Biology and the Royal Ontario Museum, the Centre for Global Change, and the School of the Environment. The University owns a nearby field station dedicated to ecological and evolutionary research (the Koffler Scientific Reserve, www.ksr.utoronto.ca). The department also has a partnership with the Ontario Ministry of Natural Resources that helps provide access to infrastructure, including lab facilities in Algonquin Provincial Park (www.harkness.ca), funding, and long-term data sets. Genomic analyses are supported by a number of high-performance computing resources, multi-lab

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Vienna PolygenicAdaptation

Polygenic adaptation: a postdoctoral position is available at the Institute of Population Genetics, Vetmeduni Vienna (https://www.vetmeduni.ac.at/en/population-genetics/). The research focus of the Institute of Population Genetics is on understanding the genetics of adaptation. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including experimental evolution, quantitative genetics, functional genetics, empirical population genetics, bioinformatics and statistics.

In addition to a high quality of living, Vienna offers an outstanding community of evolutionary biologists (https://www.univie.ac.at/evolvienna/).

The position is associated with a research priority program on polygenic adaptation uniting a unique cluster of scientists with a keen interest to understand polygenic adaptation (e.g.: N. Barghi, N. Barton, R. Bürger, J. Hermisson, R. Kofler, M. Nordborg, H. Sachdeva and K. Swarts).

Adaptation to new environments is frequently driven by traits with a polygenetic basis. Nevertheless, the characterization of the adaptive architecture, in particular in natural populations, is challenging. The contribution of individual loci to the phenotypic changes associated with adaptation to new environmental conditions is so small that their identification and functional characterization is frequently not possible.

The successful candidate will join a team of scientists taking advantage of experimental evolution to study the adaptive architecture of temperature adaptation - a highly polygenic trait. Manipulating the genetic composition of a series of founder populations provides an unmatched opportunity to study polygenic adaptation in *Drosophila*. We are using a combination of genomic analyses with high throughput molecular phenotyping (RNA-Seq, metabolomics, proteomics) and targeted high-level phenotypes (e.g. behavior) to study these experimental populations. The goal is to understand polygenic adaptation in the context of the underlying functional variation and use this information to predict adaptive responses in the laboratory and natural populations.

We are looking for a candidate with a background in quantitative genetics and experience in handling large data sets. A solid background in population genetics and statistics will be further assets. The successful applicant will be supported by technicians for the collection of phenotypic data and the maintenance of experimental populations.

The position is available for 30 starting June 2025, but the exact starting date is negotiable. The application should be emailed to <christian.schloetterer@vu-wien.ac.at> as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be received by 2.4.2025 to ensure full consideration.

Background on our experimental system:

1. Barghi N, Tobler R, Nolte V, Jaksic AM, Mallard F, Otte KA, et al. Genetic redundancy fuels polygenic adaptation in *Drosophila*. PLoS biology. 2019;17(2):e3000128. Epub 2019/02/05. doi: 10.1371/journal.pbio.3000128. PubMed PMID: 30716062.

2. Barghi N, Hermisson J, Schlötterer C. Polygenic adaptation: a unifying framework to understand positive selection. Nature reviews Genetics. 2020;21(12):769-81. Epub 2020/07/01. doi: 10.1038/s41576-020-0250-z. PubMed PMID: 32601318.

3. Barghi N, Schlötterer C. Distinct patterns of selective sweep and polygenic adaptation in evolve and re-sequence studies. Genome biology and evolution. 2020. Epub 2020/04/14. doi: 10.1093/gbe/evaa073. PubMed PMID: 32282913.

4. Burny C, Nolte V, Dolezal M, Schlötterer C. Genome-wide selection signatures reveal widespread synergistic effects of two different stressors in *Drosophila melanogaster*. Proceedings Biological sciences / The Royal Society. 2022;289(1985):20221857. Epub 2022/10/20. doi: 10.1098/rspb.2022.1857. PubMed PMID: 36259211; PubMed Central PMCID: PMCPMC9579754.

5. Christodoulaki E, Nolte V, Lai WY, Schlötterer C. Natural variation in Drosophila shows weak pleiotropic effects. Genome biology. 2022;23(1):116. Epub 20220516. doi: 10.1186/s13059-022-02680-4. PubMed PMID: 35578368; PubMed Central PMCID: PMCPMC9109288.

6. Lai WY, Otte KA, Schlötterer C. Evolution of Metabolome and Transcriptome Supports a Hierarchical Organization of Adaptive Traits. Genome biology and evolution. 2023;15(6). doi: 10.1093/gbe/evad098. PubMed PMID: 37232360; PubMed Central PMCID: PMCPMC10246829.

7. Thorhölludottir DAV, Nolte V, Schlötterer C. Temperature-driven gene expression evolution in natural and laboratory populations highlights the crucial role of correlated fitness effects

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WorkshopsCourses

Berlin AngiospermDiversification Jul28-Aug8

Berlin Summer Course in Flower Morphology and Angiosperm diversification

28 July - 8 August 2025

There are still some spaces on this exciting course.

This is the third version of a highly successful two-week workshop based at the Biological Institute of the Freie Universität Berlin and the Berlin Botanical Garden. The workshop benefits from extensive facilities, including functional microscopy laboratories and a huge plant collection of more than 20,000 species. The course is set up as lecture-based, laboratory taught, and interactive visits of the living collections.

FORMAT:

2-week workshop, lectures and hands-on practical sessions.

INTENDED AUDIENCE:

Final year undergraduate students, PhD students, postdoctoral and advanced researchers, professionals (but no formal restriction). A basic knowledge of botany is preferred but not essential.

COURSE INSTRUCTORS AND CONTACT: Dr. Louis Ronse De Craene, Research Associate Royal Botanic Garden Edinburgh (l.ronsedecraene@gmail.com)

Prof. Julien Bachelier, Freie Universität Berlin (julien.bachelier@fu-berlin.de)

REGISTRATION FEE:

euro 800 (euro 600 for Undergraduate and Master students)

(Registration includes coffee breaks, daily lunches with snacks, but does not include travel and accommodation).

HOW TO APPLY, PAY AND SECURE A PLACE:

visit https://www.conftool.net/berlin-summer-course-2025/ For further information please contact Dr. Louis Ronse De Craene (l.ronsedecraene@gmail.com).

PROGRAMME:

Course Description and outline:

This short course will introduce students to the structure and development of flowers, with a focus on floral diversity and evolution and the significance of flowers for systematics. Major plant families will be studied within the framework of the main lineages of seed plants to understand their evolution and diversification. Additionally, students will learn to analyse, describe, and study the structure of inflorescences, flowers, and fruits, and based on their observations, to identify the main evolutionary patterns underlying their tremendous morphological diversity, as well as their potential pollination and dispersal mechanisms.

