# EvolDir

May 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

## Athens Evolution2025 Jun20-24

Dear All,

April 15th is the last day for early-bird registration rates for Evolution 2025! It is also the last day to submit talks to the in-person portion of the meeting. Please visit https://www.evolutionmeetings.org/ for more information.

Sincerely,

Evolution Organizers

This email contains links to content or websites. Always be cautious when opening external links or attachments.

Please visit https://carleton.ca/its/help-centre/report-phishing/ for information on reporting phishing messages.

When in doubt, the ITS Service Desk can provide assistance. https://carleton.ca/its/chat Alex Wong <AlexWong@cunet.carleton.ca>

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## Cardiff Online EcoGenetics Sep17-19

#EGG2025: On scales of time 17-19 September National Museum Cardiff

https://www.britishecologicalsociety.org/content/-egg2025-on-scales-of-time/ Abstract submission opens until 31 May here: https://forms.office.com/e/-G16q4ZNavq Registration opens until 31 July here: https://egg2025.eventbrite.com The Ecological Genetics Group (EGG) is pleased to invite anyone from any career stage to join us in person at Cardiff or online from 17 to 19 September 2025 for an exciting program of talks and posters.

Time is a key consideration in ecological genetics-the organisms and the processes we study work across different scales of time. A devastating loss of genetic diversity can occur within a handful of generations, while the process of speciation takes us back into deep evolutionary time.

Over the course of the three-day meeting, you can also expect to hear talks that cover every scale of time, including from every stage of a researcher's career. We welcome posters or talks from those just starting out in research, including undergraduate students, as well as those who are established researchers and look forward to the exciting talks from our keynote speakers.

While time is the highlight of EGG2025, we set no limits in the presentation topics and are interested in every ecologist's work that harnesses genetics.

EGG2025 will be a hybrid event. Talks will be livestreamed and recorded for online delegates, so that time zone or distance do not need to be a barrier. We have an eventful lineup of socials regardless you are joining in-person or remotely.

EGG2025 celebrates our 69th anniversary-we look forward to meeting you at this special time as we are stepping into our seventh decade.

Dr Michelle Davis

Lecturer in Ecology, Edge Hill University Conference Officer, Ecological Genetics Group, British Ecological Society

Edge Hill University < http://ehu.ac.uk/home/emailfooter > Modern University of the Year, The Times and Sunday Times Good University Guide 2022 < http://ehu.ac.uk/tef/emailfooter > University of the Year, Educate North 2021/21

Michelle Davis <Davism@edgehill.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/1FAIpQLSeG6P8U2DV5BBCL xzmMI76FQoB9E6IK kSTIQlTQZR4kKx6NJg/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 DhÃ¹n Ãideann, clàraichte an Alba, àireamh clàraidh SC005336.

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

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## ESEB2025 Barcelona HostAssociatedMicrobiomes Aug17-22

ESEB 20205 Symposium: 'The contribution of the microbiome to host adaptation and plasticity' (S07)

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).

We are also excited to announce a WAME support scheme for ECRs wishing to attend ESEB 2025 and participate in the symposium. See here for more details: https://www.wamestn.com/eseb-2025 S07 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).

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 20205 (link below)

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

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## ESEB Barcelona BioticInteractions Aug17-22

Call for talks and posters for ESEB symposium "Evolution of Biotic Interactions across Scales" (Symposium #S18) at ESEB 2025, in Barcelona Spain.

The ESEB 2025 Congress will be held at the International Convention Centre of Barcelona (CCIB) in Barcelona, Spain, from August 17 to 22,2025. We consider this symposium to be the home of all things biotic interactions, e.g. from host-parasite co-evolution to predator-prey interactions, from genomic conflicts to mutualisms. Specifically, we encourage contributions that study the evolutionary ecology of biotic interactions, as described below. Biotic interactions are a core component of evolutionary ecology. Understanding their evolution is key to predicting how global change will impact on ecosystems. Their nature is mediated by the costs and benefits experienced by the interacting partners. Increasingly, it is becoming clear that biotic interactions do not fall into fixed categories, but rather form a continuum from antagonism to mutualism. Moreover, the nature of any given interaction can depend on the ecological conditions currently experienced, with otherwise virulent pathogens potentially conveying stress resistance, or former mutualists starting to cheat. While the concept of a dynamic mutualism-antagonism continuum has been embraced in some fields, in others these categories remain rigid. This hinders our understanding of the evolution and the potential for plasticity of biotic interactions in rapidly changing ecosystems. Here, we want to bring together researchers across different fields and scales, i.e. from host-pathogen interactions to classical mutualisms, and from sub-cellular interactions such as transposable elements to the interactions of multi-cellular organisms such as plants and pollinators. The ultimate aim of the symposium is to work towards a common theoretical and experimental framework for studying the dynamic evolutionary ecology of biotic interactions under conditions of rapid global change. Invited speakers:

Prof. Stineke van Houte, University of Exeter, UK Prof. Jordi Bascompte, University of Zurich, Switzerland

Organizers: Prof. Lena Wilfert, University of Ulm - lena.wilfert@uni-ulm.de Dr. Peter Czuppon, University of Münster

Prof. Dr. Lena Wilfert University of Ulm Institute of Evolutionary Ecology and Conservation Genomics Albert-Einstein Allee 11 D-89069 Ulm Germany Tel.: 0049-731-5030615 Fax: 0049-731-5022683

email: lena.wilfert@uni-ulm.de Website: https://www.uni-ulm.de/nawi/evolutionary-ecology-and-conservation-genomics/prof-dr-lena-wilfert Lena Wilfert Ulm <lena.wilfert@uni-ulm.de>

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## ESEB Barcelona EvoEcoMicrobialSymbiosis Aug17-22

Call for talks and posters for ESEB symposium “Evolutionary Ecology of Microbial Symbiosis” (Symposium #S22) at ESEB 2025, in Barcelona Spain.

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

Evolutionary Ecology of Microbial Symbiosis Microbial symbiosis plays a pivotal role in shaping the ecological and evolutionary trajectories of both host and microbial species. Symbiotic microbes can confer novel metabolic capabilities, enhance nutrient acquisition, and alter host phenotypes, facilitating resilience and adaptive potential in the face of environmental pressures. In return, hosts can drive the reciprocal adaptation and diversification of microbes within these relationships, by actively selecting and shaping their microbial partners. This symposium aims to bring together researchers questioning the importance of microbial symbiosis in promoting or challenging key evolutionary processes, such as adaptation, speciation, and ecological specialization in both hosts and microbes. By showcasing cutting-edge studies across diverse systems, we will re-examine the proposed roles of host-microbe interactions as drivers of rapid evolutionary change and/or as stabilizing forces in ecological interactions. We invite contributions that explore the theoretical, molecular, ecological, and evolutionary mechanisms underpinning microbial symbiosis, to renew the dialogue around its implications for the development and diversification of life on Earth. We have two exciting invited speakers:

* Dr Marjolein BRUIJNING with a talk on ’The bacterial march to endosymbiosis: on-ramps and off-ramps’, the University of Amsterdam (https://www.uva.nl/en/profile/b/r/m.bruijning/m.bruijning.html); and * Dr Lee HENRY with a talk on ’Bacterial symbionts: a horizontal gene pool for eukaryotes?’, Queen Mary University of London (https://www.qmul.ac.uk/sbbs/staff/leehenry.html)

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. Anne DUPLOUY, University of Helsinki, Finland (anne.duplouy’at’helsinki.fi) Prof. Wolfgang MILLER, Medical University of Vienna, Austria (wolfgang.miller’at’meduniwien.ac.at)

Dr. Anne DUPLOUY Fellow of the Research Council of Finland Insect Symbiosis Ecology and Evolution (ISEE), PI Organismal & Evolutionary Biology Research Programme Faculty of Biological & Environmental Sciences Viikinkaari 1 Fi-00014 University of Helsinki, Finland

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## ESEB Barcelona GeneticControl Aug17-22

Dear colleagues,

We are pleased to invite you to contribute to our symposium at the upcoming ESEB meeting in Barcelona (August 17 to 22, 2025) entitled “Evolutionary biology meets genetic control” (Symposium 20). For more information, to register and submit your abstract before April 25th, please visit: https://eseb2025.com/ Invited speakers are: Alice Namias, IDEEV, CNRS, Université Paris Saclay Philipp Messer, Cornell University

Flo Débarre and Nicolas Rode

*S20: Evolutionary biology meets genetic control *

keywords: gene drive, /Wolbachia/, Sterile and Incompatible Insect Techniques, selfish genetic elements

Genetic control methods are characterized by the release of organisms that are genetically altered to disrupt the reproduction of target pest populations. For example, these methods could be used to either suppress mosquito populations or to reduce their vectorial capacity. Genetic control is deeply embedded in evolutionary theory, involving concepts like the fitness effect of mutations, genetic incompatibilities, population dynamics of selfish genetic elements, etc. The success of these strategies crucially depends on our ability to assess the fitness of released individuals and their impact on the dynamics of target populations.

This symposium aims to bring together empiricists and theoreticians working in evolutionary ecology and in genetic control in order to synthetize recent advances in the field. We expect this diversity of backgrounds to foster fruitful discussions that will lead to new research avenues regarding the future of genetic control and will improve our ability to predict the immediate efficacy and long-term sustainability of control strategies.

Nicolas O. RODE INRAE Researcher UMR CBGP 755 avenue du Campus Agropolis 34980 Montferrier-sur-Lez France tel: +33 430 630 443 web:https://bit.ly/nrode_cbgp Nicolas Rode <nicolas.rode@inrae.fr>

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## ESEB Barcelona GenomeArchitecture

Dear Colleagues,

I have the pleasure to invite you to contribute to our symposium at the upcoming ESEB meeting in Barcelona www.eseb2025.com entitled “Genome Architecture and Their Role in Evolution”

This Symposium is organised by Marcial Escudero, Petr Nguyen and myself

Our symposium addresses one of the most transformative areas in evolutionary biology: how genomic structures shape evolution, in particular species formation and adaptation. This topic is timely and relevant, considering recent advances in genomics that reveal the significance of structural changes - such as genomic rearrangements, satellite DNA dynamics, and structure of centromeres - in driving speciation, adaptation, and sexual system evolution. This symposium will stimulate discussion on the cellular mechanisms by which genome architecture changes influence evolutionary processes, therefore bridge between the fields of cell biology, genomics and speciation.

Our keynote speakers are: Dr. Kohta Yoshida whose experimental work on genomic rearrangements in nematodes offers a novel perspective on speciation and sexual system evolution, while

Dr. Melissa Toups whose research on sex chromosomes provides essential insights into the drivers of sex chromosome turnover and recombination suppression.

With kind regards

Kay

Prof. Dr. Kay Lucek Biodiversity Genomics Laboratory University of Neuchatel rue Emile-Argand 11 2000 Neuchatel Switzerland

LUCEK Kay <kay.lucek@unine.ch>

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## ESEB Barcelona MicrobialPangenomes Aug17-22

We invite abstract submission for the symposium "The evolution of microbial pangenomes" at ESEB https://eseb2025.com/call-for-abstracts/ (Abstract deadline: 25 April)

Invited talks:

Jesse Shapiro - Looking for Darwin's footprints in prokaryotic pangenomes

Anna Dewar - Why do pangenomes vary so much across bacteria?

Pangenomes describe the set of all genes in a microbial species. For most species, pangenomes contain substantially more genes than any single genome. Because such genes can be horizontally transferred within and across populations, the pangenome represents a pool of genes of different functions that can enhance the adaptability of microbes to changing environments. Bacterial species vary in the size and shape of their pangenomes, for example by showing a range of variation in the proportion of core and accessory genes. The shape of microbial pangenomes results from a combination of selection and non-adaptive processes, such as horizontal gene transfer, gene loss, and migration. Particularly, complex selection processes, such as frequency-dependent selection and epistasis between genes, are expected to play an important role in microbial pangenomes. Vice versa, the distribution of genes in bacterial pangenomes impacts the adaptability and evolutionary plasticity of bacterial populations. The recent steep increase in bacterial genome sequencing data and advances in high-throughput laboratory methods now provide the opportunity to describe and understand the different evolutionary factors that shape these pangenomes. This symposium will bring together scientists working on experimental approaches, comparative genomics analyses, and evolutionary modelling to develop an understanding of the different evolutionary processes that shape pangenomes and the eco-evolutionary implications of pangenome variability across prokaryotes.

"Kupczok, Anne" <anne.kupczok@wur.nl>

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## ESEB Barcelona SmallPopulations Aug17-22

Call for contributed talks and abstracts for symposium on "Evolution in small populations" (Symposium S16) 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, Maëva Gabrielli (CRBE, Toulouse), Bárbara Freitas (MNCN, Madrid) and José Cerca (CEES, Oslo) are happy to announce this exciting symposium on evolution in small populations and invite you to contribute with talks and posters.

Abstract: As human activities increasingly impact our planet, natural habitats are being reduced, leading to the decline in the population sizes of numerous species. Understanding the evolutionary dynamics in small populations, such as those in insular, fragmented, or isolated environments (e.g. sky-islands and lake populations), is therefore critical, not only for conservation biology but also for advancing fundamental evolutionary theory.

Currently, a synthesis integrating both genomic and phenotypic data in small populations is lacking. To fill this gap, we propose a symposium that focuses on the evolutionary processes in small populations from an integrative point of view. It will cover key areas of molecular evolution, evolutionary and population genomics, including genetic load and demographic history, as well as micro- and macro-evolution studies and evolutionary ecology with an emphasis on understanding how phenotypes and behaviours are modified in small populations' traits.

To enrich discussions and develop a cohesive understanding of the evolution in small populations, we will welcome contributions from diverse study systems, as well as multidisciplinary approaches including various sources of data (genetics, morphology, ecology, physiology). Together with the symposium participants, we will collaborate to develop and submit a manuscript on this topic to the Journal of Evolutionary Biology (JEB).

We have two exciting invited speakers, Eva Ringler (University of Bern) "Who let the frogs out? Insights from an experimental island population" and Hernán Morales (University of Copenhagen) "Genomic erosion in small populations: evolutionary dynamics and conservation implications".

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 on evolution in small populations.

Best regards,

Dr. Maëva Gabrielli, Centre de Recherche sur la Biodiversité et l'Environnement (CRBE)

Bárbara Freitas, Centre de Recherche sur la Biodiversité et l'Environnement (CRBE), Museo Nacional de Ciencias Naturales

Dr José Cerca, Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biosciences, University of Oslo

Maëva Gabrielli <maeva.gab@hotmail.fr>

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## ESEB Barcelona SociallyTransferredMaterials Aug17-22

Call for Abstracts *Closing Soon*

We are excited to invite you to our Symposium on "Cooperation, Conflict and the Evolution of Socially Transferred Materials" at ESEB 2025 (17th-22nd August, Barcelona). Please note that the submission deadline is coming up: 25th April 2025 via https://eseb2025.com/call-for-abstracts/ Our invited speakers are:

Jen Perry Department of Biology, St. Francis Xavier University, Canada

Aileen Berasategui Amsterdam Institute for Life and Environment, Section Ecology & Evolution, VU Amsterdam, Netherlands

Symposium abstract Many organisms have evolved to transfer materials to conspecifics which go beyond simple gametes or nutrients. These are defined as socially transferred materials and include components that have been metabolized by the donor and induce a direct physiological response in the receiver, bypassing sensory organs. Examples include components of milk, seminal fluids, skin secretions and regurgitate and may even extend to the transfer of symbiotic microbes, with the method of transfer itself ranging from active uptake by recipients (e.g. consumption of externally deposited spermatophores), passive transfer (e.g. in ejaculates or milk) or even forced transfer (as in various forms of hypodermic injection). Although these transfers benefit the donor, they can influence the fitness of the recipient in different ways, either positively or negatively. Hence, whilst many social transfers may originate in cooperation, they also provide significant scope for conflict when the evolutionary interests of donors and recipients diverge.

This broad and emerging field of integrative biology contains many parallels and research opportunities in dramatically different transfer systems that have to date been studied in isolation, within their own scientific fields (ranging from evolutionary ecology, via dairy production to medicine). An important early goal of the nascent STM community is thus to connect researchers focusing on different transfers to foster cross-fertilization, and to collectively identify unifying concepts and experimental priorities for understanding their role in evolution. In this symposium, we therefore aim to showcase the wide diversity of biological phenomena that can usefully be captured by the framework of socially transferred materials, and to identify the commonalities and key differences in their origins, properties and evolutionary fates.

The symposium is organized by the ESEB Special Topic Network on Socially Transferred Materials.

Organizers

Steve Ramm UMR 6553 ECOBIO, Universitï¿½ de Rennes, France

Joris Koene Amsterdam Institute for Life and Environment (A-LIFE), VU Amsterdam, Netherlands

Mariana Wolfner Department of Molecular Biology and Genetics, Cornell University, USA

Symposium details: https://eseb2025.com/list-of-symposia/#S08 For more information about (and to join!) the Special Topic Network: https://www.socialtransfer.net < https://www.socialtransfer.net/ >

Dr. Steven RAMM Chaire de Recherche Rennes Mï¿½tropole Chaire de Professeur Junior

UMR 6553 ECOBIO - Ecosystï¿½mes, Biodiversitï¿½, Evolution Universitï¿½ de Rennes Campus de Beaulieu 263 avenue Gï¿½nï¿½ral Leclerc 35042 Rennes Cedex FRANCE

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## ESEB Barcelona Symposium44 ClimateChange Aug17-22

Call for Talks and Posters for ESEB2025 Symposium 44: The Ecological and Evolutionary Implications for Climate Change on Reproduction

Annual meeting of the European Society for Evolutionary Biology (ESEB) will be held at the International Convention Centre of Barcelona (CCIB) in Barcelona, Spain, from August 17 to 22, 2025.

The ESEB funded Special Topics Network (STN) on The Evolutionary Ecology of Thermal Fertility Limits is pleased to announce a contributed symposium on The Ecological and Evolutionary Implications for Climate Change on Reproduction

We have two symposium plenary speakers.

Dr. Belinda van Heerwaarden (University of Melbourne) who will speak about: "Can evolution and plasticity buffer fertility loss under climate change?"

And

Dr. Matthew Koski (Clemson University) talking about: "Variation in gametophytic thermal performance across an elevation gradient and its influence on floral thermoregulatory evolution"

Please consider sending in an abstract for this symposium. Abstract submission deadline is 25th April 2025. For more information, to register and submit your abstract, please visit: https://eseb2025.com/ We look forward to receiving your abstracts and networking with you in Barcelona this summer.

Claudia Fricke, Amanda Bretman, Liam Dougherty, and Rhonda Snook Co-leaders, ESEB STN Thermal Fertility Limits.

Rhonda R Snook Professor Ecology Division Department of Zoology Stockholm University, Sweden

Rhonda Snook <rhonda.snook@zoologi.su.se>

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## Liverpool UK Bioinformatics Jul20-24

BOSC 2025 dates: July 21-22, as part of ISMB/ECCB 2025

Location: Liverpool, UK, and virtual

Website: https://www.open-bio.org/events/bosc-2025 Key Dates

April 17: Deadline for submitting talk/poster abstracts

May 13: Talk/poster acceptance notifications

May 15: Deadline for submitting late poster abstracts

July 20-24: ISMB/ECCB 2025

July 21-22: BOSC 2025

July 23-24: ISMB CollaborationFest

About BOSC

Since 2000, BOSC has provided a forum for sharing ideas and results in open-source bioinformatics and open science. Our annual two-day program includes keynote talks, talks chosen from submitted abstracts, posters, a panel discussion, and more!