Course objectives and learning outcomes:

Through this course students will acquire the following skills:

- guidelines to identifying plants using morphological characters in the context of the molecular classification system. - a better understanding of the origin and evolution of floral structures, including their importance for classification, and of the main developmental patterns and evolutionary trends which underlie the tremendous diversity of reproductive structures. - an ability to observe and recognise key characters through the study of live floral material and the building up of floral diagrams.

Contents:

Introduction to morphology of vegetative structures and flowers, inflorescence and flower structure (floral diagrams and formulas). Overview of major groups of flowering plants; major characteristics of Flowers and special attributes (phyllotaxis, aestivation, merism, symmetry, floral tubes and hypanthia). Floral evolution of the major clades of angiosperms with special emphasis on morphological adaptations and diversification.

The Royal Botanic Garden Edinburgh is a charity registered in Scotland (No SC007983) |

Louis Ronse De Craene

<LRonseDeCraene@rbge.org.uk>

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Ferrara Italy SIBESummerSchool Sep7-11

Dear all,

We are pleased to inform you that applications for the first edition of the "SIBE Summer School" are now open.

IMPORTANT DATES for this workshop: Deadline for applications: 20/04/2025 Course dates: 7-11/09/2025

Full details, including the course programme, invited speakers and the application form, at: https://sites.google.com/view/sibesummerschool/home-page The SIBE (Italian Society of Evolutionary Biology, https://www.sibe-iseb.it/) is organizing its new "SIBE Summer School" which will take place in Ferrara from September 7th to 11th. It will offer both theoretical and practical lessons on pangenomics, conservation and population genetics.

The participation fee is 200 euro for non-SIBE members (175 euro workshop fee + 25 euro two-year SIBE membership) and euro 175 for SIBE members, and members will have the opportunity to apply for two travel grants.

For any questions or further information, feel free to get in touch.

Giobbe Forni, University of Bologna, IT Alessandro Formaggioni, University of Bologna, IT Giulia Fabbri, University of Ferrara , IT Maria Teresa Vizzari, University of Ferrara, IT Patrícia Santos, University of Ferrara, IT Rajiv Boscolo Agostini, University of Ferrara, IT Roberto Biello, University of Ferrara, IT Valentina Peona, Swedish Natural History Museum, SE

Best regards, Patrícia

Patrícia Santos, PhD Postdoctoral Researcher Department of Life Sciences and Biotechnology University of Ferrara (IT)

Patricia Alexandra Silva Santos <sntprc1@unife.it>

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Ilmenau Germany SpeciesIdentification May10-23

Dear colleagues,

The Young Modellers in Ecology (YoMos) are thrilled to invite you to this year's workshop from 19th to 23rd of May in Ilmenau, Germany. This is a peer-organized get-together for PhD-, Master- and Bachelor students working on projects related to ecological modelling - our participants work on everything from statistical modelling approaches over machine learning for species identification to mathematical models. The workshop will be in English, so international guests are very welcome.

The participation fee incl. accommodation is 240 euro for funded and 150 euro for non-funded students. We will have three amazing keynote speakers, experienced ecological modellers from very different fields. Lisa Hülsmann from University of Bayreuth will introduce us to her work on ecosystem analysis, Philip Papastefanou from Max-Planck-Institute for Biogeochemistry has exciting research on biosphere modelling to share and Thilo Gross from Helmholtz Institute for Functional Marine Biodiversity will have a contribution on modelling complex systems.

So, if you are curious to meet Thilo, Philip or Lisa, exchange with enthusiastic young modellers in ecology and learn about the variety of ecological models, join us for the 2025 YoMos workshop. You can register here until the 31st of March: https://www.yomos.org/next-workshop Best, Charlotte

Charlotte Bunnenberg (she/her) Ph.D. Student | University of Aberdeen Greta Bocedi's Research Group | School of Biological Sciences c.bunnenberg.24@abdn.ac.uk

The University of Aberdeen is a charity registered in Scotland, No SC013683.

Tha Oilthigh Obar Dheathain na charthannas clàraichte ann an Alba, Ã. SC013683.

"Bocedi, Greta" <greta.bocedi@abdn.ac.uk>

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MaxPlanckPleon EvolRescueTheoryExpts Jun30-Jul3

In case you missed it the first time, we are happy to announce the second edition of our Evolutionary Rescue workshop series at the Max Planck Institute for Evolutionary Biology in Plon, Germany.

In 2023 we organised a workshop on Mathematical models of evolutionary rescue. In this second edition we now aim to bring modelers and experimentalists together to discuss (1) which theoretical insights should be tested experimentally and how this could be done, (2) which experimental observations could be clarified with the help of theoretical models, and (3) which open questions could be addressed by the co-development of models and experiments. In addition to invited and contributed talks and posters there will be discussion sessions designed to increase cross-talk between theory and experiments.

Invited speakers: Helen Alexander, Lutz Becks, Robert D Holt, Laure Olazcuaga, Jitka Polechova.

The workshop will take place from June 30 (evening) to July 3. Before the workshop (June 29-30) we are offering a "pre-school" for those who would like to obtain an introduction to modeling evolutionary rescue. Registration is open until March 15. We hope that all participants present a talk or poster but it is not mandatory. Registration is free. For more information see https://workshops.evolbio.mpg.de/event/128/ . Matt Osmond and Hildegard Uecker

Matthew Osmond <mm.osmond@utoronto.ca>

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MountainLake GraduateEvolution Jul27-Aug2

Join Drs. Amanda Gibson (University of Virginia), Corlett Wood (University of Pennsylvania), Lynda Delph (Indiana University), and Curt Lively (Indiana University) for a six-day workshop on evolutionary biology for early career graduate students. During this week, you'll have the time and support to think deeply about the evolutionary questions that excite you and to engage in focused conversations with a small group of peers. As your group shapes ideas into a research proposal, you'll practice communicating with one another and articulating yourself in writing. The workshop will also include tutorials on the art of science writing and question development.

We have found this workshop to be particularly valuable for students who are early in their PhD, prior to writing their dissertation proposal. We assume some prior experience working in the field of evolutionary biology. The research proposal is an exercise in scientific thought and communication; it will reflect the mutual interests of your group and does not need to focus on your specific dissertation research. So, come prepared to work with your group on a wide range of evolutionary questions and approaches that may fall outside your area of expertise!

Workshop dates: July 27 - August 2, 2025 Enrollment limit: 16 Cost: $300 (with financial assistance available, including registration awards for student members of the American Society of Naturalists) Deadline for cancelation with refund: July 13, 2025 Location: Mountain Lake Biological Station, Pembroke, Virginia

For more information and to register, visit https://mlbs.virginia.edu/evolutionary-biology-workshop Amanda Kyle Gibson, Ph.D. Assistant Professor (she/her)

Physical Life Sciences Building, RM 408 Department of Biology University of Virginia Charlottesville, VA

Email: akg5nq@virginia.edu Website: https://coevolving.org/ "Gibson, Amanda K (akg5nq)" <akg5nq@virginia.edu>

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MountainLakeVA EvolQuantGenetics Jun9-13

We are pleased to announce the return of the 2025 Evolutionary Quantitative Genetics Workshop (EQG25) at a new location, scenic Mountain Lake Biological Station in the heart of the Appalachian Mountains. This five-day workshop has been given yearly since 2011-2019 and virtually in 2021-2022 under the leadership of Dr. Joe Felsenstein and Dr. Stevan J Arnold, most recently at Friday Harbor Labs. Steve and Joe have had to take a step back in organizing the workshop, but we will rely heavily on the groundwork they have built for this course; with Dr. Felsenstein participating virtually.

This years' workshop will be led by Dr. Josef Uyeda (Virginia Tech) and Dr. Fabio Machado (Oklahoma State U.), with additional instructors Drs. Pat Carter (Washington State U.), Jacqueline Sztepanacz (U. of Toronto), Laura Alencar (Yale), and Joel McGlothlin (Virginia Tech) joining us at MLBS.

Dates of instruction: Monday, June 9th - Friday, June 13th, 2025 (five-day workshop) Location: Mountain Lake Biological Station, Pembroke, VA Enrollment limit: 20 Application Deadline: April 4, 2025, 5:00pm Eastern Standard Time

Cost: The cost is $375. The fee pays for all housing accommodations (June 8-14), meals, lecturer expenses, facilities, administration, and travel between MLBS and the Roanoke Airport, arriving Sunday June 8th and departing Saturday June 14th. It does NOT cover airfare or other travel expenses to Roanoke. Applicants will be notified of their acceptance or wait list standing by April 11th, and the tuition fee will be paid after the participant has confirmed that they will attend.

Who should apply: The intended participants for this workshop are graduate students, postdoctoral fellows, and junior faculty members in evolutionary biology, particularly those interested in big questions in trait evolution.

For more information, including the registration link, please visit: https://eqgw.github.io The workshop will teach evolutionary frameworks for studying trait evolution from micro to macroevolutionary scales. We will cover the basics of theory in the field of evolutionary quantitative genetics in microevolutionary studies before transitioning to teaching phylogenetic comparative methods for studying trait evolution over macroevolutionary scales. Our primary aims are to build bridges between the traditionally separate disciplines of quantitative genetics and phylogenetic comparative methods, contextualize each others research in the outstanding questions across scales, and learn cutting edge computational methods of analysis of continuously-varying traits.

For questions, please contact Josef Uyeda, juyeda@vt.edu

"Uyeda, Josef" <juyeda@vt.edu>

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Online AdvancedRProgramming Apr14-17

Dear all,

Are you ready to take your R programming skills to the next level? Join the Physalia online course, Beyond Beginner R: Advancing Your Coding Skills, from April 14-17.

Course website: (https://www.physalia-courses.org/courses-workshops/course47/)

Designed for researchers and professionals with basic R knowledge, this hands-on course will help you write more efficient code, enhance data visualization, build interactive dashboards, and generate professional reports. Main topics covered: Advanced R programming techniques (functional programming, loops, and apply functions) Mastering the Tidyverse for data manipulation and visualization Building interactive dashboards with Shiny Creating high-quality figures, tables, and reports Collaborative coding and version control with GitHub For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/course47/)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

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Online AnalysisRNASeqData Apr17-May22

Hi everyone

Instats is excited to offer a 6-day seminar, Analysis of RNA-Seq Data, running once per week from April 17 to May 22, being led by senior biostatistician Dr. Rosina Savisaar. This comprehensive workshop demystifies the RNA-seq analysis pipeline by focusing on data analysis and interpretation, fostering an intuitive practical understanding of key concepts. You'll gain hands-on experience with data visualization in genome browsers and R, learn descriptive statistics (such as RPKM, FPKM, TPM, and L2FC), and explore advanced techniques including hierarchical clustering with heatmaps, Principal Component Analysis, differential gene expression analysis using DESeq2, and functional enrichment methods like over-representation analysis and Gene Set Enrichment Analysis. Ideal for researchers new to gene expression analysis or those seeking deeper insights into RNA-seq methodologies, this seminar uses real-world datasets (including a reanalysis of a schizophrenia study) to reinforce learning through interactive weekly Zoom sessions.

https://instats.org/seminar/analysis-of-rna-seq-data Sign up today to secure your spot, and feel free to share this opportunity with colleagues and students who might benefit!

Best wishes

Michael Zyphur Director Institute for Statistical and Data Science instats.org

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mzyphur@instats.org

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Online BasicBioinformatics

Hi EvolDir community,

Zoom course in Bioinformatics (covering basic Python and R coding), offered through my academic institution in Greece.

https://kedivim-apply.ihu.gr/en/progs/prog-380 Below are the sections that we will cover together:

- Section 1 (4 hours): Jupyter IDE & work with variables in Python. - Section 2 (4 hours): Data types and strings in Python. - Section 3 (4 hours): Logical Operators in Python. - Section 4 (4 hours): Python loops and functions. - Section 5 (4 hours): Pandas & Capstone I: DNA transcriber project; also python dictionaries and Nesting. - Section 6 (4 hours): Exception handling & Capstone II: biallelic SNP finder project - Section 7 (4 hours): API & biological databases - Section 8 (4 hours): Basic Unix commands. - Section 9 (4 hours): Basic R functionality. - Section 10 (4 hours): Visualisation with ggplot2.

Feel free to share this with anyone who might be interested.

Kind regards,

Spiros

Spiros Papakostas, Assist. Prof. Head of the lab of Molecular Ecology Dept of Science and Technology International Hellenic University mob: +30 6981099530

Spiros Papakostas <spapakostas@ihu.edu.gr>

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Online ClusteringDataWithChatGPT Mar28

Hi everyone

Instats is excited to offer a one-day seminar, Clustering High-Dimensional Data with ChatGPT, on March 28 with Professor Nikolay Oskolkov from Lund University. In the era of big data, effectively analyzing high-dimensional datasets is critical in areas such as evolutionary biology and ecology where researchers must deal with complex environmental and genetics variables that have uncertain relationships. In this workshop, you'll learn to harness both classic and advanced clustering techniques using R and Python with ChatGPT serving as your AI assistant to help write code, interpret results, and streamline your workflow. Dr. Oskolkov, an expert in bioinformatics, statistics, and machine learning, will guide you through methods to tackle the curse of dimensionality, apply dimensionality reduction (PCA, t-SNE, UMAP), and implement a range of clustering algorithms from basic (K-means, GMM, hierarchical) to advanced graph-based techniques (SNN, (H)DBSCAN, Louvain, Leiden). Designed for PhD students, academics, and professional researchers, this hands-on session will equip you with the skills to extract meaningful insights from complex, multi-dimensional data.

https://instats.org/seminar/clustering-high-dimensional-data-with-ch Sign up today to secure your spot, and feel free to share this opportunity with colleagues and students who might benefit!