BOSC 2025 will include a joint session with the newly renamed Bio-Ontologies and Knowledge Representation (BOKR) COSI. Learn more at https://www.open-bio.org/2025/03/17/BOSC-BOKR-2025 Our panel topic this year will be Data Sustainability. A range of experts will share their thoughts on this important and timely subject and take questions from the audience.

This year, our popular collaborative work event, CollaborationFest ( https://www.open-bio.org/events/bosc-2025/ismb-collaborationfest-2025/), will be part of ISMB. Choose it as a free "add-on" when you register for ISMB.

Submit an abstract!

Abstract submission is open until April 17 (end of the day, "anywhere on Earth"). We encourage you to submit abstracts on any topic relevant to open source bioinformatics or open science. After review, some abstracts will be selected for lightning talks, longer talks, or posters.

Abstract submission is via ISMB's EasyChair, which is linked from our submission page at https://www.open-bio.org/events/bosc-2025/submit. A short ( $<$ 250 words) text-only abstract is required for all submissions (talk or poster), plus a "long abstract" (PDF, 2 pages max) if you want to be considered for a talk.

BOSC topics include (but are not limited to):

Open Science and Reproducible Research

Open Biomedical Data

Citizen/Participatory Science

Standards and Interoperability

Data Science

Workflows

Translational Bioinformatics

Open Science

Developer Tools and Libraries

Outreach and Training

AI/ML: Open Approaches

Data Sustainability

Knowledge Representation and Ontologies (for joint session with BOKR)

Sponsors: We are thrilled to announce the first two sponsors of BOSC 2025 (with more coming soon)! Big thanks to these excellent organizations for supporting open source bioinformatics and enabling us to offer free registration to some qualified participants! Learn more at https://www.open-bio.org/events/bosc/sponsors/ Platinum sponsor: Chan Zuckerberg Initiative. The aim of CZI's Open Science program is the universal and immediate open sharing of all scientific knowledge, processes, and outputs. Learn more at https://chanzuckerberg.com/ Gold sponsor: Seqera. Developed by the creators of Nextflow, Sequera empowers researchers to develop and deploy scalable bioinformatics pipelines faster. Learn more at https://seqera.io Helpful links:

Website: https://www.open-bio.org/events/bosc/ LinkedIn: https://www.linkedin.com/groups/14344023/ Bluesky: https://bsky.app/profile/bosc.bsky.social Slack: https://join.slack.com/t/obf-bosc/shared_invite/zt-n5ur1gsj-z2C~69_4lYTFPg5tbWA8Ew We hope to see you, in person in Liverpool or virtually, at BOSC 2025!

Sincerely,

BOSC 2025 Organizing Committee - Nomi Harris, Karsten Hokamp, Jessica Maia, Hervé Ménager, Mónica Muñoz Torres, Tazro Ohta, Deepak Unni, Jason Williams.

Monica Munoz Torres <monimunozto@gmail.com>

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## Online BrainEvolution Apr22

Join us TOMORROW for the inaugural seminar in The Integrative Biology of Brain Evolution (TIBBE) seminar series. This event brings together 2 outstanding evolutionary neuroscientists who will present their work, followed by an interactive discussion with the audience. Our first topic is: Brain size, neuron number and connectivity.

April 22, 2-3pm UTC

Sign up here: https://www.crowdcast.io/c/brain-size-neurone-number-and-connectivity The Integrative Biology of Brain Evolution (TIBBE - tibbe-network.github.io) seminar series launches tomorrow April 22, 2-3pm UTC. Come join us as Kristina Kverková will present on "Counting what counts: Why neuron numbers matter but are not the whole story" and Kei Yamamoto will present on "Different encephalization strategies: telencephalization in amniotes, mesencephalization in teleost fish" and lead a lively discussion about "Brain size, neuron number and connectivity" hosted by Katja Heuer and Carmen Falcone. Sign up here: https://lnkd.in/grTEzTms . Join the TIBBE ESEB special topic network here: tibbe-network.github.io

Alexandra Allison de Sousa <alexandraallisonsousa@gmail.com>

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## Online ESEB InternalConflictsSTN Apr30

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 April 30th at 08:00 UTC. Our speakers for this seminar are:

Perran Ross (University of Melbourne): Evolutionary impacts of endosymbionts for pest and disease control

Filip Husnik (OIST): The fate of obligate endosymbionts: reduction, integration, or extinction

We expect the meeting to take approximately 1.5 hours.

Meeting details:

Link: https://zoom.us/j/94433691509?pwd=-REaAyzb8QUd75q5b5u0GIzb3m5oSqJ.1 Date: April 30th, 2025

Time: 08:00 UTC

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,

Thomas Hitchcock, Manus Patten, Arvid ï¿½gren, Martijn Schenkel, and Nina Wedell

The Internal Conflicts and Organismal Adaptation STN

ESEB-funded Special Topic Network "Internal Conflicts and Organismal Adaptation" https://-internalconflictsstn.wordpress.com/ https://eseb.org/-prizes-funding/special-topic-networks/ Internal Conflicts STN <internalconflictsstn@gmail.com>

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## Online ESEB STN DispersalAndMatingSystems Thu24

Dear all,

We are pleased to announce the second virtual seminar of the ESEB Special Topic Network on

Dispersal and Mating Systems!

Themed "Sex-biased dispersal", the seminar will take place on Thursday, 24th April, at 15:00 CETand will last approximately 1.5 hours. This includes two talks and some time for questions and discussions.

Our two speakers are:

Dr. Tom Miller, Associate Professor, Rice University Title: Sex biases in demography and dispersal: implications for population dynamics and range expansion

Dr. Xiang-Yi Li Richter, Professor, University of Konstanz Title: What causes sex-biased dispersal, and how does mating system play a role?

To join the seminar live on Thursday, 24th April, at 15:00 CET:

Link: https://unibe-ch.zoom.us/j/61015199425?pwd=-3DcHSN29ycn0bFCYGLupDYxUKvmDgZb0.1 Meeting ID: 610 1519 9425

Passcode: 903495

The seminars will be recorded and subsequently posted on our YouTube channelfor those who cannot make it live.

It is open to all;please feel free to share it with anyone who might be interested.

We hope to see many of you there!

Ella, Louise, Xiaoyan and Dhanya

ECR Organising Team

"dhanya.bharath@students.unibe.ch"
<dhanya.bharath@students.unibe.ch>

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## Online ESEB STN Speciation May13

Dear colleagues,

The next instalment of the online seminar series organised by the ESEB-funded STN network ï¿½ Integration of Speciation research ï¿½ ( [ https://speciation-network.pages.ist.ac.at/ ] ) will be held on 13 May 2025 at ** 5pm CET **

The upcoming session addresses the topic of "Global change and speciation". We welcome speakers Scott Taylor (University of Colorado Boulder, USA) and Sï¿½ren Faurby(University of Gothenburg, Sweden).

The session will last 1.5 hours, with the first hour dedicated to talks from our speakers followed by questions. The last half-an-hour is dedicated to a more general discussion.

To attend the session live, please use the following link: https://gu-se.zoom.us/j/67870592345 Talks (but not the discussion session) are recorded and made available here: https://www.youtube.com/channel/-

UClEkDdE_5sDw70SQq78DIAA . The IOS network aims to promote scientific integration and also integration of the community. A main objective is to foster diversity and inclusion across the field. The seminar series and subsequent discussion is open to everyone, from students to established researchers and non-scientists alike. To maximise the geographic diversity of attendees we alternate time slots every month. Please share this email with anyone who may be interested, especially those in countries that are typically underrepresented in scientific discourse.

The programme of the seminar series is announced by email, on Twitter (@Speciation_net) and on the IOS network website. To automatically receive the programme and other news from the IOS network, sign up to the network mailing list via the IOS website.

We look forward to seeing you there!

The STN IOS organising committee:

Jonna Kulmuni (chair), Chris Cooney, Sean Stankowski, Carole Smadja (co-chairs), Sonal Singhal, Liz Scordato, Joana Meier, Richard Merrill, Konrad Lohse, Nick Barton and Roger Butlin

NERC Research Fellow School of Biosciences University of Sheffield www.cooneylab.co.uk Chris Cooney <c.cooney@sheffield.ac.uk>

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## Online SORTEE Oct15-16

2025 SORTEE Conference: Submit Your Content Proposal by June 2nd

Dear Colleague,The fifth annual SORTEE conference (The Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology) will be held virtually in October 2025. The conference will run continuously from 15 October 07:00 UTC to 16 Oct

Dear Colleague,

The fifth annual SORTEE conference (The Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology) will be held virtually in October 2025. The conference will run continuously from 15 October 07:00 UTC to 16 October 10:00 UTC to cover all time zones.

To submit a content proposal, please go to: https://www.sortee.org/upcoming We accept the following types of proposals:

1) Unconferences: Facilitated discussions of ideas for how to make ecology, evolutionary biology, and related disciplines more open, reliable, and transparent. Facilitation involves moderating the conversation with ideas and examples, but there are no formal presentations.

2) Hackathons: Group projects with well-defined goals (papers, techniques, software, protocols, organizations, etc.).

3) Workshops: Teach tips and tools for producing open, reliable and transparent research practices.

Submissions will close on June 2nd.

The conference is a forum to discuss and develop ideas, while also exploring current practices for advancing research in fields related to ecology and evolutionary biology. If these topics interest you then please consider becoming a member:

https://www.sortee.org/join. The conference will be FREE for SORTEE members.

You are also welcome to submit a proposal and facilitate your session in a language other than English. We will organise live translation during the conference to support this.

Conference registration will also soon open on the SORTEE webpage:

https://www.sortee.org/upcoming . For more information on the conference, do not hesitate to contact us at conference@sortee.org

We hope to see you in October.

Sincerely, The SORTEE Conference Committee

SORTEE Conference Committee <conference@sortee.org>

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## QMUL London EvoDevo Jul11

Dear all,

We are pleased to announce the support of the Genetics Society for the upcoming UK EvoDevo 2025 symposium, which will happen on July 11th (Friday) at Queen Mary University of London.

This will be a day-long (10 am to 6:30 pm) meeting with two exciting keynote speakers (Edwige Moyroud from the University of Cambridge and Chris Lowe from Stanford University) and plenty of opportunities for oral and poster contributions. Registration is only ï¿½5 and will include coffee breaks, a light lunch and drinks for the poster session.

To register, please visit: < https://eshop.qmul.ac.uk/-conferences-and-events/conferences-events/-conferences-events/uk-evodevo >

To submit your abstract, go to: < https://forms.gle/-FKyaFp2TZrCDNi699 >

As always, more information about sponsors, the venue, and the programme is at londonevodevo.co.uk < http:/-/londonevodevo.co.uk/ >

Please feel free to share this information with your contacts and within your institutions. We look forward to seeing you all in July!

Best wishes,

London EvoDevo committee

Jose M (Chema) Martin Duran Reader in Organismal Biology Queen Mary University of London School of Biological and Behavioural Sciences Mile End Road. Fogg Building E1 4NS London UK

https://martinduranlab.com @Chema_MD

Chema Martin <chema.martin@qmul.ac.uk>

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## Roscoff France PolyploidyInPlants Sep15-19

Dear colleagues,

As previously announced, we are organizing a CNRS funded Jacques Monod Conference on "*/Evolutionary and ecological genomics of polyploidy in plants:temporal dynamics across scales of biological organization from molecules to ecosystems/*" to be held in Roscoff (France), September 15-19, 2025.

_*Deadline for registration is approaching (5 may 2025)*_, and details on the Conference can be found at

< https://www.insb.cnrs.fr/fr/evolutionary-and-ecological-genomics-polyploidy-plants-temporal-dynamics-across-scales-biological > (English version)

< https://www.insb.cnrs.fr/fr/genomique-et-ecologie-evolutive-des-plantes-polyploides-dynamique-temporelle-differentes-echelles > (French version)

_Invited speakers_:

*BARKER Michael*—(Department of Ecology & Evolutionary Biology, University of Arizona, USA) *BONNEMA Guusje*—(Department of Plant Sciences, University of Wageningen, Netherlands) *CASACUBERTA Josep *(Center for Research in Agricultural Genomics, Barcelona, Spain) *CHOULET Frédéric*—(INRAE Site de Crouël, Clermont-Ferrand, France) *CONOVER Justin*—(Molecular and Cellular Biology Department, University of Arizona, Tucson, USA) *D'HONT Angélique*—(CIRAD, Montpellier, France) *GLEMIN Sylvain*—(CNRS UMR Ecobio, Université de Rennes, France) *HU Guanjing*—(Agricultural Genomics Institute at Shenzhen, China) *KOLAR Filip*—(Department of Botany, Faculty of Science Charles University, Praha, Czech Republic) *KOVARICK Ales*—(Institute of Biophysics, Academy of Sciences of the Czech Republic, Brno, Czech Republic) *LASCOUX* *Martin*—(Uppsala University, Sweden) *LEITCH Andrew*—(Queen Mary University of London, England) *LEITCH Ilia*—(Royal Botanic Gardens Kew, England) *MANDAKOVA Terezie*—(Mazaryk University, Brno, Czech Republic) *MASON Annaliese*—(INRES, Pflanzenzüchtung Bonn, Germany) *NOVIKOVA Polina *(Max Planck Institute for Plant Breeding Research, Köln, Germany) *PARISOD Christian*—(Département de Biologie, Université de Fribourg, Switzerland) *ROUSSEAU-

GUEUTIN Mathieu*—(IGEPP, INRAE, Le Rheu, France) *SALMON Armel*—(UMR CNRS Ecobio, Université de Rennes, France) *SERRA Heïdi *(Institut de Génétique, Reproduction et Développement, CNRS/ INSERM/Université Clermont Auvergne, Clermont-Ferrand, France) *SOLTIS Pamela *(Florida Museum of Natural History, USA) *VAN DE PEER Yves*—(VIB UGent Center for Plant Systems Biology, Belgium) *VEKEMANS Xavier *(Université de Lille, Villeneuve d'Ascq, France) *WINCKER Patrick *(Genoscope, Evry, France)

Best regards,

Malika AINOUCHE (U. Rennes, France) & Jonathan WENDEL (Iowa State University, USA)

Malika Ainouche Professeur Emérite, Université de Rennes UMR CNRS 6553 Ecobio Bât 14 A Campus de Beaulieu 35 042 Rennes Cedex (France) https://ecobio.univ-rennes.fr/evolution-des-genomes-traits-dhistoire-de-vie-et-adaptation Malika Ainouche <malika.ainouche@univ-rennes1.fr>

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## Roscoff Speciation Oct20-24

Speciation lies at the intersection of microevolution, which focuses on variation within species, and macroevolution, which examines speciation rates and extinction patterns at global scale. The Jaques Monod conference "A multidimensional view of speciation: bridging micro and macro-evolution" aims to bridge across fields by addressing key topics in four sessions:

1. Species diversification 2. The biogeography of speciation 3. Hybridization 4. Components of reproductive isolation

Conference Information: https://cjm.sb-roscoff.fr/en/conference/multidimensional-view-speciation-bridging-micro-and-macro-evolution Registration: https://cjm.sb-roscoff.fr/en/apply/85 Important dates:

* Conference: Monday, October 20 - Friday, October 24, 2025 * Abstract submission deadline: Friday, June 6, 2025 * Deadline for payment of registration fees: September 12, 2025 * Deadline to return completed forms: September 2, 2025 * Organisers: Nick Barton (IST Austria), Camille Roux (Lille, France)

Nick BARTON <nick.barton@ist.ac.at>

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## SwissAlps EvolutConservBiol 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, post-graduate 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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## UMiami EvoDevoBiology Jul22-25

We are excited to announce that registration for Biennial Meeting of the Pan American Society for Evolutionary Developmental Biology at the University of Miami, Coral Gables Campus, July 22-25 is now open.

Please register early to secure your preferred housing. We have an incredible line up of activities and speakers, including four satellite symposia that will take place on the first day (July 22, Spiralia, Arthropods, Fishes and Non-bilaterian EvoDevo). Register for 5 nights if you would like to attend one of the satellite symposia, or come for four nights to attend the regular meeting. We are really looking forward to seeing you there. We are also organizing professional development and community building workshops, as well as an EvoDevo poetry slam, and karaoke night. We are so looking forward to coming together as a community!

Register here:

https://evodevo.wildapricot.org/event-6007396 Hope to see you this summer,

Karen Crow

PASEDB President

Tetsuya Nakamura <tn241@rutgers.edu>

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## ViladoConde Portugal ARGEvol Nov12-14

Dear all,

We have the great pleasure of inviting you to */ARGEvol/* - a conference on the use of ancestral recombination graphs (ARGs) in evolutionary biology. The main objective of the meeting is to introduce the international community of population geneticists and evolutionary biologists to ARGs, and to promote collaborative projects further developing and implementing these new approaches.

We are organising this event that will take place over three days (12-14 November 2025) in Vila do Conde (Portugal). ARGEvol will feature both conference-style sessions (including talks from invited speakers and submitted abstracts) and more practical hands-on sessions where participants can get experience directly working with ARGs and tree sequences. Our invited speakers are Yun Deng (University of California, Berkeley), Dï¿½bora YC Brandt (University College London), Daria Shipilina (ISTA Vienna), James Kitchens (University of California, Davis) and Yan Wong (BDI, Oxford).

If you are interested in attending, please fill in the poll < https://framaforms.org/argevol-conferenceworkshop-interest-survey-1742308127 > which comprises an interest survey. For more detailed information, please see the flyer < https://listes.umontpellier.fr/sympa/d_read/evolmontp/ARGEvol/ARGEvol_flyer_international.pdf > which will be updated with links toï¿½abstract submission and registration. If you have any questions, please contact laura.meyer@umontpellier.fr.

Kind regards, The organisers

Laura Meyer and Pierre-Alexandre Gagnaire (ISEM, France) Pierre Barry and Rui Faria (CIBIO, Portugal)

Poll: https://framaforms.org/argevol-conferenceworkshop-interest-survey-1742308127
Flyer: https://listes.umontpellier.fr/sympa/d_read/evolmontp/ARGEvol/ARGEvol_flyer_international.pdf
Laura Meyer <meyerlaura373@gmail.com>

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# GradStudentPositions

## BayreuthU Germany MicrobesAndParentalCare

PhD position: Parental Care and Microbial Control in Burying Beetles Evolutionary Animal Ecology, University of Bayreuth (Germany)

We are seeking a highly motivated PhD candidate (f/m/d) to investigate how parental care enables /Nicrophorus/ burying beetles to control beneficial and harmful microbial communities during family life. This three-year position is part of an ERC-funded project exploring the socioecology of animal-microbe interactions, focusing on how interactions between animals and microbes shape - and are shaped by - animal social behaviors.

*** The challenge *** Animals continuously interact with a vast array of harmful and beneficial microbes, and natural selection has shaped sophisticated strategies enabling them to manipulate these interactions. However, we still know little about the role of animal social behaviors in exerting such host control. Burying beetles are ideally suited to tackle this issue, because they show complex social behaviors (parental care) and intimately interact with both beneficial symbionts and harmful environmental microbes during their social (family) life. In this project, we will examine how different parental care strategies: (i) enable beetles to mitigate the threat posed by harmful microbes, (ii) affect the transmission of beneficial symbionts to offspring, and (iii) vary across beetle species in their fitness effects and role in host control. The interdisciplinary project will involve an exciting combination of behavioral observations, laboratory and field experiments, as well as the profiling of microbial communities via metabarcoding.