Best wishes

Michael Zyphur Director Institute for Statistical and Data Science instats.org

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Online ComparativeGenomics Apr7-11

Dear all,

We are pleased to announce that a few seats remain for the upcoming Physalia online course: Comparative Genomics.

Dates: (online) 7-11 AprilCourse website: (https://www.physalia-courses.org/courses-workshops/course34/)

This five-day course provides a comprehensive introduction to comparative genomics, with a focus on structural variation. Participants will explore a range of tools and workflows, covering: Genome assembly and annotation for eukaryotic genomes Identification of single nucleotide variants (SNVs) and structural variants (SVs) Functional analysis of genomic variations in an evolutionary context The course combines lectures with hands-on practical exercises, ensuring participants develop both theoretical understanding and practical skills.

By the end of this course, participants will: Identify SNPs and SVs using de novo assembly and read mapping approaches Evaluate sequencing technologies (Illumina, PacBio, Oxford Nanopore) for variant detection Compare multiple genomes and analyze structural variations Annotate variations and interpret their functional impacts

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/course34/)

Best regards,

Carlo

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Online GenomeAnnotation May19-22

Dear all,

We are pleased to announce our upcoming online course: Introduction to Genome Annotation, scheduled for 19-22 May.

Course website: (https://www.physalia-courses.org/courses-workshops/genome-annotation/)

This course will provide an in-depth, hands-on introduction to genome annotation strategies, covering: Data quality assessment and sequencing technologies Ab initio and de novo transcriptome assembly (short and long-read data) Evidence-guided gene prediction (including BRAKER/Augustus) Building and refining gene models Visualizing and evaluating annotation quality This course is designed for PhD students, postdocs, and researchers working on genome assembly projects and looking to improve their annotation skills. Basic knowledge of the command line (Unix Shell) is essential.

By the end of this course, you will: Understand core genome annotation strategies and technologies Develop practical skills to start annotating your genome of interest Tackle genome-specific challenges and improve annotation accuracy For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/genome-annotation/)

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

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Online IntroToPython Apr7-16

Dear colleagues,

Registration is open for the Online course "Introduction to Python".

Dates and schedule: Online live sessions on April 7th, 9th, 11th, 14th, and 16th, 2025; from 13:00 to 16:30 (Madrid time zone).

Course Overview:

Python is a user-friendly and powerful programming language commonly used in scientific computing, from simple scripting to large projects. This workshop will provide hands-on practice in a biological context for beginners with very limited prior programming experience. This course is designed to be very applied, and we will explore Python tools that can immediately help the working scientist.

After completing this course, participants will be able to apply Python programming automation to their own research problems and should be equipped to continue their own Python learning. While this course will focus on data analysis using Python, participants will gain language-agnostic principles of programming, like automation with loops and encapsulation with functions, that will serve as best practices for their scientific computing.

Check all the information and registrations: https://www.transmittingscience.com/courses/statistics-and-bioinformatics/introduction-to-python-for-biology/ or writing to courses@transmittingscience.com

Full list of upcoming Transmitting Science courses: https://www.transmittingscience.com/courses/ With best regards

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com Twitter @SoleDeEsteban Orcid: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or http://transmittingscience.com/additional-terms. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es . Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction.

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Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

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Online MachineLearningForSequenceData May6-9

Dear all,

We are pleased to announce the Physalia online course: Machine Learning Methods for Longitudinal Data with Python.

Dates: 6th-9th May Course website: (https://www.physalia-courses.org/courses-workshops/longitudinal-data/)

This course focuses on machine learning techniques for analyzing longitudinal (sequence) data data collected repeatedly over time or space with an emphasis on handling time and cause-effect relationships. You will learn how to manage the unique challenges posed by these data, from visualization and modeling to interpreting results.

By the end of the course, you will: Understand how to manage time and cause dependencies in data Recognize and address biases such as confounding, colliding, and mediator bias Apply machine learning techniques to sequence data Use graph models, Bayesian networks, and time-series forecasting Analyze real-life biological datasets, including epidemiology and gene expression data This course is designed for students, researchers, and professionals working with biological data particularly those analyzing time-based or causation-driven datasets. A basic understanding of Python and Linux is helpful but not required.

Course Schedule (Berlin time): Day 1 (2-8 PM): Introduction to sequence data, statistical models, handling biases Day 2 (2-8 PM): Graph models, Bayesian networks, machine learning for time-series prediction Day 3 (2-8 PM): Longitudinal data in epidemiology, deep learning, Transformer models Day 4 (2-8 PM): Model diagnostics, multi-omics case study, final quiz and discussion For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/longitudinal-data/)

For any questions or further information, feel free to get in touch. Best regards, Carlo

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Online MappingTraitEvolution May26-Jun4

Dear colleagues,

Transmitting Science has opened registration for a new edition of the course MAPPING TRAIT EVOLUTION (8th edition!).

This course will be held live online (synchronous) with a maximum of 16 participants to promote interaction with the instructor. Acceptance is on a first-come, first-served basis.

Dates and schedule: Online live sessions on the Online live sessions on May 26th, 28th, and 30th & June 2nd and 4th, 2025, from 14:00 to 18:00 (Madrid time zone).

Instructor: Jeroen B. Smaers [1] (Stony Brook University, USA).

Course webpage: https://www.transmittingscience.com/courses/evolution/mapping-trait-evolution/ COURSE OVERVIEW The course provides a comprehensive overview of the state-of-the-art methods in mapping phenotypic trait evolution. It will provide participants with a springboard to using these methods to answer their own research questions. We focus on analyses that use a phylogenetic tree and observed trait information from tip taxa (extant and/or extinct) to describe how traits have changed along the branches of a phylogeny. The course covers methods that estimate and test patterns related to changes in mean, covariation, and rate. Applications for continuous and categorical, and univariate and multivariate research designs are discussed. At the end of this course, participants will have developed an understanding of: (1) Brownian motion and Ornstein-Uhlenbeck models of evolution. (2) How these models can be applied to estimate and test patterns of trait evolution. (3) What the advantages and disadvantages are of different models/methods. (4) How to recognize which model/method is most appropriate given a particular dataset and research question. We provide several data sets that will be used to exemplify the application of these methods. We do, however, encourage participants to work with their own data so as to get direct experience with analysing precisely what they expect to analyse. Methods from the following R packages will be discussed: ape, geiger, phytools, evomap, l1ou, bayou, surface, OUwie, mvMORPH, geomorph (this list may change as new packages become available).