*** Your profile *** We are looking for a highly motivated candidate with: - A Master's degree (or equivalent) in evolutionary ecology, microbiome science, or a related field. - A strong interest in social evolution and animal-microbe interactions. - Prior experience with behavioral experiments and community profiling (desired but not required). - Proficiency in biostatistics (R) or a high motivation to acquire and improve bioinformatic skills. - The ability to work both independently and collaboratively in a team. - Good written and spoken English skills.

*** What we offer *** - A fully funded 3-year PhD position within an ERC-funded project. Remuneration is based on the German TV-L E13 pay scale (65%; gross salary: 3009 EUR/month) and includes social benefits such as health insurance and pension contributions. - A cutting-edge interdisciplinary research ecosystem at the University of Bayreuth, which has recently been ranked in the top 5 percent of young universities worldwide. - A vibrant and supportive research environment in a newly established team, hosted at a department with extensive experience in insect rearing, behavioral experiments, and molecular analyses. - Access to state-of-the-art facilities and equipment for behavioral and microbiome research. - Funding for conference participation and professional training, as well as opportunities for national and international collaboration. - Living in Bayreuth, a small but bustling university town in scenic Upper Franconia, with numerous opportunities for outdoor activities and cultural exploration.

*** How to apply *** Applications should include: - A cover letter (1-2 pages) describing your research interests, motivation, and relevant work experience. - A detailed CV, including your methodological skillset, B.Sc. and M.Sc. grades, and publications (if any). - A summary of the Master thesis (max. 500 words). - Names and email addresses of 2-3 academic scholars who agreed to serve as a reference.

Apply by May 16, 2025, by sending your application as a single PDF to Jos.Kramer@uni-bayreuth.de with the subject: “PhD Application - Parental Care vs. Microbes”. The ideal starting date is September 2025.

The University of Bayreuth is committed to promoting diversity and equal opportunities. We encourage applications from all qualified individuals, regardless of background. The working language in our group is English.

For more information, feel free to reach out informally: Jos.Kramer@uni-bayreuth.de

Jos Kramer <jos.kramer@env.ethz.ch>

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## BiologyCentre Czech EvolGenomicsAmphizoicProtists

PhD/MSc Position in Evolutionary Genomics of Amphizoic Microbial Eukaryotes

Join our research team to explore the genomic and metabolic underpinnings of a rare and fascinating evolutionary phenomenon amphizoic lifestyle in microbial eukaryotes. We study Hexamita inflata, a unique unicellular flagellate (Diplomonada) that thrives both freely in aquatic sediments and inside animal hosts. This project combines fieldwork, single cell transcriptomics, comparative genomics, and experimental evolution to uncover how organisms switch between host-associated and free-living lifestyles an event exceptionally rare in nature.

You will participate in: - Generating and analyzing genomic/transcriptomic data from natural populations and lab cultures - Investigating gene flow, expression patterns, and evolutionary pressures across habitats - Developing and applying cutting-edge methods in single cell biology and experimental evolution

Start date: Flexible (2025). Duration: 4 years.

Ideal candidates will have a background in evolutionary biology, parasitology, bioinformatics, molecular biology, or microbiology. Previous experience with omics data is a plus but not required. A PhD candidate has to hold a Master’s degree, be at minimum conversational in English and have good communication and organisational skills.

The position is fully funded. The minimum starting student net income will be ca 1,100 EUR/month sufficient to comfortably cover life expenses in Äeské BudÃ. Additional salary will be negotiated based on skills and results. We expect several articles to be published in the course of the study in high quality journals. Active participation at international scientific conferences will be encouraged and supported.

Our lab is based at the Institute of Parasitology, Biology Centre of the Czech Academy of Sciences, Äeské BudÃ. The PhD/MSc studies will be performed at the Faculty of Science, University of South Bohemia (https://www.prf.jcu.cz/en/study-at-the-faculty/information-for-phd-students). The Laboratory of Genomics and Diversity of Protists is a friendly and supportive environment of an international team.

Ãeské BudÃis a pleasant and safe mid-sized city of 100,000 people with relatively low living costs, situated in the South Bohemia region, less than 2 hour train ride from Prague. The BC CAS' campus is directly adjacent to the University of South Bohemia with an international student community.

All questions and applications (CV + half-page motivation letter + contact details of 1-2 references) should be sent directly to Jan Brabec.

Jan Brabec, PhD. (brabcak@paru.cas.cz)

Laboratory of Genomics and Diversity of Protists
Biology Centre of the Czech Academy of Sciences
BraniÅovská 31, Ãeské BudÃ, 37005 Czech Republic

Brabec Jan <brabcak@paru.cas.cz>

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## CEFE-Montpellier EvolutionaryGenomicsAndTheory

Hello,

I have *two* fully funded PhD opportunities in my lab (to start Oct 2025), with genomics and population genetics theory. This is part of the ERC RegEvol project dedicated to better understand the multifaceted evolutionary consequences of cis and trans regulatory variation.

One is to work on sex-asex transitions with Christoph Haag; see project description, and application instructions here: bit.ly/4hp1q1A

One is to work on allele-specific expression with Sylvain Glï¿½min; see project description, and application instructions here: bit.ly/4iuKLuQ

The PhDs will be based in the GEE < https://www.cefe.cnrs.fr/en/research/evolutionary-ecology/genetique-et-ecologie-evolutive-3 > team in CEFE lab in Montpellier, a large and international group of evolutionary geneticists and will interact with several close collaborators

Interested candidates can contact me informally for extra details if needed.

Thanks to spread the word to interested master students!

Thomas Lenormand

Thomas Lenormand CNRS research director PI ERC RegEvol < https://www.cefe.cnrs.fr/fr/recherche/ee/gee/800-c/193-thomas-lenormand > Lab website < https://www.cefe.cnrs.fr/en/ > CEFE Lab, Montpellier France

Thomas LENORMAND <thomas.lenormand@cefe.cnrs.fr>

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## DalhousieU Macrogenetics

The Biodiversity and Population genetics lab of Chloé Schmidt at Dalhousie University is inviting applications for a PhD position. Our team studies big-picture questions surrounding spatial patterns of biodiversity from a population genetics perspective. Students will work with and contribute to building a large database of population-level microsatellite datasets in terrestrial vertebrates and potentially other taxonomic groups. The position will be fully computational with no field or lab component.

Potential PhD projects include either urban evolutionary ecology or the biogeography of genetic diversity, depending on student interests. The urban ecology and evolution project will focus on understanding within-city variation in genetic diversity across Canadian cities, particularly the role of socioeconomic factors and relationships between wildlife genetic diversity across species and neighborhood racial composition. Projects on the biogeography of genetic diversity will focus on describing multi-species patterns of genetic diversity from continental to global scales and understanding how these patterns are related to environmental factors and other aspects of biodiversity. For more information about the kind of work we do, please see our research themes and publications on the lab website: https://www.schmidt-biodiversity-lab.org/ Applications are welcome from those curious about evolutionary ecology, population genetics, biogeography, and macroecology who are interested in developing quantitative skills (R coding, geographic information systems [GIS], and statistical modeling including hierarchical modeling and modeling spatial data). Previous experience with these topics is a bonus, but not required! If these types of research questions interest you please don't hesitate to get in touch.

The position is based in Halifax, Canada. Preferred start date is September 2025 or January 2026 (this is flexible). The position is fully funded.

To apply, please send (1) a motivation letter describing your reasons for applying, your research interests and how they intersect with those of the lab; (2) a CV; and (3) contact information for two academic references to Chloé Schmidt (chloe.schmidt@dal.ca). Review of applications will begin immediately and continue until the position is filled.

Chloe Schmidt <Chloe.Schmidt@dal.ca>

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## ILIM AUSTRIA EcoEvoDynamics

PhD position at the Research Institute for Limnology (ILIM) in Mondsee, University of Innsbruck, Austria: We are offering a PhD position in an FWF START project on eco-evolutionary dynamics and admixture at ILIM in Mondsee which is part of the University of Innsbruck. We investigate secondary contact in the context of global change in important aquatic grazers (Daphnia spp.) and study the consequences of admixture on eco-evolutionary dynamics on the species, communities and ecosystem level. The position is planned for 42 months with a possible extension up to a total of 48 months.

***Your project*** The goal of this PhD project is to characterize phenotypic differences among parental species and their hybrids in the Daphnia longispina species complex and to experimentally test the ecological consequences of phenotypic admixture variation in mesocosms. The lab maintains a large collection of unadmixed and admixed isofemale Daphnia lines for which whole-genome data is available and which can be used for experimental work to investigate eco-evolutionary dynamics and potential feedback loops. The lab and the University's Research Institute for Limnology (ILIM) in Mondsee are well-equipped to support life history, aquaria and mesocosm experiments.

***Your skills*** We are seeking a candidate with a pronounced interest in research and limnology. Good problem-solving skills, a high degree of self-motivation, independence and the ability to work in a team are essential. Prior experience in any of the following areas will be of advantage but is not strictly required: (i) phenotyping, life-history and/or mesocosm experiments (design, experimentation), (ii) statistical analysis and coding (e.g. R, Python, bash), (iii) genetic data analysis. The work within our international team and with international collaborators requires proficiency in English.

***What the position offers*** The annual gross salary is ˜49.320,00 EURO. The contract includes health insurance and 5 weeks of holidays per year. Furthermore, the university has additional attractive offers: https://www.uibk.ac.at/universitaet/-zusatzleistungen/index.html.en We aim to ensure an excellent working environment in which everyone can contribute their experience, ideas and ways of thinking and we offer and support professional training. Moreover, we strive for cultural and gender equity, diversity, and inclusion for anyone to be involved in this project. Candidates with a broad range of backgrounds, perspectives, and ideas will be welcomed and are encouraged to apply. For more information on the position, the project, the group, or the University, please do not hesitate to contact Markus.Moest@uibk.ac.at.

***How to apply*** We are looking forward to receiving your application and we will start reviewing applications on a rolling basis from April 30th. Please send a single pdf file including a letter of motivation, curriculum vitae, a list of publications (if any) and contact details of two references to Markus.Moest@uibk.ac.at. Applications should be written in English.

MÃST Markus, PhD University of Innsbruck Technikerstrasse 25 (Room 517) A-6020 Innsbruck Tel: +43 (0)512 507-51771 Fax: +43 (0)512 507-51799 E-mail: mailto:Markus.Moest@uibk.ac.at

"Möst, Markus Hartmann" <Markus.Moest@uibk.ac.at>

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## ISYEB Paris CommonLizardEvolution

We offer a 3-years position, working as a PhD candidate to study the link between selection, local adaptation and the genetic architecture of complex traits on the common lizard (Zootoca vivipara). The project will use whole-genome sequenced obtained by the linked-read haplotagging approach, on thousands of individuals from a wild population and a common garden experiment.

The candidate will pass their PhD at Ãcole Pratique des Hautes Ãtudes (PSL University), joining Pierre de Villemereuil's team, at the Institute for Systematics, Evolution, Biodiversity (ISYEB), located within the Muséum National d'Histoire Naturelle (MNHN) in Paris. This position is funded for 3-years as part of the EvoGenArch ERC Starting Grant.

The position will start in October 2025, although the starting date is negotiable. Applications are welcome until May 13th.

For more information and instructions to apply, see here: https://devillemereuil.legtux.org/erc-funded-phd-position-available/ Pierre de Villemereuil <pierre.de-villemereuil@mnhn.fr>

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## LaRochelleU WildlifeCancerEvolution

La Rochelle University is recruiting within the LIENSs Laboratory for a 3-year doctoral contract on the following thesis subject:

Evolution of anticancer defenses in wild animals.

Supervisors: Drs. Mathieu Giraudeau (LIENSs), Orsolya Vincze (LIENSs) and Fabrice Bertile (IPHC, Strasbourg).

Employer description

In a higher education and research landscape that has been profoundly reshaped for more than a decade, La Rochelle Universitéhas chosen to structure its research around a thematic by positioning its scientific and academic strengths on societal and environmental issues. This approach has led to the creation of a teaching and research institute called the LUDI Institute, SmUCS in English (Smart Urban Coastal sustainability), operational since the 1st September 2021.

Bringing together all the laboratories, all the PhD students and most of the institution's masters programmes. This institute aims to address the many scientific issues raised by the anthropisation of the coastal area by facilitating decompartmentalised and interdisciplinary approaches, based on a proactive policy of innovation and dissemination of results, without forgetting the fundamental principles of ethics and scientific integrity.

The creation of the LUDI Institute is surrounded by two other important projects, namely the EU-CONEXUS European university, a network of European partner universities sharing a common speciality, and the CampusInnov site initiative, intended to establish a culture of innovation in both training and research.

Website to consult: click here

Research context

Cancer is recognized as a pathology that affects almost every member of the animal kingdom. Yet while some species are highly susceptible to cancer (e.g., humans), others are highly resistant (e.g., naked mole rats). Variation in cancer resistance across wildlife taxa is an extremely valuable source of information on oncogenic processes and resistance mechanisms. The limited research conducted on non-standard model organisms in this respect has already provided tremendous insights into the natural mechanisms of cancer resistance. Within this PhD project, we propose to use a multidisciplinary approach at the interface of oncology, physiology, cellular evolutionary biology, and analytical chemistry to characterize the prevalence of cancer in wildlife and identify the genetic, physiological and life-history predictors of the cross-species pattern of cancer susceptibility.

Our project proposes to use new databases on cancer prevalence, life history traits and physiology of hundreds of vertebrate species in order to run large-scale comparative analyses to study the variability of cancer resistance across vertebrates. We propose to assess genomic tumor-suppressor mechanisms in vertebrate species through analyses of already published genomes. Finally, using primary cell cultures from cancer-resistant species exposed to carcinogenic experimental conditions, we will evaluate oncogenic susceptibility and the efficacy of putative tumor-suppressive mechanisms using a number of validated in vitro assays. This last approach might involve large-scale proteomic analyses of exposed cells. The ultimate goal of this research program is to identify natural mechanisms of resistance against cancer that might be translated to human medicine. The selected student will have the opportunity to work more specifically on some aspects of this research program, based on his background and interests.

See https://wicane.recherche.univ-lr.fr/for a full description of our research programs.

Our studies are well grounded, partly being based on pre-existent data or already available cell cultures. We hope to unravel the cross-species diversity of cancer resistance, and highlight future avenues in the identification of efficient tumor-suppressor mechanisms.

Representative publications :

Vincze, O., Colchero, F., LemaÃtre, J. F., Conde, D. A.,

Pavard, S., Bieuville, M., ... & Giraudeau, M. (2022). Cancer risk across mammals. Nature, 601(7892), 263-267.

Giraudeau, M., Sepp, T., Ujvari, B., Ewald, P. W., & Thomas, F. (2018). Human activities might influence oncogenic processes in wild animal populations. Nature Ecology & Evolution, 2(7), 1065-1070.

Firsanov, D., Zacher, M., Tian, X., Sformo, T. L., Zhao, Y., Tombline, G., ... & Gorbunova, V. (2024). DNA repair and anti-cancer mechanisms in the long-lived bowhead whale. BioRxiv, 2023-05.

Abegglen, L. M., Caulin, A. F., Chan, A., Lee, K., Robinson, R., Campbell, M. S., ... & Schiffman, J. D. (2015). Potential mechanisms for cancer resistance in elephants and comparative cellular response to DNA damage in humans. Jama, 314(17), 1850-1860.

Skills required

We are looking for a student with relevant background in evolutionary biology and/or cancer biology, with enthusiasm to learn advanced statistical analyses (experience with R is a strong asset), but also

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## MonashU EvolutionaryEcol

PhD opportunity in evolutionary ecology - Monash University, Australia

Dear colleagues

The Community Ecology and Evolution group led by Giulia Ghedini is seeking motivated PhD candidates to join the team in the School of Biological Sciences at Monash University in Melbourne, Australia.

What we do: We study how species interactions affect organismal physiology to get a better understanding of performance in complex environments. We use experiments (informed by theory) on marine phytoplankton to quantify (plastic and evolutionary) changes in growth, energy/resource use and competitive ability at the individual level; we then ask how these responses help explain the diversity and functioning of communities. Our motivation is to improve our understanding of biological systems, particularly to facilitate predictions in the context of environmental change. For examples of our recent work see here

Project details: Evolutionary dynamics in communities.The project will study evolutionary dynamics in phytoplankton communities using experimental evolution. Predicting how multi-species communities evolve remains a challenge - phytoplankton is a great system to study eco-evolutionary dynamics in eukaryotes and improve our ability to predict the evolution of communities. The goal of this project is to quantify how biotic interactions alter competitive ability, resource use and coexistence between phytoplankton strains, as well as the consequences of these responses for community properties. The specifics of the project can be defined according to interests of the candidate, within the broader research interests of the group.

Eligibility and scholarship information:

Honours or Masters of Science degree or equivalent are required. Candidates can be national (Australian) or international and will need to apply for PhD scholarships with the support of the group leader. Next deadline is 31 August 2025 for international students, and 31 May 2025 for domestic students. Further information about scholarship eligibility: https://www.monash.edu/graduate-research/study/scholarships/fees-scholarships Stipend and allowance rates: https://www.monash.edu/graduate-research/study/scholarships/fees-scholarships/rates Selection criteria:

- Honours/Masters Degree and knowledge in one or few of the following areas: evolutionary biology, population biology, ecology, marine biology, microbial ecology and evolution. Hands on experience in any of those areas will also be an advantage
- Strong written and verbal communication skills in English
- A demonstrated capacity to work independently and as part of a team
- A high level of motivation and enthusiasm to perform laboratory- based research
- Experience in statistical analysis in R (or similar)
- Capacity to commence studies by 2026

After checking your eligibility, please email your expression of interest to Dr Giulia Ghedini (giulia.ghedini@monash.edu). Include a motivation letter(1-2 pages) describing your expertise and interests, stating why you see yourself as a good fit for our research group. Please also include your academic transcripts and your

CV with a list of publications if available and contacts of two referees.

Giulia Ghedini <giulia.ghedini@monash.edu>

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## NewCaledonia AvianEvolution

PhD position at AMU Poznan – Song variation and interspecific communication in the fan-tailed gerygone from New Caledonia –

Project description The fan-tailed gerygone (Gerygone flavolateralis) from New Caledonia produces short stereotyped songs and calls that are used for territorial displays and intra-pair communication. Both types of vocalisation vary among populations, even across relatively short distances, strongly suggesting the presence of geographic variation in vocalisation structure and the existence of dialects in this species. The PhD candidate will quantify the variation in song and call structures at the individual and population levels and determine the ecological and behavioural factors underlying such variation. The main objectives of the research will be to 1) quantify the variation in vocalisation type across individuals and populations, 2) determine ecological and behavioural factors underlying song variation across populations and 3) conduct playback experiments to assess the behavioural responses of individual birds to vocalisations from same and other populations.

The field season will last 4 months per year (until 2027) and overlaps with the breeding period of the fan-tailed gerygone in New Caledonia (September-January). The research will be conducted primarily at our two long-term research sites on the main island of Grande Terre, in habitats of tropical dry forest and tropical moist forest. However, short excursions on other smaller islands within the archipelago of New Caledonia to collect bioacoustics data are also possible. The candidate will also conduct behavioural experiments in the field to quantify the response of individual birds to known and foreign vocalisations. Depending on the candidate interests, it will be also possible to develop molecular work to link genetics and song variation. Additionally, the candidate will have ample possibilities to develop complementary research according to their own interests.

We are looking for a student who would like to participate in a hybrid research project involving two institutions. The field portion of the research in New Caledonia will be funded by Dr. Alfredo Attisano's project (Museum and Institute of Zoology, Polish Academy of Sciences), while the doctoral fellowship will be financed by the Doctoral School of Natural Sciences at Adam Mickiewicz University in Pozna??, under the supervision of Prof. Tomasz Osiejuk. AMU will also provide equipment and expertise for the bioacoustic aspect of the project. Based on the applications, we will select a student who will be prepared for recruitment at the Doctoral School, which will take place in the second half of July 2025. After successful admission to the Doctoral School, the student must be able to complete all formalities in the 1st half of October and then join for 2 months of research in New Caledonia. The fieldwork will run from September to December in following years.

Requirements: - M.Sc. in Animal Behaviour, Biology, Zoology, Ecology or related field - good knowledge of bioacoustics techniques, analysis and management of large bioacoustics datasets - relevant ornithological fieldwork experience in mistnetting, bird handling and banding, blood sampling, behavioural observations, nest searching and nest monitoring - good knowledge of methodologies for statistical analysis. Proficiency in R and/or Python will be considered and asset - proficiency in English (spoken and written, level B2 and above), knowledge of French desirable - physical fitness, resilience and ability to work under challenging conditions (heat and UV exposure) - ability to withstand long-working hours (10-12 during the peak of the breeding season) - ability to work independently or as part of a team - category B driving license

How to apply: Send the application (deadline 15/05/2025) to Alfredo Attisano (aattisano@miiz.waw.pl) and Tomasz Osiejuk (osiejuk@amu.edu.pl) with the subject "NCBioAcoustics_NameSurname". Please include in the application: (1) a cover letter describing research interests and motivation to join our research group (max 1 A4 page); (2) CV including publications lists and contact (email, phone) of at least 2 potential referees; (3) please include a statement of EU General Data Protection Regulation (https://gdpr.eu/privacy-notice/) in the CV.

More info on our research: 1) Alfredo Attisano: https:/-/orcid.org/0000-0002-6675-4900 2) Tomasz Osiejuk: https://behaecol.web.amu.edu.pl/ Alfredo Attisano <aattisano@miiz.waw.pl>

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## NewCaledonia MiIZ PAS AvianEvolution

M.Sc. — Avian behavioural ecology in New Caledonia

We are looking for 2-3 M.Sc. students interested in conducting their research project on avian behavioural ecology in New Caledonia. The students' research projects will be part of the long-term research conducted by the Behavioural Ecology Group at the Museum and Institute of Zoology of the Polish Academy of Sciences on the behavioural ecology of small passerines and coevolutionary arms race between the fan-tailed gerygone (Gerygone flavolateralis) and the shining bronze-cuckoo (Chalcites lucidus) from New Caledonia.

We welcome applications from students interested in brood parasitism, bioacoustics, predator-prey interactions and nest ecology. The candidate's research should complement our main research topics, but we also encourage students to formulate their proposal based on their ow research interests. Possible research topics include: - dialect variation, intra-pair communication and territorial defence in the fan-tailed gerygone - antiparasitism defences of potential passerine hosts of shining bronze- cuckoo in New Caledonia - nest defence strategies of the fan-tailed gerygone against brood parasite and nest predators - choice of nest location in fan-tailed gerygone: role of nest camouflage, solar radiation and predation pressure

When: the field season will run from September - December 2025 (exact dates to be agreed). Our field sites are located on the main island of Grande Terre, in managed nature reserves with tropical dry forest and tropical moist forest habitats and abundant birdlife.

Additional duties: in addition to own research duties, the candidates will also be actively involved in all other fieldwork-related activities. These include nest searching and monitoring, mist-netting and banding, data collection and analysis and maintenance of field equipment. The full scope of tasks will vary depending on the candidate's specific research project.

Requisites: experience of behavioural research with wild birds in particular nest searching, nest monitoring (including video monitoring), mist-netting, bird banding. Additional training will be provided. Fieldwork is physically demanding (UV exposure, heat, humidity, rain) therefore physical fitness, enthusiasm and self-motivation are essential. Ability to work independently or as part of a team and to share living spaces is also essential. Previous experience of working in the tropics, driving license and knowledge of French are desirable.

Working conditions: 8-10 hours daily for 6 days a week on average, up to 10-12 hours during the peak of the breeding season with an early morning start (5-6am). The project will cover the costs of subsistence, accommodation and commute between sites in New Caledonia. Selected candidates will need to arrange their own travel to and from New Caledonia, therefore prospective students are encouraged to apply for their own research funding to support the travel costs.

How to apply: send a single PDF with the title — NC2025_MSc_NameSurname.pdf — with 1) CV with contact details of 2 referees, 2) cover letter (max 1 A4 page) describing relevant experience and research interests and 3) a short research proposal (max 1 A4 page) describing the intended research activity to aattisano@miiz.waw.pl. The initial deadline is 15/05/2025, but positions are open until filled. Only selected applicants will be contacted and invited for an online interview.

For informal enquiries please contact: Alfredo Attisano (aattisano@miiz.waw.pl).

Alfredo Attisano <aattisano@miiz.waw.pl>

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## NewZealand ComputationalPhylogenetics

We have a 3 year Ph.D. research fellowship available in computational phylogenetic biogeography. The funded research aims to develop and test computational models that link long-distance dispersal to mechanistic predictors, including palaeogeography (plate tectonics, palaeoclimate, paleoislands), evolving dispersal-related traits, and/or diversity-dependence. Students who would like to do a project on a clade of special interest, and/or on advancing the computational methods, are encouraged to apply.

Location: School of Biological Sciences, University of Auckland, Auckland, New Zealand

The University of Auckland has rolling admissions, but has some strict requirements, including (1) a previous Honours or Masters-level research project; (2) a strict requirement of a minimum GPE of 6.0, and (3) a supervisor-approved project proposal.

To begin discussions about applying, please email nzpbgie@gmail.com with:

1. A screenshot showing you meet the Grade Point Equivalent (GPE) minimum of 6.0:

University of Auckland Doctoral Entry Requirements: https://www.auckland.ac.nz/en/study/applications-and-admissions/entry-requirements/postgraduate-entry-requirements/doctoral-entry-requirements.html 2. Description of previous bioinformatics or programming experience (much of our work is in R, Julia, or with GenBank-related tools)

3. A description of your previous research, and your potential interests for a computational/phylogenetic/biogeography project.

Questions to: nzpbgie@gmail.com

NZpbgie <nzpbgie@gmail.com>

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## Norwich UK Bioinformatics

Dear Evoldir,

I wanted to highlight a bioinformatic PhD position (deadline 14th March) on gut microbial evolution in response to human disease in Norwich, UK: buff.ly/1zRakR6

Please do not hesitate to write me with further questions.

Kind regards,

Falk

Dr Falk Hildebrand

PI at Quadram Institute Bioscience & Earlham Institute

Norwich Research Park

www.falk.science "Falk Hildebrand (QIB)" <Falk.Hildebrand@quadram.ac.uk>

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## NTNU Norway ArcticAlienPlantGenomics

Application deadline: 09.05.2025 For the full description of the position and application instructions, see: https://www.jobbnorge.no/en/available-jobs/job/-278168/phd-candidate-in-arctic-alien-plant-genomics About the position. The NTNU University Museum is seeking a highly qualified, ambitious, and motivated PhD candidate for a project focusing on genomics of Arctic alien plants. A warming climate, changes in soil properties, and rising human activity in the Arctic increase the probability of introduction and establishment of alien plant species. In high-Arctic Svalbard and other Arctic regions, the wintercress (Barbarea vulgaris) is an established alien species. Hypotheses for its success include multiple introductions from different genetic sources, enemy release advantage related to plant defense compounds, and shifts in adaptive traits.

The PhD project will develop genomic datasets, making use of field collections and herbarium resources, and have the possibility to develop experimental evidence to examine links between the genomic basis of successful establishment and potential invasiveness in the high-Arctic. The wintercress will be a primary focus of the project, but complementary research on parallel systems may be developed. The project will add an important evolutionary component to ongoing interdisciplinary research on Arctic greening.

The successful candidate will be employed at the NTNU University Museum's Department of Natural History. The NTNU University Museum is the natural and cultural history museum of the Norwegian University of Science and Technology in Trondheim. The Department of Natural History conducts research in systematics and taxonomy, evolutionary genomics, as well as in phylogeography, population genetics, and ecology with an emphasis on conservation biology. Your immediate leader will be the Head of Department.

About the project. The team of supervisors will consist of Ass. Prof. Kristine Bakke Westergaard (main supervisor), as well as co-supervisors Prof. Mike Martin and Dr. Simone Fior (ETH Zürich, Switzerland). The candidate will use the NTNU University Museum's herbarium, genomics laboratory facilities and computational resources, and the work will be closely associated with a project on Arctic greening based at ETH Zürich < https://geobiology.ethz.ch/research/arctic-greening.html >. The work will also be part of the Nordic Borealization Network < https://nordborn.lbhi.is/ > that seeks to understand the processes, drivers, and consequences of changes in the species composition of tundra ecosystems.

Duties of the position. The work of the PhD candidate will likely consist of field work, herbarium work, genomics lab work and bioinformatic analyses, and common garden experimental work in an international interdisciplinary team. For a position as a PhD candidate, the goal is a completed doctoral education up to an obtained doctoral degree. Publication of the project results in peer-reviewed journals is expected.

* Carry out research of excellent quality within the framework described above * Academic publications and popular science dissemination * Participate actively in research groups * Participate in international activities such as networks and conferences * Other career-promoting work * Be prepared for changes to your work duties after employment.

Required selection criteria.

* You must have a Master's degree in in biology or equivalent with specialization in biosystematics, population genetics, phylogeography, evolutionary biology, or closely related fields. * You must have experience at the Master's level with analyses of next-generation sequencing (NGS) data to answer evolutionary questions (e.g. phylogenomic and population genomic analysis) * Your course of study must correspond to a five-year Norwegian course, where 120 credits have been obtained at master's level. Master's students can apply, but the master's degree must be obtained and documented before starting the position and no later than 20.06.2025. * You must have a strong academic background from your previous studies and have an average grade from your Master's degree study, or equivalent education, which is equal to B or better compared to NTNU's grading scale < https://i.ntnu.no/wiki/-/wiki/English/Grading+scale >. If you do not have letter grades from previous studies, you must have an equally good academic foundation. If you have a weaker grade background, you may be considered if you can document that you are particularly suitable for a PhD education.

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## OxfordBrookesU LepidopteraConsGenomics

We are looking for a PhD Student in Conservation Genomics interested in using museum specimens of extirpated (regionally extinct) butterfly populations to investigate the symptoms and causes of local extinction using genomics.

Background: Climate change and habitat degradation are causing global biodiversity declines. Extinction risk is acute for insects, which are difficult to monitor but are often of direct or indirect socioeconomic importance. Museum samples are a treasure trove for understanding past extinction events and preventing future losses, but their use remains limited. This project aims to use whole genome sequence (WGS) data from museum samples to understand genomic symptoms and potential causes of regional extinctions in insects. We will focus on the Mazarine Blue (Cyaniris semiargus) and Large Copper (Lycaena dispar) butterflies, species that went extinct within the UK in the early 20th and mid 19th centuries respectively. This will involve optimizing WGS sequencing protocols for working on museum specimens and developing best practices for museum metagenomics.

We will focus on, but not limited to, the following:

1. Evaluating the impact of historical and more recent events on the disappearance of these two species.

2. Did inbreeding and genetic load contribute to their extirpation?

3. Did fungal or other microbial pathogens play a role in their demise?

There is also a possibility to explore other Lepidoptera or insect species depending on student interests.There is also a possibility of combining the analysis above with those from stable and threatened species.

Requirements: We are looking for someone interested in conservation genomics, working with museum specimens and a desire to develop bioinformatics/data science skills. Additionally, the following are required:

- Degree (BSc. or MSc. in relevant study area - Interest or background in conservation genomics - Bioinformatics experience/aptitude, some knowledge of R or Python - Molecular Biology experience (PCR, DNA extraction, pipetting) - Experience working with museum samples would be a plus

This project will be in collaboration with the Natural History Museum (London), Oxford University Museum of Natural History and the University of Edinburgh and potentially other museums. We are looking for someone interested in conservation genomics, working with museum specimens and a desire to develop bioinformatics/data science skills. Lab and Bioinformatics training will be provided as part of the programme of study. There will also be opportunities to participate in LepEU activities ( lepeu.github.io) for interested candidates. For more information, interested candidates are encouraged to contact Saad Arif ( sarif@brookes.ac.uk)

For full details on the project (including stipend and and additional info), studying at Oxford Brookes and how to apply, see the advert here: https://www.findaphd.com/phds/project/using-museomics-to-investigate-the-disappearance-of-the-mazarine-blue-and-large-copper-butterflies-in-the-uk/?p184018 Further reading: https://onlinelibrary.wiley.com/doi/10.1111/mec.17518 https://elifesciences.org/articles/87928 https://www.nature.com/articles/s44358-025-00033-0 Dr. Saad Arif Senior Lecturer Department of Biological and Medical Sciences Faculty of Health and Life Sciences Oxford Brookes University Gipsy Lane Oxford, OX3 0BP UK Tel. +44 (0)1865 483437 Mob: +44 (0) 7985378194 email: sarif@brookes.ac.uk web: saadarif.github.io

Saad Arif <sarif@brookes.ac.uk>

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## Rennes France ModellingAquaticInvasivePop

Rennes_France.DemogeneticsInvasivePopulations

Dear all,

Please find below a fully funded 3-years PhD position. Feel free to share this opportunity with your students and networks. Thanks.

We propose a fully funded 3-years PhD position in *Predictive Demogenetics of the ecological and evolutionary dynamics of freshwater and coastal populations* at DECOD Unit Research (Ecosystem dynamics and sustainability: from source to sea) in Rennes, France, supervised by Eric j. Petit et Solenn Stoeckel.

This thesis is 100% funded by INRAE: approximately euro 27,600 gross per year + ~5% coverage of incidental costs (teleworking package, sustainable mobility, public transport subscription, family supplement, mutual insurance). Starting in November 2025.Deadline for applicants: May 31th, 2025.

Workplace: https://ouvaton.link/mdHjAg If you are interested in:

§exploring scientific questions at the frontiers of ecology and evolution, through modelling and analysis of tracked population datasets, based on genotyping and abundance data acquired on invasive species (including Northern Hemisphere water primroses, crayfishes in France, freshwater and coastal algae, and Kerguelen Islands trout);

§acquiring or implementing mathematical, statistical, and programming methods to produce methodological results, to understand microevolutionary phenomena, to then apply advances on tracked population datasets in partnership with natural area managers;

§working on a thesis involving international collaborators, in a living laboratory located in a young and vibrant city, with a reasonable cost of living and connected to Europe (TGV, airport);

This thesis position may be for you.

In this case, please feel free to contact us if you have any questions, or to express your interest in this position: Eric J. Petit (eric.petit@inrae.fr) et Solenn Stoeckel (solenn.stoeckel@inrae.fr) If you wish, you may come and visit our lab, meet us and talk with the doctoral students and postdoctoral fellows to feel the workplace environment.

*Context* Biological invasions are long monitored by scientists and natural area managers. They provide an opportunity to understand the biological processes and mechanisms that enable rapid biological evolution of populations facing major environmental changes. By coupling demographic and landscape genetic models, population demogenetics offers a suitable framework for analyzing the monitoring of contemporary populations and for predicting their short- and medium-term fates under constrained spatio-temporal scenarios. This formalism allows for the integration and full exploitation of time series data.

The objective of this thesis will be to study the methodological strengths and limitations of a mathematical demogenetic model for inferring the demographic, biological, and eco-evolutionary processes occurring in such populations. This study will provide a better understanding of how repeated foundation effects, the complex demographies of invasion fronts, and the random variability of reproductive success can explain the emergence and maintenance of biological specificities in populations at the periphery of their ranges. We will apply these analytical approaches to real-life monitoring of invasive populations in aquatic environments and along waterways to infer their demographic and evolutionary dynamics.

The acquired knowledge will inform management actions and planned regulations.

The lab: https://www.umr-decod.fr/en Funding research institutes: https://www.inrae.fr/en/divisions/ecodiv https://www.inrae.fr/en/divisions/aqua The city: https://www.tourisme-rennes.com/en/ sstoeckel <solenn.stoeckel@inrae.fr>

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## Seville Spain InsectEvolution

Our lab currently have one research internship position open for 7 months (fully Funded, 600 Eur/month. Suitable Master and Bachelor students (Suitable for Spanish citizens and foreign graduates of Spanish Universities, as well as people who have Spanish equivalencia of their foreign degree completed. Our position is JAE_INT_EX0881 “Drivers of gigantism in the Australian Miocene Insects”.

Applications at https://sede.csic.gob.es/tramites/programa-jae/jae-intro-2025 Deadline: 2nd of May, 2025

Factors Driving evolution of Insect Gigantism in Subtropical Miocene Environments of Australia

Insect size is a crucial functional trait that influences dispersal, productivity, and the ability of insects to survive rapid global change events, including mass extinctions.

The McGrath’s Flat fossil site offers a unique window into the much warmer and wetter past of eastern Australia during the Miocene (approximately 16 million years ago). At this site, our team discovered millions of insect fossils between 2018 and 2025. (https://www.australiangeographic.com.au/news/2022/11/billabong-of-ancient-life/)

We have described numerous insect species from the site, including several species of cicadas, flies, and wasps, as well as spiders and fish. Many of the insects described are as large or even larger than any of their modern relatives. This gigantism is especially evident in the cicadas Tithopsaltria titan, which are among the largest cicadas to have ever existed in Earth’s history.

The causes of the prevalent gigantism in the insects of McGrath’s Flat are unclear, but there are multiple poorly understood factors that may influence insect size, such as predation pressure, temperature, or partial oxygen pressure. Our hypothesis is that, in the warmer Miocene environments of eastern Australia, insect groups affected by this gigantism experienced a higher rate of phylogenetic radiation, leading to the exploitation of a broader spectrum of niches and the emergence of numerous “giant” taxa.

Call for JAE INTRO Fellowship Applicant

We invite an undergraduate student to join this project, participating in the work of a Spanish-Australian-German international team aiming to analyze the phylogenies of various insect groups described from McGrath’s Flat.

The fellow will:

Learn to carry out trait evolution analyses on both fossils and modern animals.

Learn statistical methods to analyze diversification rates in animals (primarily using R).

Become part of the activities of a dynamic, multidisciplinary international group.

Tasks to be performed:

Assemble phylogenetic data for analysis (mainly from open-access molecular data sources such as GenBank).

Create trait (size) databases for the insect groups being analyzed.

Participate in writing the manuscript resulting from the study.

VIKTOR BARANOV <viktor.baranov@ebd.csic.es>

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## SGN Frankfurt Paelobotany

Job Announcement Ref. #01-25029

The Senckenberg Gesellschaft für Naturforschung (SGN) was founded in 1817 and is one of the most important research institutions in the field of biodiversity. At its twelve locations throughout Germany, scientists from almost 40 nations conduct cutting-edge research on an international scale. The Society's headquarter is in the Main metropolis of Frankfurt in the heart of Germany. This is also where one of the best-known Senckenberg facilities, the Senckenberg Natural History Museum, is located.

The Senckenberg Society for Nature Research (SGN) at the location in Frankfurt am Main is seeking to fill the following position starting 01.09.2025

Doctoral student (m/f/d) in Paleobotany

(Part time, 75%)

As part of the Emmy Noether Project "Spatial signal and bias in the fossil record of seed plants in the late Mesozoic" led by Dr. Mario Coiro, we are hiring a doctoral student (m/f/d) for a 30 month term contract with possibility of a 6 month extension.

The project aims to identify the geological and biological causes of the patterns observed in Jurassic and Cretaceous floras by combining spatially explicit data from the rock record with trait-based data from the plant fossil record, in order to fully disentangle the different causes of the apparent quasi-synchronous radiation of seed plants. This position will focus on estimating the variation in plant trait diversity at a global scale during the Jurassic-Cretaceous interval.