Important note: Please bear in mind that this course is not about reconstructing (building) phylogenetic trees, the methods we cover in this course assume that a phylogeny is known.

If you have any doubts or questions do not hesitate to write to courses@transmittingscience.com

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com Twitter @SoleDeEsteban Orcid: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or http://transmittingscience.com/additional-terms. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es . Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

Links:

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Online MassSpecProteomicsWithR Mar17-19

Dear all,

We have two open spots left for next week's online course "R/Bioconductor for Mass Spectrometry and Proteomics" (March 17-19). If you're interested in joining on short notice, this is your chance! This hands-on course will guide you through analyzing MS-based proteomics data using R and Bioconductor, from raw data processing to statistical interpretation. It's designed for both proteomics practitioners and bioinformaticians looking to enhance their skills.

Dates: March 17-19Schedule: 2 PM - 8 PM (Berlin time) Course website:(https://www.physalia-courses.org/courses-workshops/course58/)

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/)

For more details or to secure your spot, feel free to reach out.

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

"info@physalia-courses.org" <info@physalia-courses.org>

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Online MultivariateAnalysisCommunities Mar31-Apr4

ONLINE COURSE - Multivariate Analysis Of Ecological Communities Using R With The VEGAN package (VGNR07)

Only 2 places left!

https://www.prstats.org/course/multivariate-analysis-of-ecological-communities-using-r-with-the-vegan-package-vgnr07/ 31st - March - 4th April 2025

Please feel free to share!

We encourage attendees to bring their own data, you will receive opportunities to discuss your data with the instructor throughout the course, if you would like guideline on how to organize your data prior to the course please askoliverhoooker@prstatistica.com

This course is suitable for researchers (PhD and MSc students, post-docs, primary investigators) and environmental professionals who are interested in implementing best practices and state-of-the-art methods for modelling species' distributions or ecological niches, with applications to biogeography, spatial ecology, biodiversity conservation and related disciplines.

This 5-day course will cover R concepts, methods, and tools that can be used to analyze community ecology data. The course will review data processing techniques relevant to multivariate data sets. We will cover diversity indices, distance measures and distance-based multivariate methods, clustering, classification and ordination techniques using the R package VEGAN. We will use real-world empirical data sets to motivate analyses, such as describing patterns along gradients of environmental or anthropogenic disturbances, and quantifying the effects of continuous and discrete predictors. We will emphasise visualisation and reproducible workflows as well as good programming practices. The modules will consist of introductory lectures, guided computer coding, and participant exercises. The course is intended for intermediate users of R who are interested in community ecology, particularly in the areas of terrestrial and wetland ecology, microbial ecology, and natural resource management. You are strongly encouraged to use your own data sets (they should be clean and already structured, see the document: "recommendation if you participate with your data".

Classes will run from 08:00 - 13:00 for the morning lecture and 14:00 - 16:00 for the practical (UK time) with an evening time session tbc for US, Canada etc. attendees. The course will be recorded and made available each day and will remain available for 28 days after the course for you to revisit any lectures.

DAY 1 - Module 1: Introduction to community data analysis, basics of programming in R - Module 2: Diversity analysis, species-abundance distributions

DAY 2 - Module 3: Distance and transformation measures - Module 4: Clustering and classification analysis

DAY 3 - Module 5: Unconstrained ordinations: Principal Component Analysis - Module 6: Other unconstrained ordinations

DAY 4 - Module 7: Constrained ordinations: RDA and other canonical analysis - Module 8: Statistical tests for multivariate data and variation partitioning

DAY 5 - Module 9: Overview of Spatial analysis, and recent Hierarchical Modeling of Species Communities (HMSC) methods - Modules 10: Special topics and discussion, analyzing participants' data.

Email oliverghooker@prstatistics.com with any questions.

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca)

Online MultivariateEcolAnalysis Mar31-Apr4

ONLINE COURSE - Multivariate Analysis Of Ecological Communities Using R With The VEGAN package (VGNR07)

https://www.prstats.org/course/multivariate-analysis-of-ecological-communities-using-r-with-the-vegan-package-vgnr07/ 31st - March - 4th April 2025

Please feel free to share!

We encourage attendees to bring their own data, you will receive opportunities to discuss your data with the instructor throughout the course, if you would like guideline on how to organize your data prior to the course please ask oliverhoooker@prstatistica.com

This course is suitable for researchers (PhD and MSc students, post-docs, primary investigators) and environmental professionals who are interested in implementing best practices and state-of-the-art methods for modelling species' distributions or ecological niches, with applications to biogeography, spatial ecology, biodiversity conservation and related disciplines.

This 5-day course will cover R concepts, methods, and tools that can be used to analyze community ecology data. The course will review data processing techniques relevant to multivariate data sets. We will cover diversity indices, distance measures and distance-based multivariate methods, clustering, classification and ordination techniques using the R package VEGAN. We will use real-world empirical data sets to motivate analyses, such as describing patterns along gradients of environmental or anthropogenic disturbances, and quantifying the effects of continuous and discrete predictors. We will emphasise visualisation and reproducible workflows as well as good programming practices. The modules will consist of introductory lectures, guided computer coding, and participant exercises. The course is intended for intermediate users of R who are interested in community ecology, particularly in the areas of terrestrial and wetland ecology, microbial ecology, and natural resource management. You are strongly encouraged to use your own data sets (they should be clean and already structured, see the document: "recommendation if you participate with your data".

Classes will run from 08:00 - 13:00 for the morning lecture and 14:00 - 16:00 for the practical (UK time) with an evening time session tbc for US, Canada etc. attendees. The course will be recorded and made available each day and will remain available for 28 days after the course for you to revisit any lectures.

DAY 1 - Module 1: Introduction to community data analysis, basics of programming in R - Module 2: Diversity analysis, species-abundance distributions

DAY 2 - Module 3: Distance and transformation measures - Module 4: Clustering and classification analysis

DAY 3 - Module 5: Unconstrained ordinations: Principal Component Analysis - Module 6: Other unconstrained ordinations

DAY 4 - Module 7: Constrained ordinations: RDA and other canonical analysis - Module 8: Statistical tests for multivariate data and variation partitioning

DAY 5 - Module 9: Overview of Spatial analysis, and recent Hierarchical Modeling of Species Communities (HMSC) methods - Modules 10: Special topics and discussion, analyzing participants' data.

Please email oliverhooker@prstatistics.com with any questions

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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Online MultivariateTraitEvolutionR May12-21

Dear colleagues,

Registration is now open for the Transmitting Science course: "Modelling and Analysing Multivariate Traits Evolution using R" (4th edition).

Max capacity: 16 participants Format: Live online sessions Dates: May 12th, 14th, 16th, 19th, and 21st Schedule: 10:00-12:30 & 13:00-15:00 (Madrid time)

Instructor: Dr. Julien Clavel (CNRS, France), co-author of the R package mvMORPH (alongside Aaron King & Emmanuel Paradis).

This course is ideal for researchers working with phylogenetic comparative methods and multivariate data.

Learn more and register here: https://www.transmittingscience.com/courses/evolution/modelling-and-analysing-multivariate-traits-evolution-using-mvmorph/ Course overview:

In this workshop students will be introduced to multivariate phylogenetic comparative methods with the mvMORPH R package.

The mvMORPH package contains tools for modelling the evolution of correlated continuous traits (e.g. morphometric measurement, geometric morphometric datasets, life history traits, gene expression data, etc.) on phylogenetic trees [with either fossil species, extant species or both] as well as statistical tools such as multivariate generalized least squares (GLS) linear models -e.g. multivariate regression, MANOVA, MANCOVA - for studying comparative datasets.

In this course, students will be first introduced to some theory with illustrative examples (both from simulated data as well as students' own datasets) and will learn how to interpret the models, their parameters, as well as how to assess their reliability.

If you have any questions do not hesitate to contact us at courses@transmittingscience.com

Best regards,

Haris

Check the full list of upcoming courses here: https://www.transmittingscience.com/courses/ Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com [1]

Links:

[1] http://www.transmittingscience.com [2] http://www..es Haris Saslis - Transmitting Science <haris.saslis@transmittingscience.com>

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Online MultivariateTraitsEvolution May12-21

Dear colleagues,

Registration is open for Transmitting Science course "Modelling and Analysing Multivariate Traits Evolution using R"- 4th edition.

This course only accepts 16 participants, acceptance on "first come, first served" basis.

Dates and schedule: Online live sessions on May 12th, 14th, 16th, 19th, and 21st, 2025; from 14:00 to 10:00 to 12:30 and from 13:00 to 15:00 (Madrid time zone).

Instructor: Dr. Julien Clavel [1] (NNRS, France), author of the package mvMORPH [2] (together with Aaron King and Emmanuel Paradis).

This course is addressed to any researcher studying phylogenetic comparative methods using multivariate data.

For all the information, please check the course webpage: https://www.transmittingscience.com/courses/evolution/modelling-and-analysing-multivariate-traits-evolution-using-mvmorph/ Course overview:

In this workshop students will be introduced to multivariate phylogenetic comparative methods with the mvMORPH R package.

The mvMORPH package contains tools for modelling the evolution of correlated continuous traits (e.g. morphometric measurement, geometric morphometric datasets, life history traits, gene expression data, etc.) on phylogenetic trees [with either fossil species, extant species or both] as well as statistical tools such as multivariate generalized least squares (GLS) linear models -e.g. multivariate regression, MANOVA, MANCOVA - for studying comparative datasets.

In this course, students will be first introduced to some theory with illustrative examples (both from simulated data as well as students' own datasets) and will learn how to interpret the models, their parameters, as well as how to assess their reliability.

If you have any questions, do not hesitate to contact the course coordinator at courses@transmittingscience.com

With best regards

Sole

– Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com [3]

Check the full list of Transmitting Science upcoming courses here: https://www.transmittingscience.com/courses/ X @SoleDeEsteban Orcid: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or http://transmittingscience.com/additional-terms. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es . Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

Links:

[1] https://www.transmittingscience.com/instructors/julien-clavel [2] https://cran.r-project.org/web/packages/mvMORPH/index.html [3] http://www.transmittingscience.com Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

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Online NetworkAnalysis Mar9-12

Hi everyone

Instats is pleased to announce a four-day seminar on "Methods of Hypergraph/Hypernetwork Analysis," taking place March 9'12 and led by Professor Moses Boudourides from Northwestern University. This seminar is especially relevant for evolutionary and population biologists as hypergraph techniques offer innovative approaches to deciphering the complex, multi-dimensional interactions inherent in ecological and evolutionary systems. Unlike conventional network models, hypergraphs enable the simultaneous analysis of multiple, interconnected interactions'an approach that can illuminate patterns in genetic, ecological, and social networks. Over the course of this seminar, participants will engage in both foundational and advanced topics, with practical, hands-on experience using Python tools to model and interpret higher-order interactions.

https://instats.org/seminar/hypernetworks-in-theory-and-practice Sign up today to secure your spot, and please feel free to tell your colleagues and students about this unique opportunity!

Best wishes

Michael Zyphur Director Institute for Statistical and Data Science instats.org

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mzyphur@instats.org

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Online NGS DataForPopGeneticsAnalyses May5-14

Dear colleagues,

I am happy to announce the 6th edition of the Transmitting Science course "Manipulation of NGS Data for Genomic and Population Genetics Analyses", this course will be run online.

Schedule: Online live sessions on May 5th, 7th, 9th, 12th and 14th, 2025; 13:00 to 17:00 (Madrid time zone).

This course offers a comprehensive introduction to Next-Generation Sequencing (NGS) data analysis, guiding participants through second and third-sequencing technologies, command-line operations, and data management. Key topics include quality assessment, variant detection, and large-scale genomic analyses.

Participants will gain hands-on experience with computational pipelines and explore analytical approaches to address diverse biological research questions.

Course webpage: https://www.transmittingscience.com/courses/genetics-and-genomics/manipulation-ngs-data-genomic-population-genetics-analyses/ Course programme:

* Introduction to NGS sequencing platforms. * Introduction to basic command lines. * Basic raw data manipulations (counting sequences, listing files). * Raw data QC & Cleaning. * Mapping: principle, tools, execution, cleaning, data control, * SNP calling: raw calling, cleaning calling, filtering. * VCF manipulations: filtering on MAF, heterozygosity * Impact of SNPs on genes. * Population genomics using sNMF. * Assembling genomes with long reads * Comparing assembled genomes and SV detection * Testing tools and different conditions to answer different biological questions. * Discussion about bioinformatic strategies related with sientific projects of participants.

Do not hesitate to contact us at courses@transmittingscience.com if you have any doubt or question.