Your tasks

Study and photograph vegetative fossil specimens of gymnosperms from the collections of the Senckenberg networks as well as other collections around the world.Score traits from vegetative fossils of gymnosperms from the Jurassic and Cretaceous based on literature searches and direct observations.Quantify morphological variation through time and space using disparity measures.Disseminate results in scientific journals and international conferences.

Your Qualifications

Essential

Diploma or Masters degree in Botany, Biology, Paleontology, Paleobiology or a related discipline Knowledge of botany and plant anatomy Strong interest in trait-based analyses and macroevolution Good communication skills, in order to work in a highly collaborative and international environment Very good command of written and spoken English

Desirable

Good knowledge of the statistical programming language R Experience with vegetative fossils of seed plants, i.e. leaf venation and architecture Knowledge of cuticular anatomy and microscopy, including fluorescence and confocal microscopy

We offer

An attractive and challenging position in a motivated team Independent work in an international and professional environment The possibility to conduct a PhD thesis Flexible working hours - mobile working - Support with childcare or caring for family members (certified by the "audit berufundfamilie" (work and family audit) - Employee ID card with free admission to municipal museums - Annual bonus - Company pension plan

Location: Frankfurt Employment scope: Part Time (75%) Contract type: Limited until 28.02.2028 with the possibility of a 6 month extension

Compensation: E 13 TV-H / Collective agreement of the state Hesse

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.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.

Would you like to apply?

Please send us your complete and comprehensive application documents (cover letter, detailed CV, training and employment references) electronically (as a single PDF file) quoting reference #01-25029 by 11th of May 2025 to recruiting@senckenberg.de.

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt a.M. E-Mail: recruiting@senckenberg.de

For any job-related inquiries, Dr. Mario Coiro will be happy to assist you at mario.coiro@senckenberg.de.

For more information about the Senckenberg

Gesellschaft für Naturforschung, please visit www.senckenberg.de . Mit freundlichen Grüßen

Sabine Heinrichsohn

Referentin Recruiting/HR Department & Personalmarketing

Tel.: 069 7542 1309

Mail: recruiting@senckenberg.de

Sabine Heinrichsohn <recruiting@senckenberg.de>

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## Smithsonian InvertEvolution

Hello All, Please see below the announcement for a 10-week graduate student fellowship opportunity at the Smithsonian National Museum of Natural History.

The Robert D. Hevey, Jr. and Constance M. Filling Fellowship in Invertebrate Zoology

Applications due 28 April 2025 8 am EDT

The Robert D. Hevey, Jr. and Constance M. Filling Fellowship in Invertebrate Zoology was established to support short-term, resident, graduate student fellowships focused on invertebrate zoological studies in the Department of Invertebrate Zoology < https://naturalhistory.si.edu/research/invertebrate-zoology > at the National Museum of Natural History (NMNH) < https://naturalhistory.si.edu/ > in Washington, DC. Priority will be given to applicants who have not previously visited the NMNH.

Robert Hevey is currently pursuing a PhD in Plant Conservation Biology at Northwestern University and the Chicago Botanic Garden focused on tolerance ranges of native bush clovers. Previously, his nearly 40-year business career provided him a variety of opportunities ranging from public accounting to distribution, corporate restructuring, and inventory appraisals. Constance Filling, EdD, serves as the Chief Learning Officer at the American Association of Medical Colleges (AAMC). In this role, Constance Filling is responsible for building a highly effective learning unit with the goal of providing AAMC members the education, training, research, and clinical care models to succeed in newly emerging fields. Robert Hevey and Constance Filling established this short-term graduate student fellowship at NMNH to complement their suite of giving and to help contribute toward the training and inspiration of the next generation of natural history researchers.

Eligibility - You must be a currently enrolled graduate student. Fellowships are available to U.S. and non-U.S. citizens. Applicants must write and converse fluently in English. Awardees are expected to be resident in the Department of Invertebrate Zoology at Smithsonian's National Museum of Natural History in Washington, DC full-time and actively engaged in the NMNH community during the entire fellowship tenure. Fellows cannot hold any other position at the Smithsonian during the tenure of their fellowship. Fellowship tenure must be continuous and start within one year of notification.

Term - Ten weeks. Stipend - The ten-week fellowship includes a stipend, research funds, and relocation allowance for travel to/from Washington DC.

* Stipend: $10,000 * Research Allowance: $5,000 * Relocation Allowance: as appropriate for location To apply - Proposals for the Hevey/Filling Graduate Student Fellowship in Invertebrate Zoology should be submitted through SOLAA. Prior to preparing your application, you should identify an appropriate IZ Research Staff (Ellen Strong < https://naturalhistory.si.edu/staff/ellen-strong >, Chris Meyer < https://naturalhistory.si.edu/staff/christopher-meyer >, Karen Osborn < https://naturalhistory.si.edu/staff/karen-osborn >, Anna Phillips < https://naturalhistory.si.edu/staff/anna-j-phillips >, Andrea Quattrini < https://naturalhistory.si.edu/research/invertebrate-zoology/research/nmnh-coral-lab >, or John Pfeiffer < https://naturalhistory.si.edu/research/invertebrate-zoology/research/pfeiffer-lab >) and confirm with them that they are willing to serve as the advisor for your project.

>From SOLAA < http://solaa.si.edu/solaa/#/public >, click "start your application". Search for the frellowship program "NMNH Fellowships in Invertebrate Zoology". Upload only a CV and research proposal. The proposal should include: (1) an abstract, (2) a proposal narrative (max 4 pages, double spaced, 12 pt.) that details the purpose and significance of the project, methods to be used, rationale for use of the Smithsonian National Museum of Natural History Collections, (3) a budget for the $5000 research funds, and (4) a detailed timeline of activities with proposed start and end dates. Figures do not count toward the maximum number of pages. Start date must be after 21 July 2025. Two references letters should be requested through SOLAA.

Applicant proposals are reviewed to assess applicant's eligibility, whether the proposed research meets the highest intellectual and ethical

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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

## Southampton UK AccessoryGenome

Southampton_UK.AccessoryGenome

PhD opportunity to join the growing Microbiology community in Southampton, UK

Interested in how bacteria adapt to challenges like temperature changes and antibiotics? Join Nikolic lab at the University of Southampton to explore the role of accessory elements!

PhD Project: "Accessory Genomes and Evolutionary Strategies of Antibiotic-Resistant Bacteria"

How do bacteria respond so effectively to the myriad of environmental insults they face? This Project will investigate the flexibility of these resilient bacteria that is encoded in their 'accessory' genome, which can add novel functions to their core genome. Despite our advances in DNA sequencing technology, accessory elements still form the genetic 'dark matter' in bacteria as we know little about the functions of the genes they encode, making it difficult to develop control strategies against disease-causing bacteria.

This Project will investigate how accessory systems work, and how they re-route bacterial core regulatory networks enabling bacteria to survive in harsh conditions and endure antimicrobial treatments. The PhD student will have the opportunity to employ microbiology, molecular biology, time-lapse microscopy, microfluidics and flow cytometry alongside bioinformatics and genome analysis tools. The roles of accessory systems will be studied in a set of Escherichia coliantibiotic-resistant pathogenic strains. The specific research questions that will be addressed will range from 'How do accessory genetic systems help bacteria to respond so quickly to environmental changes?' to 'How do accessory systems control the development of stress-tolerant 3D-structures called biofilms?'.

The results of this Project will not only help us better understand how to successfully combat bacterial diseases but will also give us insights of how accessory elements supercharge bacteria to adapt to new environments, which is an increasingly important topic in light of the evolutionary pressure posed by pollution and climate change.

More details here https://tinyurl.com/PhDbacteriaUoS Apply here https://tinyurl.com/MicroUoS For initial discussions, email Nela: N.Nikolic@soton.ac.uk Starting date: September 2025

Nela Nikolic, PhD Lecturer in Microbiology Office 2056 School of Biological Sciences Life Sciences Building 85 University of Southampton SO17 1BJ

University Profile webpage Google Scholar ORCID

Please note, I may send emails out of core working hours, as this fits my own work-life balance. I do not expect a response outside of your own working hours.

Nela Nikolic <N.Nikolic@soton.ac.uk>

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

## StockholmU EvolutionaryGenomics

*PhD student position at Stockholm University*

We have an open 4-year PhD student position in Plant Evolutionary Genomics.

The PhD student will investigate the evolutionary drivers and genomic consequences of pollen evolution in association with shifts in pollination mode in flowering plants. The work will involve comparative genomic analyses in a phylogenetic framework, as well as population genomic and transcriptomic analyses in suitable plant systems.

For this position, we are looking for a highly motivated candidate with a strong interest and training in evolutionary genomics. Skills in coding and/or botany are beneficial but not required.

The complete ad with information on qualification requirements and instructions on how to apply is at: https://su.varbi.com/en/what:job/jobID:805144/where:4/ Application deadline: April 22, 2025

The PhD position is fully funded and is part of the large interdisciplinary project "Harnessing evolutionary transitions, machine learning, and genomics to decode pollen evolution and unravel sexual selection mechanisms shared across kingdoms" led by Prof. Tanja Slotte in close collaboration with co-investigators Prof. John Fitzpatrick, Prof. Catarina Rydin, and Dr. Allison Hsiang at Stockholm University.

The PhD student will join the research group of Prof. Tanja Slotte (http://tanjaslottelab.se) and will be enrolled in the research subject Ecology and Evolution at the Dept. of Ecology, Environment and Plant Sciences, Stockholm University. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both evolutionary geneticists, plant biologists, and ecologists. The city of Stockholm is known for its beauty, its buildings and architecture and its abundant clean and open water.

For informal inquiries about the position, please contact Tanja Slotte at tanja.slotte@su.se

Tanja Slotte Professor Department of Ecology, Environment and Plant Sciences (DEEP) Stockholm University 106 91 Stockholm Sweden

Lab website: tanjaslottelab.se

Tanja Slotte <Tanja.Slotte@scilifelab.se>

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## StockholmU PollenEvolution

*PhD student position at Stockholm University*

We are recruiting a fully funded 4-year PhD student position for a project on 'Using artificial-intelligence-based image analysis to determine how animals shape pollen evolution'.

The PhD student will develop AI-assisted tools for automated pollen image analyses and conduct macroevolutionary analyses of pollen evolution. A key aspect of this project will be to assess how shifts in pollination mode influence pollen evolution in flowering plants.

For this position, we are looking for a person with a strong interest and training in evolutionary biology. Skills/experience in AI-assisted analyses, phylogenetic analyses and programming are beneficial but not required. Experience in animal-plant interactions and/or experience working with gamete evolution is also a merit, but not required.

The PhD student will join the research group of Prof. John Fitzpatrick (https://sites.google.com/view/fitzpatrick-lab/home) at the Department of Zoology, Stockholm University, located in the city of Stockholm, Sweden. The Department of Zoology has an international working atmosphere, with researchers and students from across the world. The working language is English and the position offers plenty of opportunities for scientific exchange with evolutionary biologists and ecologists. Overseas applications are encouraged.

The PhD project is funded as part of a interdisciplinary project "Harnessing evolutionary transitions, machine learning, and genomics to decode pollen evolution and unravel sexual selection mechanisms shared across kingdoms" that will be done in close collaboration with co-investigators Dr. Allison Hsiang, Prof. Tanja Slotte, Prof. Catarina Rydin at Stockholm University.

The complete ad with information on qualification requirements and instructions on how to apply is at: https://su.varbi.com/en/what:job/jobID:805542/where:4/ Application deadline: April 22, 2025

For informal inquiries about the position, please contact John Fitzpatrick: john.fitzpatrick@zoologi.su.se

John Fitzpatrick Professor Department of Zoology Stockholm University 106 91 Stockholm Sweden

Lab website: https://sites.google.com/view/fitzpatrick-lab/home John Fitzpatrick <john.fitzpatrick@zoologi.su.se>

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## StockholmU Sweden EvolutionSeasonalCamouflage

Dear colleagues,

We have extended the deadline for this PhD position until *4 of May 2025*.

We are offering a fully funded PhD Position in Evolutionary Genomics of Seasonal Camouflage, at Stockholm University-

*Link to job application* https://su.varbi.com/en/what:job/jobID:805048/where:4/ *Contact* Mafalda Ferreira: mafalda.ferreira@zoologi.su.se

*Context* The project focus on characterizing phenotypic and genomic variation associated with seasonal camouflage variation in willow grouse (Lagopus lagopus). The analysis will combine state-of-the-art computer vision, modeling and archived specimens to determine biotic and abiotic factors driving spatial variation in molt phenology. It will use museum genomics to recover DNA from museum specimens and population genomics to study signatures of selection in populations with different mol phenology while accounting for demographic history. It will use comparative genomics to study the evolutionary history of molt phenology across related species of grouse. The project will also use functional genomics to study the regulatory mechanisms of molt phenology in grouse. The position will be associated with Assoc. Prof. Mafalda Ferreira's research group located at SciLifeLab (Solna) and the Department of Zoology, Stockholm University.

We are looking for candidates with a strong interest in evolutionary biology, ideally with experience in population and adaptation genomics. Prior training in bioinformatics, image processing with computer vision, molecular work (both modern or museum samples), fieldwork, and/or evolution and ecology of birds, camouflage or seasonal biology is a plus. Applicants should be motivated to learn, think critically, work in an international team and be well organized. Proficiency in English is required since this is the team's working language. Applicants should also hold a MSc degree (or equivalent qualification) in biology.

The position is based in Stockholm and at SciLifeLab (main location), and at the Department of Zoology, Stockholm University. The candidate will have the opportunity to be trained in evolutionary genomics, molecular genetics, bioinformatics, statistic, sampling and handling of museum collections. The position is mostly lab based, but includes opportunities for fieldwork and experimental work. The position is fully funded with social benefits and there is opportunity for teaching at a maximum of 20%.

Please apply by 4 of May 2024 follow the link to the official Stockholm University job portal: https://su.varbi.com/en/what:job/jobID:805048/where:4/

Applicants should right a strongly motivated cover letter including how their skills and interests align with the project.

Start date is negotiable but preferably within 2025.

Mafalda Ferreira, Ph.D. (she/her) Assistant Professor, SciLifeLab Fellow

Department of Zoology, SciLifeLab Stockholm University Tomtebodavägen 23A, Gamma 7 SE-171 65 Stockholm, Sweden mafalda.ferreira@zoologi.su.se seasonalgenomics.wordpress.com

Mafalda Ferreira <mafalda.ferreira@zoologi.su.se>

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## TrinityC Dublin PopulationGenetics

PhD Position in Population and Evolutionary Genetics at Trinity College Dublin Fully Funded for 4 Years - Project “ArchEvo”

A fully funded PhD position is available in the Population and Evolutionary Genetics group at the Smurfit Institute of Genetics, Trinity College Dublin, as part of the project “ArchEvo”, funded by Research Ireland. This position is for 4 years and offers an exciting opportunity to contribute to cutting-edge research in human evolution.

Project Overview:

The PhD student will work under the supervision of Dr. Marco Rosario Capodiferro and mentor Prof. Emilia Huerta-Sanchez. The project focuses on studying archaic introgression in ancient DNA (aDNA) from Eurasia and the Americas. The student will be responsible for imputing and analyzing aDNA data from the Americas, employing a recently developed method to investigate archaic introgression in ancient genomes. This research will be entirely bioinformatics-based, analyzing publicly available ancient genome data.

Qualifications and Requirements:

- A Bachelor's or Master's degree in Biology, Molecular Biology, Genetics, or a related field (minimum 2.1 or equivalent). - A high level of competence in the English language, demonstrated through one of the examination systems recognized by Trinity College Dublin. - Basic coding knowledge in Python, R, and Bash. - Prior experience in bioinformatics and genomic data analysis is desirable but not essential.

Funding and Salary:

- The position is fully funded with a salary of euro 25,000 per year. - Course-related fees will also be covered for EU and non-EU students. - 3-month research stay in Prof. Flora Jay's group at Université Paris-Saclay.

How to Apply: Interested candidates should send their CV, a cover letter, and contact details for two referees to marcorosario.capodiferro@gmail.com.

For more information on the Postgraduate program, please visit the Department of Genetics website < https://www.tcd.ie/Genetics/postgraduate/ > or contact the PI.

Application Deadline: Applications will be evaluated on a rolling basis until the position is filled.

Starting Date: September 2025.

Marco Rosario Capodiferro, Ph.D Huerta-Sanchez Lab

Smurfit Institute of Genetics Trinity College Dublin

Dublin 2, Ireland

Marco Rosario Capodiferro <marcorosario.capodiferro@gmail.com>

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## UAdeBarcelona BioinformaticsPopGenomics

PhD Opportunity in Bioinformatics & Population Genomics - FI-STEP Fellowship

The Bioinformatics of Genome Diversity group at Institute of Biotechnology and Biomedicine (UAB) is seeking a PhD candidate interested in applying for an FI-STEP fellowship funded by AGAUR. We are looking for a motivated student with a strong academic background in bioinformatics and genomics to join our team.

Project Description The selected candidate will join the PopLife project, a novel genomic browser designed to integrate large-scale population genomic datasets from diverse species. PopLife aims to facilitate comparative and meta-analyses of genome-wide variation, enabling the exploration of patterns of genomic diversity, adaptation, and evolutionary dynamics across species. By joining this project, the PhD candidate will work at the intersection of bioinformatics and evolutionary genomics, contributing to the development of computational methods and the analysis of big-data in genomics.

Eligibility Requirements European citizenship Bachelor's degree in sciences Enrolled in or completed a Master's program that allows for 300 ECTS credits Academic record with average grade >8.5

Key DATES Deadline for contacting us: April 4, 2025 Start date: No later than November 1, 2025

The Bioinformatics of Genome Diversity group is a Consolidated Group funded by AGAUR, offering a dynamic and interdisciplinary research environment.

APPLY NOW: Contact SÃ²nia Casillas at sonia.casillas@uab.cat until April 4, 2025

SÃ²nia Casillas Viladerrams <Sonia.Casillas@uab.cat>

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## UAuckland PlantMicrobePollinatorInteractions

PhD Scholarship - Ecology & Evolution of interactions between floral microbes, pollinators and plant reproductive fitness Supervisors:Dr Manpreet Dhami and Professor Jacqueline Beggs Closing date:15/05/2025 Location:Manaaki Whenua Landcare Research in Lincoln, New Zealand. Start date: Immediately, upon enrollment via the University of Auckland Background:Flower-associated microbes can alter the pollination success of the plant, by modifying nectar composition and chemistry. This project is focused on understanding how certain microbes may alter the nectar chemistry of Kowhai (Sophora spp.) flower nectar. Kowhai flowers produce a large volume of nectar, which is an especially important resource for birds and insects. We have identified the key microbes that dominate Kowhai nectar. But it remains unknown whether these microbes have any impact on the production of nectar, its quality in the flowers and its consumption by pollinators. Project scope:The student will develop questions investigating the role of floral microbes in shifting the value of Kowhai nectar resources to potential pollinators and whether this affects the reproductive fitness of Kowhai trees. The student will develop new understanding of these multi-partite interactions to contribute to the growing body of research on the ecology and evolution of the role microorganisms play in mediating pollination. Qualifications & skills:The applicant should hold a first class honours degree, or Masters in Biological Sciences or Microbiology, with a strong background in Ecology or Evolutionary Biology. The applicant should have skills in microbiology, ecology, biochemistry, statistics and competent with the use of R and other analytical environments. The candidate satisfies the PhD enrolment requirements as described here: https://www.auckland.ac.nz/en/-study/applications-and-admissions/apply-now.html Personnel specifications:The applicant should be curious, self-driven and able to work effectively independently and in a team environment. The applicant is able to disseminate their research in written and spoken English, effectively and communicate with others well. Proven ability to conduct and publish research, experience with field work and/or lab work, sterile methods or basic molecular methods (DNA extraction, PCR, genome resequencing) are desirable. The applicant will work collaboratively with scientists, technicians, postdocs and While this position is open to international applicants, preference will be given to candidates already residing in NZ with valid permission to work or study. Stipend:Tax-free stipend of NZ$35,000 per annum for 3 years and PhD fees are covered. Additional support towards research operating expenses available. How to apply:Applications should include evidence of qualifications and research experience, together with a curriculum vitae and contact details of two academic referees who can be contacted. Applications should be supported by a cover letter that states a) why you are interested in continuing your studies to obtain a PhD; b) what specific aspects of this particular PhD attracted you; c) how your qualifications and experience would map onto the proposed research; and d) your GPE as calculated here: https://www.gpecalculator.auckland.ac.nz/. Please email complete applications to dhamim@landcareresearch.co.nz before 15th May 2025. Preferred candidates would then need to apply to study at the University of Auckland and meet the institutional criteria for entry prior to the scholarship being confirmed. Contact:All enquiries may be directed to Manpreet Dhami dhamim@landcareresearch.co.nz

Manpreet Dhami

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## UBasel SpeciationInTheAfricanGreatLakes

The research group of Dr. Jeremias Brand at the Department of Environmental Sciences at the University of Basel is offering a fully funded 4-year PhD position to explore a recently discovered radiation of Macrostomum flatworms in the African Great Lakes region.

Project description Adaptive radiations characterized by rapid speciation and remarkable morphological diversity are key drivers of biodiversity on our planet. Ecological opportunities such as the colonization of new environments like islands or lakes often trigger adaptive radiations. Yet a fundamental question remains unanswered: Why do some lineages radiate while closely related ones do not? This project investigates this evolutionary puzzle by studying the newly discovered Macrostomum flatworm radiation in the African Great Lakes. While cichlid fishes in these lakes represent one of biology's most celebrated examples of an adaptive radiation, we have recently uncovered evidence that tiny flatworms have undergone a parallel but independent radiation in the same waters. This provides a unique opportunity to compare two different animal groups that evolved in the same environment but with fundamentally different biology.

The project brings together two complementary research areas: 1. Speciation Research Conduct fieldwork along lake shores in Zambia and Tanzania to collect flatworm samples Use phylogenetic and population genetic approaches to study speciation patterns Identify and describe new species, contributing to biodiversity research Investigate the role of two contrasting mating systems on speciation rates

2. Meiofauna Ecology Study the role of Macrostomum flatworms in sediment ecosystems Use stable isotope analysis to explore their position in the food web Examine morphological and behavioral adaptations to sediment environments using phalloidin staining and confocal microscopy Analyze population structures to understand biodiversity patterns This project represents the first investigation of an adaptive radiation in free-living flatworms and will substantially contribute to understanding why speciation occurs in certain lineages but not others. We will directly compare the Macrostomum radiation with the extensively studied cichlid radiation, thus disentangling taxon-specific from general factors.

Position Details

Full-time (100%) PhD position with a salary of 47,040-55,000 CHF per year Funding secured for 4 years via a competitive Swiss National Science Foundation Ambizione grant awarded to Dr. Jeremias Brand.

Training in evolutionary biology, phylogenetics, and molecular techniques Field research in East Africa, with the opportunity to contribute to fundamental questions in biodiversity science Dynamic research environment in Basel, with connections to the Biozentrum, ETH Zurich, and the Swiss Institute of Bioinformatics Regular seminars with international researchers Candidate Profile Essential Requirements

MSc in Biology, Evolutionary Biology, Ecology, or a related field Fluency in spoken and written English Strong motivation to develop as a scientist Willingness to conduct regular multi-week field expeditions in East Africa

Preferred Experience

Knowledge of evolutionary biology concepts Experience with phylogenetics or genomics Familiarity with stable isotope analysis Experience with confocal microscopy or automated image analysis Previous fieldwork experience National and international collaborations

Natural History Museum London: Dr. Chris Laumer for nanopore sequencing-based molecular analyses

University of Basel: Prof. Walter Salzburger for field work and comparative studies with cichlid fish radiations and Prof. Moritz Lehmann for stable isotope analysis

University of Dar es Salaam: Field work, training, and knowledge dissemination

Location Basel is a vibrant academic city at the border of Switzerland, Germany, and France. It offers an excellent quality of life and strong international connections. The University of Basel, founded in 1460, is Switzerland's oldest university and is consistently ranked among the world's top institutions for research.

Commitment to Diversity We are committed to fostering diversity in science and encourage applications from underrepresented groups and candidates from developing countries.

Application Process Please submit the following documents to jeremias.brand@unibas.ch:

CV One-page cover letter explaining your motivation and relevant experience Two reference letters Application Deadline: May 31, 2025 Starting Date: September 1, 2025 For further inquiries, contact Dr. Jeremias Brand at jeremias.brand@unibas.ch and see the group website at: https://jeremias-brand.github.io/

Jeremias Brand <jeremias.brand@unibas.ch>

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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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## UEdinburgh OnlineBreedingAndGenetics

Dear colleagues (apologies for any double-posting),

We are excited to announce the launch of our new postgraduate online programme in Data-Driven Breeding and Genetics, set to begin in September 2025. This programme is led by academics from The Roslin Institute and the Division of Global Agriculture and Food Systems at the University of Edinburgh.

Our programme is part-time and thus offers flexible learning paths, from individual credit-bearing PPD courses a full MSc, catering to the diverse needs of professionals seeking to upskill in the field without having to leave their current positions.

Full information on the programme and how to apply is available here: edin.ac/pgt-data-driven-breeding-genetics

We would appreciate if you could help us disseminate this information to those that might benefit from it.

For enquiries, you can reach us at DDBG@ed.ac.uk

In brief:

This is a globally-unique online programme that will train the next generation of breeders and geneticists in the statistical and computational skills to design and implement sustainable genetic improvement programmes for key aquacultural and agricultural animal and plant species across global food systems, raw material, heat, and power production.

The programme will equip graduates with practical, applied statistical and computational skills to manage, analyse and interpret large, real-world data and address context-specific genetic challenges using specialised skills in genetics, data science, and underpinning technologies.

By bringing together animal and plant species, this programme opens-up career prospects.

By engaging with colleagues in industry and institutions such as ILRI and CTLGH, the programme will give a diverse range of global perspectives and representation of systems across Global North and South and prepare students with key transferable skills valued by employers.

Graduates from this programme will be equipped to address the shortage of data scientists in the Agri-Tech sector globally and locally, strengthening the pipeline into industry research and development, academia, governmental and non-governmental organisations (GOs and NGOs) amongst others, and will serve as advocates for the importance of coordinated international efforts in tackling global challenges equitably.

Thank you very much for your support with dissemination. Pau

Pau Navarro, PhD, SFHEA My pronouns are she/her Senior Lecturer in Quantitative Genetics and Group Leader Data-Driven Breeding and Genetics programme director The Roslin Institute and the Division of Global Agriculture and Food Systems, University of Edinburgh

The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336. Is e buidheann carthannais a th' ann an Oilthigh Dh?n ?ideann, cl?raichte an Alba, ?ireamh cl?raidh SC005336.

Pau Navarro <Pau.Navarro@ed.ac.uk>

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## UExeter EvolAnimalBehaviour

APPLICATIONS OPEN FOR MSC IN ANIMAL BEHAVIOUR

Applications are now open for the September 2025 student cohort on the MSc programme in Animal Behaviour at the University of Exeter UK!

The MSc programme is designed to provide students with a strong background in a broad cross-section of theory and research methods used in the study of animal behaviour, animal cognition and behavioural ecology. The programme gives students the opportunity to advance and expand their knowledge in the field of animal behaviour and gain expertise in the research and statistical methods generally used in Psychology, Biology and related sciences. Students learn how to formulate and test relevant research questions, as well as critically evaluate research published by others. The programme enables students to get an insight into the varied means of doing animal behaviour research in a wide array of locations: zoo, laboratory and in the wild.

The teaching and learning methods are a mix of lectures, seminars, practicals and field courses. Overall there is a strong practical and demonstration element to the programme, using innovative teaching practices.

The Department of Psychology at Exeter has a long tradition of interdisciplinary teaching and research in animal behaviour, and offers PhD degrees in animal behaviour in addition to this MSc.

The full-time MSc is a 12-month course starting in September. The programme is also offered for part-time study over 2 years.

For more information, visit our web site for prospective postgraduate students: https://www.exeter.ac.uk/study/postgraduate/courses/psychology/animal/ If you have specific questions on the MSc course not covered in the information available on these pages, or enquiries about your own qualifications, please feel welcome to contact the Course Director, Dr Andy Higginson (A.Higginson@exeter.ac.uk).

Dr Tim W. Fawcett Room 235 Centre for Research in Animal Behaviour Washington Singer Laboratories University of Exeter Exeter EX4 4QG United Kingdom

+44 1392 725273 (office)

tim.fawcett@cantab.net

www.timwfawcett.com Tim Fawcett <tim.fawcett@cantab.net>

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## UFreiburg Germany ForestAdaptation

MSc program in "Forest Ecology Research" at the University Freiburg, Germany

Forests are highly diverse ecosystems that provide habitat for a wide range of organisms, recreation for people, timber and other resources, and carbon sinks. At the same time, they are challenged by rapid climate change, emerging pests and diseases, and other anthropogenic impacts. While forests are under threat, there is a shortage of scientists specifically trained to use modern methods to study organismal interactions in these ecosystems. They are currently being sought in university and non-university research to help understand how our forests can respond to these challenges. In the MSc Program "Forest Ecology Research" at the University Freiburg, Germany, students will learn state-of-the-art research techniques to address pressing questions in forest ecosystems - from elucidating the interactions between trees and their biotic and abiotic environment, to incorporating all scales from the molecular to the landscape level.

What to expect

- Deep insights into the interactions between plants, micro- organisms and animals in forests

- Applied research training experiences; regular in collaboration with other leading forest research institutes

- Field and laboratory research, using modern microbiological, chemo- ecological, behavioral and molecular techniques, and data analyses

- Acquire skills relevant for working as an internationally visible researcher

Target group of students & career opportunities

Students with a BSc in Life or Natural Sciences (e.g. Biology, Forestry, Environmental Sciences, Ecology) who are interested in learning research approaches and methods specifically aimed at understanding organismal interactions in forest ecosystems and developing methods to investigate future challenges facing forests. Training for future research careers in universities, non-university research institutes, national parks and government departments.

For more details and application until May 15th see https://www.msc-forst.uni-freiburg.de/de/forest-ecology-research

peter.biedermann@forento.uni-freiburg.de

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## UGroningen AdaptiveSocialFlexibility

Adaptive social flexibility ï¿½“ a powerful mechanism to cope with a rapidly changing world

Job description

The Groningen Institute for Evolutionary Life Sciences (GELIFES) offers a 4-year NWO-funded PhD position for a project on “Adaptive social flexibility ï¿½” a powerful mechanism to cope with a rapidly changing world”, with the Seychelles warbler (Acrocephalus sechellensis) as a model system.

The project is coordinated by Prof. Jan Komdeur (see: https://research.rug.nl/en/persons/jan-komdeur), in collaboration with Prof. Martijn Egas <https://research.rug.nl/en/persons/martijn-egas)and> and Prof. Hannah L. Dugdale (University of Groningen, see < https://research.rug.nl/en/persons/hannah-dugdale >, Prof. David S. Richardson (University of East Anglia, UK, see: < https://research-portal.uea.ac.uk/en/persons/david-richardson-2 > and Prof. Terry Burke (University of Sheffield, UK, see: < https://www.sheffield.ac.uk/biosciences/people/academic-staff/terry-burke >. The student will join a lively and highly international team of post-doctoral researchers, PhD and master students working on the evolution of social behaviours and life history patterns in social animals, supported by laboratory technicians.

Especially now, in this era of rapid climate change, organisms need to adapt to reduced and unpredictable food availability. We argue that such adaptive flexibility may be facilitated by sociality, whereby animals form groups and cooperate on tasks that affect survival and reproduction (cf cooperative breeding). This project will investigate whether âflexibility’, i.e. the capacity of individuals to flexibly change from solitary breeding to cooperative breeding and vice versa throughout their lifetime, is a fast and potent adaptation mechanism that provides fitness benefits to individuals and buffers populations against decline and extinction in times of environmental deterioration. We will identify when and how environmental change elicits changes in social life and how this in turn affects the capacity to cope with environmental variation and change, which has not been tested.

Our long-term study of the facultatively cooperative Seychelles warblers (SW) on Cousin Island, Seychelles, provides a uniquely suitable natural system in which to investigate this question. SWs can breed as solitary dominant pairs, but can also form breeding groups with subordinates that may or may not breed cooperatively. Hence, the SW system is a rare instance where we can study the causes and consequences of social behaviour at the individual and group levels simultaneously. They inhabit an environment where food availability ï¿½“ which shows considerable spatio-temporal variation ï¿½” has become more erratic and unpredictable over the last couple of decades, apparently linked to changing local and global climatic conditions. Using >38 years of data our project will investigate the impact of food availability on life histories. We hypothesise that observed adjustments in social behaviour are strategic and enhance individual fitness, and consequently improve group persistence. Our project comprises three integrated and complementary work packages: First, we will investigate whether individuals react to environmental change (change in food availability and fluctuations) by forming groups and cooperating with each other. Second, we will test if this cooperation facilitates adaptation to extreme and unpredictable change (long-term dataset, experiments and three seasons of fieldwork on SWs). Then, we will use demographic models ï¿½“ tailored to SWs, but applicable to other species - to investigate the long-term implications of rapid environmental change on the population dynamics of social species.

Organisation Founded in 1614, the University of Groningen enjoys an international reputation as a dynamic and innovative institution of higher education offering high-quality teaching and research. Flexible study programmes and academic career opportunities in a wide variety of disciplines encourage the 34,000 students and researchers alike to develop their own individual talents. As one of the best research universities in Europe, the University of Groningen has joined forces with other top universities and networks worldwide to become a truly global centre of knowledge.

Qualifications

We are looking for an enthusiastic and talented PhD candidate with a Master's degree (or equivalent) in Biology with a strong interest

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## UJagiellonian Cracow 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), goodcommunication 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

Two PhDï¿½ positions are available in the university of Lille (France), in Evo-Eco-Paleo lab. PhD will start onï¿½ Oct. 2025 for a duration of 3 years.

- the first subject < https://eep.univ-lille.fr/wp-content/uploads/2025/02/PhD_advert_eep_TOUZET_SeCSSi_2025.pdf > concerns the implication of sex chromosomes in reproductive isolation inï¿½ the otites section of Silene.

- the second subject < https://eep.univ-lille.fr/wp-content/uploads/2025/02/PhD_advert_EEP_UGSF_Touzet_Cenci_PIE.pdf > concerns the study of cytonuclear genetic incompatibilities in Silene nutans.

The deadline to apply is April 21rst 2025. Interviews will occur in the first week of May 2025.

Best regards, Pascal Touzet

Pascal Touzet Professor Evo-Eco-Paleo, Univ. Lille, UMR-CNRS 8198 tel: 03-20-43-40-32 https://eep.univ-lille.fr/ Pascal Touzet <pascal.touzet@univ-lille.fr>

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## UMelbourne Phylogeography

We are seeking a suitably qualified student for a fully funded PhD scholarship based in Melbourne, Australia, to study “Genetic Variation and Comparative Phylogeography of Warm Temperate Rainforest Species in Southeastern Australia,” a joint project between the University of Melbourne and the Royal Botanic Gardens Victoria.

See also: https://plantsystematicsblog.wordpress.com/jim-ross-phd-studentship-2/ About the Project We are seeking a PhD student to study genetic variation and phylogeography of selected Warm Temperate Rainforest (WTR) species in southeastern (SE) Australia. The project will focus on understanding the biogeography, phylogeography and conservation genetics of key species, such as Syzygium smithii, Acronychia oblongifolia, Notelaea venosa, Cissus hypoglauca, or other taxa with appropriate WTR distributions in SE Australia.

This research aims to uncover how genetic diversity in these species is distributed across the landscape, identify which populations harbour most genetic variation, and explore historical processes that have shaped this diversity. This will assist understanding the history and connections of now fragmented WTR areas in SE Australia and provide insight into conserving WTR species, and also preserving the biodiversity of Australia’s unique Warm Temperate Rainforest ecosystems.

About the studentship The student will be enrolled at The University of Melbourne and supervised by Dr Mike Bayly (School of BioSciences), Dr Dan Murphy (Royal Botanic Gardens Victoria) and Prof. David Cantrill (Royal Botanic Gardens Victoria).

This studentship is supported by the Cybec Foundation, and honours Jim H. Ross, former Chief Botanist of the National Herbarium of Victoria. It includes a scholarship of A$38.5K per annum (increasing to A$42K in the final year) and funds to support research and fieldwork costs.

The studentship will be offered on a competitive basis, and applicants will be judged on academic merit, research experience and research performance. Candidates must be eligible to enrol in a PhD at The University Melbourne, should have a strong background in genetics, biogeography, systematics, or a related field, and an Honours or Masters degree with a grade of H1 (>80%).

Experience with field-work, molecular techniques and bioinformatics will be highly regarded. This is an exciting opportunity to contribute to cutting-edge research in plant conservation genetics and phylogeography.

The successful applicant must be able to commence in 2025. The application deadline is May 4 2025. Interested candidates should contact Mike (mbayly@unimelb.edu.au) or Dan (Daniel.Murphy@rbg.vic.gov.au), and include a CV and summary of their academic and research experience.

Daniel Murphy Senior Research Scientist (Molecular Systematics) Research Royal Botanic Gardens Victoria Birdwood Avenue Melbourne Victoria 3004

T +61 3 9252 2377 Daniel.Murphy@rbg.vic.gov.au

rbg.vic.gov.au

Daniel.Murphy@rbg.vic.gov.au

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## UMemphis BearAdaptation

The Puckett Lab in the Department of Biological Sciences at the University of Memphis is recruiting a highly motivated student for a PhD position in Evolutionary Genomics. The Puckett Lab utilizes population and comparative genomics to understand the evolutionary history of bears with a particular emphasis on translating work for conservation and management decision makers. The successful applicant will contribute towards projects on the genomic basis of adaptive traits in bears. Specifically, the project will utilize comparative transcriptomics to investigate tissue-specific gene regulation.

Required Qualifications: Academic interests in evolution, genetics/genomics, and/or bioinformatics. Candidates should be organized, persistent, a team-player, and have strong writing skills. Availability to begin graduate school in August 2025.

Preferred Qualifications: A Master's degree, 2 years work experience, or a post-bac. Experience analyzing transcriptomic data. Experience working within Unix/Linux or a programming language (R, perl, python, etc).

Students will receive five years of stipend support via TA-ships and tuition waivers. To learn more about the graduate program and intellectual community within the department, visit: http://www.memphis.edu/biology/ Due to funding constraints, this position is only open to US applicants.

Please email Emily Puckett (Emily.Puckett@memphis.edu) with application materials (person statement including relevant experience and future goals, CV, and contact information for two references) as a single pdf. Applications will be reviewed on a rolling basis until May 28, 2025 for entrance to the program in Fall/August 2025. The successful applicant will then be asked to fill out the formal University of Memphis application.