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses X @SoleDeEsteban Orcid: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or http://transmittingscience.com/additional-terms. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es . Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

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Online PopulationGenomics May26-30

Dear all,

We're excited to announce the Physalia upcoming online course: Introduction to Population Genomics, running from 26-30 May.

For details and registration, visit: (https://www.physalia-courses.org/courses-workshops/population-genomics/)

This five-day, hands-on program offers a comprehensive introduction to key population genomics concepts and techniques from basic bioinformatics to population structure, introgression, demographic modeling, genome scans, and landscape genomics. Each day includes a mix of lectures (˜2 hours) and practical exercises (˜3 hours), helping participants build both foundational knowledge and practical skills.

This course is ideal for graduate students, postdocs, and researchers with a basic understanding of genetics/genomics and evolutionary biology, along with prior experience in a programming language (UNIX command line and R required).

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/population-genomics/) Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

“info@physalia-courses.org” <info@physalia-courses.org>

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Online PreservingBiolSpecimens May5-8

Hi everyone

Instats is excited to offer a 4-day seminar, Fluid Preservation for Research and Collection Management, running May 5-8 and led by renowned conservator Simon Moore from the National History Conservation Group (formerly with the British Museum). This advanced workshop is designed for PhD students, researchers, and collection managers in natural history (botany and zoology) and evolution who want to deepen their expertise in preserving biological specimens. Through a balanced mix of lectures and hands-on activities, you’ll explore the science and art of fluid preservation from understanding the histological impacts and selecting the right preservation fluids to mastering practical techniques like glass cutting, drilling, and sealant application. Simon Moore will guide you through troubleshooting common preservation challenges, managing contaminants, and ensuring the long-term integrity of your collections. Equip yourself with the skills to prepare specimens for research and display, and take your conservation practice to the next level.

https://instats.org/seminar/fluid-preservation-for-research-and-coll Sign up today to secure your spot, and feel free to share this opportunity with colleagues and students who might benefit!

Best wishes

Michael Zyphur Director Institute for Statistical and Data Science instats.org

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mzyphur@instats.org

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Online ProteomicsInR Mar17-19

Dear all,

the Physalia course on R/Bioconductor for Mass Spectrometry and Proteomics, will take place online from March 17-19, 2025.

Course website: (https://www.physalia-courses.org/courses-workshops/course58/) This hands-on course will guide you through the analysis of mass spectrometry (MS) data using R and Bioconductor. Learn how to handle raw MS data, identify and quantify proteins, and perform statistical analysis for proteomics research. At the end of the course, youï¿½ll have practical skills to: Manipulate MS and proteomics data in R.

Leverage Bioconductor packages for exploratory and statistical analysis

Interpret results from typical shotgun MS experiments. Prerequisites: A basic working knowledge of R (data frames, vectors, syntax) is required. Familiarity with MS or Bioconductor is helpful but not essential, as we provide a comprehensive introduction. For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-course58/)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846

(https://www.linkedin.com/in/physalia-courses-a64418127/)

“info@physalia-courses.org” <info@physalia-courses.org>

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Online ScientificIllustration Apr14-17

Dear all,

We are excited to announce our upcoming online course, Art (Science) Attack, running 14-17 April.

This course bridges the gap between art and science, empowering researchers to create engaging visuals that effectively communicate their work. Using open-source software such as Krita and Inkscape, participants will learn how to design figures, project mascots, and compelling graphics for presentations, papers, and public engagement.

Course website: (https://www.physalia-courses.org/-courses-workshops/art-science-attack/)

Who should attend? Researchers, students, or anyone interested in improving how they visually communicate scientific ideas no prior artistic experience required.

What you will learn:

- Strategies to simplify complex scientific concepts into clear, attractive designs Creating logos, project mascots, and journal cover art Developing scientific schematics, one-panel figures, and outreach materials Practical training with Krita (rasters) and Inkscape (vectors)

Bring your ideas to life: Participants are encouraged to submit a “portfolio” this can be anything from a rough sketch to figures or visual concepts related to their projects.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-art-science-attack/)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

“info@physalia-courses.org” <info@physalia-courses.org>

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Online SpatialOmicsInR May19-21

Dear all,

there are still a few seats available for the online Physalia course on Spatial Omics in R/Bioconductor.

Dates: 19-21 May Course website: (https://-www.physalia-courses.org/courses-workshops/spatial-omics-1/)

This course provides a comprehensive introduction to spatial omics, covering both imaging and sequencing methodologies. Participants will gain practical skills in data analysis, experimental design, and applying tidy data principles in R/Bioconductor.

By the end of this course, attendees will be able to: - Understand spatial omics technologies and differentiate between imaging- and sequencing-based approaches.- Design and implement spatial omics experiments, considering key analytical and technical challenges. - Analyze sequencing-based spatial data using Bioconductor and Seurat in R.- Analyze imaging-based spatial data with MoleculeExperiment and Seurat.- Apply tidy data principles for spatial omics analysis using tidySpatialExperiment and tidySeurat.- Perform advanced spatial analyses, including spatial differential expression, cell-neighbor analysis, deconvolution, and multi-modality integration.- Interpret and extract biological insights from spatial omics datasets.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-spatial-omics-1/)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846

(https://www.linkedin.com/in/physalia-courses-a64418127/)

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Online WritingAboutResearch Apr1-Jun22

COURSE DESCRIPTION: Effective science communication has long held the power to reshape our world by driving changes in policy and public opinion. As society struggles with pandemic effects, anthropogenic climate change, and dwindling biodiversity, there is an acute need for scientist-communicators who can effectively convey the spectacular power of research to address these obstacles. In this course, early-career researchers will learn skills for high-impact, immediate engagement with readers, including decision-makers, colleagues, and members of the lay public. Unlike traditional writing courses, this course is focused on capturing audience attention in concrete ways that compel action, using common professional formats such as op-eds, memoranda, press releases, one-pagers, and blog entries. The workshop-driven program also includes instruction on publishing mechanics, covering topics such as pitching your work to editors, establishing an online presence, and achieving proficiency with graphic design fundamentals.

DATES: - Course opens April 1st and closes June 22nd - Live instruction: Thursdays, April 3rd - May 8th

PRICE: Begins at $500 students / $600 professionals

LEARN MORE & REGISTER HERE:

https://www.centerforwildlifestudies.org/courses/p/writing-research-impact Center for Wildlife Studies is a 501(c)(3) nonprofit organization whose global mission is to provide accessible environmental education and promote wildlife conservation through science.