Emily E. Puckett, PhD University of Memphis Memphis, TN 38152 https://puckettresearch.org/ Emily.Puckett@memphis.edu

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## Uppsala HostUseTropicalButterflies

A PhD 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 centers around understanding how species interactions change over time and space, with a focus on 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.

The aim of this PhD position is to develop a novel phylogenetic approach to predict unknown species interactions. For that, the student will compile all available data on host use for Nymphalinae butterflies, apply recent methods to predict interactions, and test these predictions by rearing caterpillars of various butterfly species on the predicted host plants. The project will result in a pipeline for faster collection of interaction data and the generation of valuable new data on tropical species.

The PhD position is fully funded by an ERC Starting Grant (project SPECTRO: Causes and consequences of higher host specialisation in the tropics - the role of ecological and evolutionary processes, and of data bias), and the successful applicant will work in the Evonets lab (evonetslab.github.io)

The successful candidate will be based in Uppsala but expected to spend extended periods in Brazil for field and lab work over four years.

Fluency in English is essential as it is the team's common language. The candidate should be proactive, independent, solution-oriented, and adaptable in solving technical problems. Strong collaborative skills, excellent communication, goodwill, and reliability are required, as the role involves close teamwork.

Read more about the position and how to apply here https://www.slu.se/en/about-slu/work-at-slu/jobs-vacancies/?rmpage=job&rmjob=12583&rmlang=UK Please submit your application by April 30, 2025.

For informal enquiries about the position, please contact me at mariana.braga@slu.se.

Mariana P. Braga, Ph.D.

Associate Senior Lecturer Data-Driven Life Sciences Fellow Department of Ecology Swedish University of Agricultural Sciences SciLifeLab Uppsala - Sweden

Mariana P Braga <mpiresbr@gmail.com>

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## UppsalaU MolecularEvolution

PhD student in Molecular Evolution

Are you interested in working with molecular data, with the support of competent and friendly colleagues in an international environment? Are you looking for an employer that invests in sustainable employeeship and offers safe, favourable working conditions? We welcome you to apply for a PhD position at Uppsala University.

The Department of Cell and Molecular Biology is divided into seven research programs, each focusing on different areas within cell and molecular biology: computational biology and bioinformatics, microbiology and immunology, molecular biology, molecular biophysics, molecular evolution, molecular systems biology, and structural biology. The scientific foundation of what we do lies in biology, but our research overlaps with other fields such as medicine, computer science, mathematics, chemistry, engineering, and physics. The department has over 200 employees, including around 60 doctoral students. Please read more about our work at https://icm.uu.se. The position is placed in the Molecular Evolution program, with main supervisor Jennifer James

Project Description This PhD position will be entirely computational, focusing on the large-scale bioinformatic analysis of proteome data from a wide range of existing species. The research will focus on understanding mutational robustness. Mutational robustness is the capacity of individuals within populations to express similar phenotypes despite the existence of underlying genetic variation. The project will uncover how mutational robustness relates to phenotypic diversity, and whether mutational robustness promotes evolvability. The project could also expand in scope to the consideration of DNA data. Further specific projects will be developed collaboratively with the successful candidate, depending on their project findings and research interests.

Duties At the start of the project, the successful candidate will create a protein dataset collaboratively with other group members, collecting amino acid sequence data from across multiple fully sequenced genomes. The student will conduct a variety of measures of protein phenotypic diversity, in the form of variation in protein structure and function, using simple measures such as overall hydrophobicity, in addition to modern protein structural prediction techniques.

The student will then be responsible for estimating measures of mutational robustness. These measures could include the relative proportion of amino acid changing mutations per codon, and the proportion of changes that result in a radical versus conservative amino acid change, i.e., what proportion of mutations will lead to an exchange between dissimilar amino acids as opposed to similar amino acids.

To investigate the relationship between phenotypic diversity and mutational robustness, the student will conduct a variety of statistical analyses. Further projects could include assessing whether adaptive substitution rates relate to degree of mutational robustness, and whether levels of genetic diversity relate to levels of phenotypic diversity.

Requirements

To meet the entry requirements for doctoral studies, you must: - hold a Master's (second-cycle) degree in a field of biology, or - have completed at least 240 credits in higher education, with at least 60 credits at Master's level including an independent project worth at least 15 credits, or - have acquired substantially equivalent knowledge in some other way.

Candidates must be able to express themselves fluently in spoken and written English. The applicant should have a strong grasp of key concepts in evolutionary biology. The applicant should also have an interest in learning, or previous experience in, computer programming, particularly using languages such as Python. The ideal candidate is driven and a creative thinker, with a passion for discovery. We are looking for a person with excellent communication skills who will thrive in a collaborative environment but is also able to work on their own initiative. We're excited to support you in developing your skills and following your scientific interests.

Additional qualifications Prior experience in computational biology, bioinformatics or generally in computer programming is desirable. Experience working in population genetics and evolutionary biology/genomics or proteomics is also desirable. Experience with statistical analyses will be considered advantageous. Rules governing PhD students are set out in the Higher Education Ordinance chapter 5, çç 1-7 and in Uppsala University's rules and guidelines.

About the employment The employment is a temporary position according to the Higher Education Ordinance chapter 5 ç 7. Scope of employment 100%. Starting date 2025-05-05 or as agreed. Placement: Uppsala

For further information about the position, please contact: Jennifer James, jennifer.james@icm.uu.se.

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## URegensburg InfectionBeeBehaviour

PhD candidate (m/w/d) in behavioural physiology and infection ecology of bumblebees

The BEE Lab at the University of Regensburg (Germany) studies the behavioural and evolutionary ecology of social insects, with a special focus on bee health. As part of a DFG-funded project titled 'Sublethal Effects of an Emerging Infectious Disease on Foraging Efficiency in Bumblebees,' we are seeking a highly motivated PhD candidate (salary: 65% TV-L E13, fixed-term for 3 years, WissZeitVG), starting in July 2025 or soon thereafter. The PhD candidate will study the impact of an emerging viral infection on the foraging efficiency of bumblebees, combining classical physiology with cutting-edge behavioural experiments.

Your Responsibilities:

- Conducting and detailed analysis of infection experiments with bumblebees - Designing, conducting, and analysing sophisticated behavioural experiments to investigate interactions between bumblebees and their environment - Applying classical physiological methods and conducting molecular analyses - Active collaboration with interdisciplinary and international research groups within the University of Regensburg (Prof. Dr. Lena Wilfert) and with external cooperation partners (Prof. Dr. Robert Paxton at MLU Halle and Prof. Dr. Tom Wenseleers at KU Leuven) - Presenting research results at national and international scientific conferences - Contributing to the preparation of scientific publications in renowned journals

Requirements:

- Completed master's degree (or equivalent) in biology or a related discipline - Solid knowledge and practical experience in statistical modelling (R and/or Python), molecular biology, virology, animal physiology, and/or behavioural ecology are advantageous - Ideally, experience with laboratory experiments on insects, especially bees - High motivation to conduct and further develop behavioural and physiological experiments on bumblebees - Excellent communication skills in English (written and spoken) - Ability to work independently and as part of a team in a dynamic research environment

We Offer:

- Scientific qualification (doctorate/PhD) - Access to a modern infrastructure with excellent laboratory equipment - An inspiring, interdisciplinary research environment at the Institute for Zoology & Evolution (new chair: Prof. Dr. Lena Wilfert) and at the Faculty of Biology and Preclinical Medicine - The opportunity to present and publish your research results at international conferences and in renowned journals - Support for developing your scientific career, both at the Chair of Zoology & Evolutionary Biology and through the Regensburg International Graduate School of Life Sciences (RIGeL, https://www.rigel-regensburg.de, section Molecular Ecology & Evolution), with additional opportunities such as workshops and annual summer schools.

The University of Regensburg aims to increase the proportion of women and therefore explicitly encourages qualified women to apply. The University of Regensburg is particularly committed to reconciling family and work (further information at http://www.uni-regensburg.de/chancengleichheit). In the case of essentially equal suitability, severely disabled applicants will be given preferential consideration. Please indicate any existing severe disability in your application.

Please note that we cannot cover any costs incurred by you for a potential interview. If you have any questions, please contact Dr. Christoph Kurze (email: christoph.kurze@biologie.uni-regensburg.de).

We look forward to receiving your application in English with the usual documents: (I) cover letter/letter of motivation (1-2 pages), (II) short CV with copies of relevant academic degrees, and (III) letters of recommendation or contact details of 2-3 references.

Please send the documents in a single PDF file by April 30, 2025, via email to christoph.kurze@biologie.uni-regensburg.de with the subject: PhD position SEED-FEB.

Christoph <christoph.kurze@ur.de>

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## UStrasbourg TurtleEvolution

bonjour,

We are seeking a keen and motivated applicant to the forthcoming entrance exam (concours) of the Doctoral School ED414 at the University of Strasbourg, France on the PhD project entitled Comparative behavioral ecology and ecophysiology of the European pond turtle Emys orbicularis along a latitudinal gradient.

The PhD will be hosted by Institut Pluridisciplinaire Hubert Curien(IPHC, UMR7178 CNRS-Université de Strasbourg, France,https://iphc.cnrs.fr), as part of the Biodiversa+ funded Emys-R project (https://emysr.cnrs.fr/) and the Long-term Studies in Ecology and Evolution (SEE-Life) program of the CNRS on Neu-Woerr.

The applicants are invited to contact the PhD supervisor (Jean-Yves Georges,jean-yves.georges@iphc.cnrs.fr)before 14 April 2025. Applications should include a detailed CV, marks, scores and ranks during the Master degree(s) and a motivation letter that clearly shows the match between the candidate's expertise and the goals and needs of the project.

Full details about the proposed research and application procedure can be found below.

We would be grateful if you could circulate this announcement widely to likely candidates within your networks.

Thank you in advance, Best wishes,

JYGeorges

§§§§§§DrJean-Yves Georges (.-.¾Ñ€¶)

IPHC UMR7178 CNRS UniStra 23 rue du loess, Building 60 67087 Strasbourg France +33 388 107 459 / 619 675 175

DR2 CNRS

https://emysr.cnrs.fr/ https://iphc.cnrs.fr/en/professional-pages/jean-yves-georges/ last publications Nekrasova et al. (2025)Ensemble modelling for smart conservation strategies.Geography and Sustainability, 100266.https://doi.org/10.1016/j.geosus.2025.100266 Meinard Y & Georges JY (2024)Frontiers of conservation.Conservation Biology, e14432. https://

doi.org/10.1111/cobi.14432 Standing with Ukraine ≫º²º£o̲Ñ€ºÑ½Ñ!

20 days in Mariupol https://archive.org/details/youtube-gvAyykRvPBo let's let go https://youtu.be/1VCQDoYop64?si=SBa9HCDDF1P9mfnD 1000 days together with Ukraine https://www.youtube.com/watch?v=TJxgOU1tx_A Jean-Yves Georges <jean-yves.georges@iphc.cnrs.fr>

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## UVienna Austria PlantGenomics

PhD position in Plant Ecological Genomics University of Vienna, Austria

We invite applications for a PhD position in Plant Ecological Genomics at the University of Vienna, Austria. The position is part of an international research project co-funded by the Austrian Science Foundation (FWF) and the French National Research Agency (ANR), aimed at gaining novel insights into the accumulation of reproductive barriers in radiated versus non-radiated plant lineages. The PhD student will be integrated in the Vienna Doctoral School of Ecology and Evolution (https://vds-ecology-evolution.univie.ac.at/).

***The project. The PhD research will focus on the genomic drivers underlying the diversification of a highly speciose North and Central American group of Tillandsia subg. Tillandsia, compared to a slowly-radiating group within the same subgenus, found in the ancestral area of South America. The potential causal factors that will be investigated will include gene family evolution, transposable element polymorphism, signatures of selection (e.g., selective sweeps), patterns of non-synonymous variation, and heterogeneity in recombination rates along the genome. Previous findings in a handful of species indicate that the radiated clade exhibits increased dynamics of gene gain/loss, including some related to ecological adaptation. However, the role of structural variants in driving diversification remains to be rigorously evaluated, in particular against the non-radiated relatives. The results can be integrated in the general context of plant adaptive radiation, in line with ongoing projects in other plant systems in our group. Further reading: https://doi.org/10.1093/plcell/koae130; https://doi.org/10.1101/2023.11.16.567341; https://doi.org/10.1111/pce.13847; https://doi.org/10.1101/2024.05.09.593278 ***Your profile. We are looking for a highly motivated candidate with - a MSc degree (or equivalent) in evolutionary biology, genomics, bioinformatics, plant biology or a related field; - a strong interest in evolutionary genomics and ecological adaptation; - good data analyses skills and programming knowledge (R, Phyton or bash); - teamwork, communication and problem-solving abilities; - proficiency in English (working language of the lab); knowledge of Spanish or French will be a plus for the activities within the project.

***What we offer. The PhD position provides an exciting opportunity to gain broad experience working at the interface of population, comparative and ecological genomics within an international team, including Ovidiu Paun (University of Vienna), Camille Roux and Christelle Fraisse (University of Lille, France) and Thibault Leroy (INRAE Toulouse, France), and will include short visits within the network. The position is available for 3 years with a potential extension depending on future funding. The salary will follow FWF rates (currently ca euro 39,000 per year before Tax) for a 30h/week employment. The contract includes health insurance and 5 weeks of holidays per year. The start date should be no later than 1 October 2025. For more information on the group see https://plantgenomics.univie.ac.at. For enquiries regarding the position or the project, please contact ovidiu.paun@univie.ac.at.

***How to apply. Applications will be reviewed on a rolling basis starting May 5th, until the position is filled. Please send a single pdf file including a motivation letter, curriculum vitae and contact details of two referees to ovidiu.paun@univie.ac.at.

Assoc Prof Ovidiu Paun Botany and Biodiversity Research University of Vienna Rennweg 14 1030 Vienna Austria https://plantgenomics.univie.ac.at Ovidiu Paun <ovidiu.paun@univie.ac.at>

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## VetMedUni Vienna PopGenetics

PhD positions in Population Genetics

Over the past years, Vienna has developed into one of the leading centres of population genetics. The Vienna Graduate School of Population Genetics has been founded to provide a training opportunity for PhD students to build on this excellent on-site expertise.

We invite applications from highly motivated and outstanding students with a love for evolutionary research and a background in one of the following disciplines: evolutionary genetics, functional genetics, theoretical or experimental population genetics, bioinformatics, mathematics, statistics.

Topics include:

The role of deleterious mutations for adaptation and maintenance of variation. Long-term adaptation of local Drosophila populations. The evolution of ageing. Inference of selection signatures from time-series data. Studying the genotype-phenotype map. Stabilising selection during polygenic adaptation. Evolution of regulatory networks.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by 14 May 2025 will be considered. Two letters of recommendation need to be sent directly by the referees.

PhD students will receive a monthly salary based on currently euro 2.786,10 before tax according to the regulations of the Austrian Science Fund (FWF).

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at Mag. Elisabeth Wagner-Weigerstorfer PhD

Coordinator,Joint Research Program (SFB)–Polygenic Adaptation Coordinator,Vienna Graduate School of Population Genetics E-Mail: Elisabeth.Wagner-Weigerstorfer@vetmeduni.ac.at Tel. +43 (1) 25077 - 4302

Wagner-Weigerstorfer Elisabeth <Elisabeth.Wagner-Weigerstorfer@vetmeduni.ac.at>

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# Jobs

## EAWAG Switzerland MolecularLabManager

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is an internationally networked aquatic research institute within the ETH Domain (Swiss Federal Institutes of Technology). Eawag conducts research, education and expert consulting to achieve the dual goals of meeting direct human needs for water and maintaining the function and integrity of aquatic ecosystems.

The Department of Fish Ecology and Evolution has an open vacancy starting January 2026 or as agreed upon for a

Manager of our Molecular Biology Laboratory 100% (m/f/d) We are looking for a person responsible to manage the Eawag Kastanienbaum molecular biological laboratory. Your tasks will be to independently organize the operation of the laboratory, instruct students, laboratory apprentices and researchers, as well as perform analyses to support our research.

Your tasks: - Independently maintain and manage the molecular laboratory its infrastructure and associated data - Train and assist trainees, students, PhDs and researchers in laboratory techniques and good laboratory praxis and contribute to the training of laboratory apprentices - Maintain laboratory instruments (e.g., ABI sequencer, corvaris, tapestation) - Independently conduct molecular analyses (e.g., microsatellite analysis, PCR, library preparation for transcriptomics, genomics, and reduced representation approached, DNA and RNA extraction) - Participate in research projects, a.o. development of new molecular and analysis methods

To qualify for this position, you have an education as a biology laboratory technician (Laborant:in EFZ, Fachrichtung Biologie) or comparable qualifications e.g., FH/Bachelor/Master of Science. You are interested in biology and environmental sciences and have experience with research activities relevant in molecular ecology, molecular biology or molecular genetics.

You appreciate working in collaborative national and international research projects that require independence, flexibility, teamwork, and individual responsibility and offer opportunities to develop new skills. You enjoy sharing your knowledge and expertise and are patient in supporting students, trainees, PhDs and researchers from a diverse background while working in the molecular laboratory and instructing the usage of analytical equipment. You are proficient in English and standard IT tools. Proficiency in German is a benefit, but not a requirement.

Eawag is a modern employer and offers an excellent working environment where staff can contribute their strengths, experience, and ways of thinking. We promote gender equality and are committed to staff diversity and inclusion. The compatibility of career and family is of central importance to us. For more information about Eawag and our work conditions please consult www.eawag.ch and www.eawag.ch/en/aboutus/-working/employment.You will be based in Kastanienbaum Lucerne, Switzerland. For further information, please email Dr Philine Feulner.

Evaluation of applications starts 1 June 2025 and continues until the position is filled. We look forward to receiving your application. Please send it through this webpage, as any other way of applying will not be considered. A click on the link below will take you directly to the application form. https://-apply.refline.ch/673277/1249/pub/2/index.html "Feulner, Philine" <Philine.Feulner@eawag.ch>

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## FulbrightU Vietnam EvolutionaryBiology

Location District 7, Ho Chi Minh City

Open Date Apr 15, 2025

Description TWO OPEN RANK POSITIONS IN BIOLOGY AND CHEMISTRY

The Integrated Sciences Program of Fulbright University Vietnam invites applications for two open rank full-time positions in (1) biology and (2) chemistry, to begin August 2025. We welcome candidates from all areas of either field. The Integrated Sciences major at Fulbright University Vietnam is both theoretically rigorous and highly interactive and interdisciplinary.

Fulbright University Vietnam seeks scholars and educators who care deeply about developing students as engaged learners and citizens, working in a transdisciplinary environment, and contributing to the evolution of a start-up university.

Successful candidates are expected to teach 5 courses per academic year, including: §Introductory Biology (for the biology candidate) §General Chemistry (for the chemistry candidate) In addition to the above required courses, faculty will be expected to teach core courses, foundational and intermediate courses, and upper-level courses related to their area of specialization. These courses should broadly align with the two concentrations within the major: (1) Environmental Science and Sustainable Development, or (2) Biology and Health Sciences. We are also interested in faculty whose teaching and research includes an interest in the intersections of AI and Data Science within their fields. In addition to teaching, faculty will also participate in advising undergraduate student research projects and capstone experiences.

Successful candidates should have demonstrated excellence in both teaching and research, as well as a desire to work with and develop undergraduate students. Candidates are expected to have completed their Ph.D. by the time of employment.