[image: Logo] < https://www.centerforwildlifestudies.org/ > *Emily J. Uhrig*, PhD Director of Education Center for Wildlife Studies < https://www.centerforwildlifestudies.org/ >

*Center for Wildlife Studies is a 501(c)(3) nonprofit organization whose **global mission is to provide accessible environmental education and promote wildlife conservation **through science.*

CWS Admin <info@centerforwildlifestudies.org>

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StAndrew SpeciationGenomics-ML Jun24-27

*** Call for Participationand Abstracts***

We a happy to announce the workshop "Short and long timescales in speciation genomics: Machine Learning approaches" (ML Speciation Genomics) to be held on 24th-27th June 2025 at University of St Andrews/ Scotland.

ABOUT THE WORKSHOP

How new species emerge is one of the big questions in evolutionary biology. Speciation genomics investigates the genetic basis of this process. Until recently researchers were only able to sequence a few individuals at a single time-point. Yet, with the growing affordability of genome sequencing, it is now possible to consider multiple individuals at multiple points in time.

These multiple time-points could include samples from Natural History Museums, they could be multiple generations of a population housed in controlled laboratory environments or diverse samples collected from the wild. This workshop will bring researchers together to make the best use of the new data. We will have introductory lectures, contributed talks as well as hands-on sessions on museum genomics, phylogenomics and machine learning methods.

We have conference rates for students of ï¿½30 and ï¿½70 for all academics and industry participants. Reduced rate conference accommodation can be booked at Agnes Blackadder Hall.

*** Faculty ***

Nick Bailey, Rui Borges (University of St Andrews); Svitlana Braichenko (University of Edinburgh); Martin Kapun (Natural History Museum of Vienna); Carolin Kosiol (St Andrews); Manolo Perez (Imperial College London); Antonio Pacheco, Mike Ritchie (St Andrews); Alexander Suh (Research Museum Koenig Bonn) among others.

*** Important dates ***

Registration opens: 17thMarch 2025 Abstract submission: 11thApril 2025 (please send an email to: MLSpeciationGenomics@gmail.com)

Reduced rate accommodation: 24thApril 2025 Registration closes: 2ndJune 2025 Conference: 24th- 27thJune 2025

For registration and more information see

https://www.eventsforce.net/standrews/264/home https://ckosiol.github.io/MLSpeciationGenomics/ Looking forward seeing you in St Andrews!

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(to subscribe/unsubscribe the EvolDir send mail to golding@mcmaster.ca<mailto:golding@mcmaster.ca>)

Venice EvoSysBioMultiLevel Aug17-22

Dear all,

Registration deadline is TOMORROW (Mar 31) for the:

*** Venice Summer School 2025: Emergence & Evolution of Multi-Level Regulatory Systems

This is a FEBS/EMBO Lecture Course that will take place on *** Aug 17 - Aug 22, 2025, at Centro Culturale Don Orione Artigianelli, Venice, IT

Organizers: James DiFrisco, The Francis Crick Institute, UK Nicole Repina, Friedrich Miescher Institute, Basel, CH Johannes Jaeger, University of Vienna, AT

Teaching Panel:

Daniel S. Brooks, Fresh Pond Institute, USA Thibaut Brunet, Institut Pasteur, Paris, FR

James DiFrisco, The Francis Crick Institute, UK Zena Hadjivasiliou, The Francis Crick Institute, UK Johannes Jaeger, University of Vienna, AT Ronald Jenner, Natural History Museum, London, UK Nicole King, University of California, Berkeley, USA Wallace Marshall, University of California, San Francisco, USA MIhaela Pavlicev, University of Vienna, AT Rashmi Priya, The Francis Crick Institute, UK Nicole Repina, Friedrich Miescher Institute, CH Merlijn Staps, Princeton University, USA Ben Steventon, University of Cambridge, UK Gï¿½nter Wagner, Yale University, USA

*** REGISTRATION is open on EMBO's course website: https://meetings.embo.org/event/25-multi-level-reg-sys Applicants are required to submit an academic CV, and a motivation letter. You are also encouraged to submit an abstract if you would like to present your own work as an elevator pitch on the first day of the course.

*** Application/abstract submission deadline: Mar 31, 2025. Applicants will be notified whether they have been accepted (or not) by Apr 30, 2025. The payment deadline for successful applicants is May 31, 2025.

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Course Description:

Biological systems comprise multiple levels of organization, from molecules, organelles, and cells, to the multi-cellular structures that form whole tissues, organisms, and ultimately societies and ecosystems. During organismal development, these levels emerge from the dynamic interactions of system components and give rise to complex structures and functions across scales. Similarly, over the course of evolution, the emergence of phenotypes involves more than the transmission of genetic material, as selection works at all levels to generate novel phenotypes. However, we are only at the beginning of understanding how such levels of organization can emerge de novo in evolution or how levels self-organize and feed back on one another during growth and development. This is no simple task, as studying these fundamental questions in evolution and development requires quantification and modeling approaches that cross biological scales, alongside conceptual frameworks for understanding dynamical systems and emergent phenomena.

To tackle the issue, we need novel, empirically grounded, systems-biology theories that integrate philosophical, mathematical, and experimental approaches across biological scales. During our lecture course, we will look at the emergence and evolution of multi-level regulatory systems from an interdisciplinary theoretical vantage point to assess the requirements, mechanisms, and consequences of multi-level phenomena.

Specifically, we will focus on the following four questions: 1. How do new levels of organization (molecular, organelle, cellular, tissue, organismal, and beyond) originate and integrate in development and evolution? 2. What is the nature of causal-mechanistic interactions between levels of organization? 3. How do we measure and manipulate biological systems across multiple scales? 4.

How can we model feedback interactions across different levels of organization in regulatory systems?

Over recent years, it has become increasingly evident that dynamical processes, mechanical and physical forces, signaling feedback, and metabolic constraints play critical roles in patterning and coordinating emergent phenotypes. In addition, systems biology and metabolomics approaches, along with single-cell quantification of live or fixed samples, have revolutionized how we can empirically study emergent phenomena. Computational modeling and dynamical systems approaches have shed light on how network components and interactions can lead to spatial and temporal patterning, division of labor, and increased complexity and integration above the level of cells. A synthesis of these interdisciplinary approaches can now allow us to refine and develop new conceptual frameworks for understanding the mechanisms, and consequences, of multi-level processes in evolution and development.

Follow @VeniceEvoDevo on BlueSky or Twitter for updates.

On behalf of the organizers, Yogi Jaeger

Dr. Johannes Jaeger Freelance Researcher, Philosopher & Educator Project Leader, JTF Project "Pushing the Boundaries", Dept of Philosophy, Uni Vienna

Associate Faculty, Complexity Science Hub (CSH), Vienna

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.mcmaster.ca/~brian/evoldir.html

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. …plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.