About Us Fulbright University Vietnam is Vietnam's first non-profit liberal arts university. We are an expanding international team of educational innovators, committed to serving Vietnamese society through rigorous research and responsible civic engagement, with strong political and financial backing, and connections to educational institutions around the world. We believe in the power of collaboration and transdisciplinary thinking. Globally integrated but deeply embedded in Vietnamese society, Fulbright is dedicated to utilizing the latest advancements in institutional design, research, teaching, and technology to create an institution that is both innovative and globally relevant.

Application Instructions Interested applicants should submit a cover letter, curriculum vitae, and the names and contact information of three references to the application dossier in Interfolio: https://apply.interfolio.com/166491 The position will remain open until filled. Applications received before May 21, 2025, will be considered with highest priority.

Fulbright University Vietnam is an equal opportunity employer that is committed to diversity and inclusion. All eligible candidates are encouraged to apply.

Jesse Hollister <jesse.hollister@fulbright.edu.vn>

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## GEOMAR Kiel MarineEvolGenomics

The GEOMAR Helmholtz Centre for Ocean Research Kiel, and Kiel University, Germany, jointly invite applications for a 3+3 yr (non tt)

Junior professorship (W1) “Marine Evolutionary Genomics”

The junior professorship is initially for a period of 3 years and will be extended for another 3 years upon successful evaluation. The post is located at the GEOMAR Helmholtz Centre for Ocean Research Kiel (www.geomar.de) and embedded into the research unit “Marine Evolutionary Ecology” (head Thorsten B.H. Reusch).

We are expecting applications from early career researchers with a very good doctoral degree in the area of genetics of aquatic organisms, evolutionary biology, evolutionary genomics or related areas, ideally with a few years of postdoctoral experience. The successful applicant will have in-depth knowledge in evolutionary genomics and bioinformatics and intends to or has already started to develop an independent research line after their doctorate, best demonstrated through excellent scientific publications. The research area should be in an innovative field of marine evolutionary biology and genomics, involving multicellular marine animals, algae or plants (no microbes).

The successful applicant is expected to have deep proficiency in population genetics and ecological genomics, as well as in bioinformatic scripting, which also forms the basis for the associated teaching commitments. Teaching will mainly take place within the Master’s program “Biological Oceanography” at GEOMAR.

Highly desirable would be a track record of successful third-party funding acquisition as well as experience in teaching topics such as genetics, genomics, evolutionary biology or marine biology. Experience in supervising students would be advantageous.

We offer support of technical staff and support scientists in marine cultivation and bioinformatics. Through the Kiel Marine Organism Culture Center KIMOCC at GEOMAR (http://www.futureocean.org/de/kimocc/), state-of-the-art cultivation facilities are available that allow the combination of evolutionary genomics with experimental work. Preferred access to high-performance computing and the sequencing centre at Kiel University (https://ccga.uni-kiel.de) is provided.

Applications (curriculum vitae, copies of academic degree certificates, list of publications and third-party funding, short research and teaching perspective (max 2 pages each) should be sent by 6 June 2025 to the Dean, Faculty of Mathematics and Natural Sciences, Kiel University, Germany, in electronic form in a single PDF file to bewerbung (at) mnf.uni-kiel.de

Starting date: 1 October 2025 or later (negotiable)

For more information pls visit the complete position description:

https://www.geomar.de/en/karriere/job-single-en/junior-professorship-w1-in-marine-evolutionary-genomics-1 Further informal inquiries can be addressed to: treusch(at)geomar.de

Thorsten Reusch <treusch@geomar.de>

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## Greifswald Germany Biomathematics

Dear colleagues,

We are seeking a highly motivated candidate for an ASSISTANT PROFESSORSHIP IN BIOMATHEMATICS.

So if you know anyone who would be a suitable candidate to join our institute, please don't hesitate to forward this job ad!

Greifswald is one of the biomaths hubs in Germany, research opportunities here are fantastic. Biomathematicians get the great opportunity to also teach the very subject they are passionate about as we offer a unique biomaths study program for our students. Plus, it's of course a bonus to work in a small historic town directly at the Baltic Sea (and yes, we do have a nice beach €).

Knowledge of the German language would be helpful, but is not strictly required.

Details can be found here: https://www.uni-greifswald.de/universitaet/information/stellenausschreibungen/professuren/stellenausschreibung/n/juniorprofessur-w1-fuer-biomathematik-ohne-tenure-track-238641/ If you have any questions, please go ahead and contact me!

Kind regards, Mareike Fischer

Prof. Dr. Mareike Fischer

Biomathematics and Stochastics

Institute for Mathematics & Computer Science Greifswald University Walther-Rathenau-Str. 47 Office 3.15 17487 Greifswald GERMANY

+49 (0) 3834 420 46 43

mareike.fischer@uni-greifswald.de

"Prof. Dr. Mareike Fischer" <mareike.fischer@uni-greifswald.de>

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## Idaho GeneticsLabTech

Genetics Lab Technician

Genetics Laboratory Technician is a position that is part of CRITFC's Fishery Science Department, but will be located with the genetics group at the Hagerman Fish Culture Experiment Station in Hagerman, ID.

This research group is involved in testing conservation, evolution, and ecological theories related to salmonids and other fishes. The Genetics Laboratory Technician will work under the Lead Geneticist and Lab Managers, in association with CRITFC geneticists and other technicians, as well as staff of the Fishery Science Department in Portland, OR. Efforts will focus on applying empirical genetics/genomics data to address questions related to conservation and recovery of steelhead, Chinook, sockeye, and coho salmon, sturgeon, lamprey, and other fishes of the Columbia River Basin.

This is an in-person position located in Hagerman, Idaho.

Responsibilities Prepare sampling materials for collecting fish tissue samples in the field Extract DNA from fish tissues Prepare DNA libraries for next-generation sequencing (e.g., RAD-seq, RNA-seq, GT-seq)Analyze genetic markers on specialized laboratory equipment Data entry into Microsoft Excel spreadsheets and Progeny database Complete QA/QC protocols Communicate effectively with project leaders Participate in inter-agency work groups, as necessary Other duties as assigned and as appropriate to CRITFC goals and purposes.

Pay Rate $ 23.98 to $ 27.17 per hour Location: Hagerman Idaho

Closing Date: Open until filled.

For additional information and to apply: https://critfc.org/jobs/genetics-lab-technician/ Rebekah L. Horn, PhD

Fisheries Geneticist, Columbia River Inter-Tribal Fish Commission

P: (208) 837-9096 x1128 E: rhorn@critfc.org W: www.critfc.org Hagerman Genetics Lab 3059-F National Fish Hatchery Rd Hagerman, ID 83332

PUTTING FISH BACK IN THE RIVERS AND RESTORING THE WATERSHEDS WHERE THEY LIVE

"Rebekah L. Horn" <rhorn@critfc.org>

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## MHNG Switzerland Invertebrates nonArthropods

The Natural History Museum of Geneva (MHNG) holds prestigious collections highlighted by a multidisciplinary scientific team of international renown, and by its exhibitions and public activities attracting hundreds of thousands of visitors per year, making it the largest institution of this type in Switzerland.

Wishing to complete its team, the Natural History Museum of Geneva is looking for a:

RESEARCH OFFICER IN INVERTEBRATES NON-ARTHROPODS full time Your mission and responsibilities: You conduct scientific research autonomously, in accordance with the scientific policy of the institution. You write scientific publications at the national and international level and ensure the training of young scientists. You participate in the management (organization, digitization, loans, and conservation) and development of collections of non-arthropod invertebrates within the Invertebrate sector. You ensure the transmission of knowledge to a wide audience by participating in outreach activities and the design of exhibitions.

Your profile: Holder of a Ph.D. in biology, you have at least one year of postdoctoral experience. Your expertise lies in non-arthropod invertebrates, preferably in the following groups: terrestrial or freshwater molluscs, annelids, or nematodes. You are experienced in managing and researching collections and conducting study programs in taxonomy, systematics, and evolution, as well as in valorizing regional and international biodiversity. You are autonomous in your tasks, able to work in a team, and have the skills to collaborate with other similar institutions nationally and internationally. You are proficient in English, both orally and in writing, and ideally also in French, or keen to learn it. You have excellent analytical and synthesis skills, initiative, and proven skills in getting funding, organization, and popularization of science.

Send your application to recrutement.mhn@ville-ge.ch Documents letter of motivation; CV; copies of diplomas; recent picture (passport format)

Contact for information on scientific matters isabel.blasco-costa@geneve.ch

Entry into office to be agreed Closing date 05.05.2025 (extended) Original announcement in French https://www.geneve.ch/administration-municipale/offres-emploi/charge-chargee-recherche-invertebres-non-arthropodes-100 Isabel Blasco-Costa Curator in-chief of the Invertebrates sector

Dr Isabel BLASCO COSTA Conservatrice, resp sect invertébrés

Invertébrés

T. +41 22 418 6387 isabel.blasco-costa@geneve.ch

Muséum d'histoire naturelle (MHN) Département de la culture et de la transition numérique Route de Malagnou 1 1208 GENEVE www.museum-geneve.ch Notre environnement est fragile, merci de n'imprimer ce message qu'en cas de nécessité.

Isabel BLASCO COSTA <Isabel.Blasco-Costa@geneve.ch>

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## MississippiUWomen 9mnth EvolutionaryBiology

Applications are invited to apply for a nine-month position in Biology at Mississippi University for Women in Columbus, Mississippi at the Visiting Assistant Professor level beginning August 2025. Applicants must have a Master's degree in Organismal Biology or related field, Ph.D. preferred. Any area of organismal biology will be considered. The successful candidate will teach Comparative Anatomy in the BS Biology Major, and introductory courses for Biology Majors and non-science majors. Service to the department, university, and community is expected along with a commitment to the scholarship of teaching and learning at a diverse, primarily undergraduate institution

In addition to campus resources, the successful applicant will have access to the Plymouth Bluff Environmental Center, a 190-acre educational and recreational center situated above the old Tombigbee River channel and located a 15-minute drive from campus. The Noxubee Wildlife Refuge and the Tombigbee, Buttahatchie, and Luxapalia rivers are nearby and available for class or research activities. Interactions and collaborations are also possible with Mississippi State University, a 25-minute drive from campus.

Applicants must have at least a master's degree in Organismal Biology or related field on or before 1 August 2025. Individuals with post-doctoral experience and/or teaching experience will be given preference.

Prior to hiring, the final candidate(s) must successfully pass a pre-employment background investigation. A prior conviction reported as a result of the background investigation DOES NOT automatically disqualify a candidate from consideration for this position. However, failure to disclose may disqualify a candidate. NOTE: MUW does not sponsor employment visas.

Required Documents

1. Cover Letter/Letter of Application 2. Curriculum Vitae 3. Teaching Philosophy 4. Unofficial Transcript 1

thagey@muw.edu

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## NTNU Norway EvolutionaryGenomics

Application deadline: May 25, 2025

About the position. Do you want to be part of an ambitious research environment at Norway's largest university? The NTNU University Museum is seeking an associate professor for a position in vertebrate evolutionary genomics. The appointment is permanent and is part of our aim to recruit ambitious and excellent researchers. The position is central to the Department of Natural History's strategy: Through the utilization of genetic information captured in natural history collections, we seek to improve our understanding of evolutionary change and processes affecting biodiversity and to advance the field of evolutionary genomics. Thus, we are looking for someone with experience and keen interests to conduct cutting edge, collection-based research that advances fundamental knowledge about genome change both within and between species over evolutionary timescales and in space.

You have a demonstrable interest in evolutionary biology and a Ph.D. in evolutionary genomics or a closely related academic discipline. Applications are welcomed from all areas of evolutionary genomics, although areas of particular interest are: the use of paleo-genomic data from natural history collections to elucidate past and present ecological and environmental interactions, the development of new mathematical and computational methods, and the application of new sequencing technologies and pangenomic methods. Preferably, you are experienced in the use of scientific collections for genomic research.

As a start-up, we offer a PhD-position. Female applicants are especially encouraged and will have special opportunities to apply to the NTNU start-up program for women in permanent scientific positions. We offer an ambitious and positive working environment and good work-life balance in one of Norway's most beautiful cities. At the NTNU University Museum's Department of Natural History, a dedicated team of faculty members, researchers, and technical and administrative staff manages and contributes to the Museum's natural history collections. Your immediate leader is the Head of Department.

Duties of the position. It is expected that the successful candidate:

* Maintains an active, international research profile. * Develops and submits competitive project applications to the European Research Council, the Research Council of Norway, and similar sources of national and international funding. * Will have the scientific governance for our vertebrate natural history collections. * Contributes to teaching at the NTNU Department of Biology, the Research School in Biosystematics (ForBio), or the Nordic Academy of Biodiversity and Systematic Studies (NABiS). * Participates in public outreach activities.

Required qualifications. You must have the qualifications required for the position of Associate Professor in the field of evolutionary genomics, as outlined in the Regulations for the Universities and Colleges Act < https://lovdata.no/forskrift/2024-06-28-1392/%C2%A73-6 >:

* Ph.D. within the field of evolutionary genomics or a closely related academic discipline. * Peer-reviewed publications in vertebrate evolutionary genomics. * Relevance of research focus in relation to the NTNU University Museum research strategy < https://www.ntnu.no/documents/10476/63382/VM+Strategi+2018+ENG.pdf/56781533-1c95-afb4-7213-0c21e573172a?t=1664351156823 >. * Excellent skills in written and spoken English. * Experience and success with any type of project acquisition and management. * You must document relevant museum-related dissemination skills, as referenced in the Regulations < https://lovdata.no/forskrift/2024-06-28-1392/%C2%A73-8 > and section 4.7 in NTNUs guidelines < https://i.ntnu.no/wiki/-/wiki/English/NTNUs+guidelines+for+academic+positions+

>. If this cannot be documented, you will be required to complete an approved course within two years of commencement. NTNU offers qualifying courses. * New employees who do not speak a Scandinavian language by appointment are required, within three years, to demonstrate skills in Norwegian or another Scandinavian language equivalent to level three of the course for Norwegian for speakers of other languages < https://www.ntnu.no/norskkurs > at the Department of Language and Literature at NTNU.

Preferred qualifications.

* Experience with the curation of natural history collections. * Experience with collaborative research using interdisciplinary approaches. * Experience with teaching and supervision.

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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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## SMNH StockholmU InsectPhylogenomics

A four-year full-time position as researcher in insect phylogenomics is available in Stockholm. The successful candidate will be a joint member of the Ronquist lab at the Swedish Museum of Natural History (https://ronquistlab.github.io/) and the van der Valk lab at the Centre for Palaeogenetics, Stockholm University / Swedish Museum of Natural History (https://www.scilifelab.se/researchers/tom-van-der-valk/).

We are looking for someone with a passionate interest in insect phylogeny and evolution, and with strong competence in de novo genome assembly and phylogenomic analysis. The successful candidate will be a key member of the DarkTree project, funded by the Knut and Alice Wallenberg Foundation. The project aims to fill the gaps in the insect tree of life using the unique global insect material from the Insect Biome Atlas (https://www.insectbiomeatlas.org/) and Lifeplan (https://www.helsinki.fi/en/projects/lifeplan) projects. The material consists of around 50,000 Malaise trap samples, containing some 50 million insects representing more than 1 million species, most of which are currently undescribed. The entire material has gone through DNA metabarcoding using mild lysis protocols, providing a detailed index to the taxonomic content of each sample.

In DarkTree, we will use this material to systematically target the species-rich insect radiations that are not covered properly (or at all) by previous and ongoing genome sequencing efforts. The aim is to generate the first reasonably unbiased view of the insect tree of life, based on a backbone of some 5,000 genomes 'decorated' with 1 million DNA barcodes. The project involves collaboration with a computer vision lab at Linköping University, focused on developing AI-assisted techniques for picking out specimens for genome sequencing, and with computer scientists at KTH in Stockholm, focused on developing scalable probabilistic machine learning techniques for online phylogenomic analysis and placement of DNA barcodes.

You will be responsible for setting up a high-throughput pipeline for de novo assembly of genomes from short-read Illumina sequencing platforms, and processing of the assemblies to generate suitable datasets for phylogenomic analysis. Together with other team members, you will also be developing and implementing the evolutionary models used in the phylogenomic analyses, and in interpreting and publishing the results. There will be considerable freedom in developing your own research projects based on the data we generate in the project.

Qualification requirements: We are looking for a candidate with a PhD and postdoctoral research experience in phylogenomics. You should have a strong background in bioinformatics, statistical phylogenetics and comparative genomics. Previous experience of working with de novo assemblies and insects would be meritorious.

About the employment: The employment is a temporary four-year position. Scope of employment 100%. Starting date September 1, or as agreed.

For further information about the position: please contact professor Fredrik Ronquist, fredrik.ronquist@nrm.se, or Dr Tom van der Valk, tom.vandervalk@nrm.se.

Application deadline: May 16, 2025.

For more information and to apply, please visit: https://recruit.visma.com/spa/public/apply?guidAssignment=12b46c01-9af4-4ec4-b181-9dc224be598c&description=True Fredrik Ronquist <Fredrik.Ronquist@nrm.se>

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## Stuttgart Germany ConservationGenomics

The State Museum of Natural History Stuttgart (SMNS) invites applications for a dynamic Junior Group Leader in Conservation Genomics (m/f/d) to join its newly established Biodiversity Monitoring Department.

Our department focuses on understanding the evolutionary drivers of genomic diversity within species, enabling their persistence amid environmental changes. Leveraging our extensive museum and monitoring collections alongside state-of-the-art genomic methods, we aim to integrate foundational insights from evolutionary genomics with practical conservation outcomes (https://biodiversitysmns.wixsite.com/rpereiralab). We are committed to creating a hub for dedicated scientists to establish independent research programs exploring the evolutionary processes that shape multiple levels of biodiversity.

This position supports the development of a collection-based research program focused on Conservation Genomics, Museomics, and related fields, bridging the gap between evolutionary genetics research and practical conservation strategies in response to the global biodiversity crisis. The position offers an initial three-year contract with the possibility of renewal, and applications are due by June 15th, 2025.

Position Details: - Lead innovative research that bridges evolutionary genetics and conservation. - Publish impactful manuscripts and secure external funding. - Foster interdisciplinary collaborations within SMNS. - Mentor students and researchers to translate findings into tangible conservation actions.

Requirements: - Ph.D. in Conservation Biology, Genetics, Bioinformatics, or a related discipline. - Strong publication record in relevant fields. - Experience with next-generation sequencing and bioinformatics. - Proficiency in relevant analytical methods and programming languages. - Proficiency in English.

Desirable: - Experience across diverse study systems. - Experience collaborating with conservation agencies. - Proven track record in funding acquisition.

We Offer: - Mentorship for a “Habilitation” degree. - Strong collaborative network with departments at SMNS and the University of Hohenheim. - Leadership role within an interdisciplinary team. - Annual research budget of 5,000 EUR. - Salary according to E13 TV-L.

Applications in English should be submitted as a single PDF (max. 10 MB) including a cover letter, CV, three academic references, and relevant certificates to biodiversity@smns-bw.de by June 15th, 2025.

For inquiries, please contact Prof. Dr. Ricardo Pereira at ricardo.pereira@smns-bw.de. SMNS is committed to diversity and encourages applications from all qualified individuals.

More info: https://tinyurl.com/biodivgen [image: photo]

Prof. Dr. Ricardo Pereira Abteilungsleitung Biodiversitï¿½tsmonitoring, Head of the Department of Biodiversity Monitoring

Naturkundemuseum Stuttgart | Natural History Museum Stuttgart

Rosenstein 1, 70191 Stuttgart, Germany <https://maps.google.com/?q=Rosenstein 1, 70191 Stuttgart, Germany>

+49 711 8936-2814 <+497118936-2814>

ricardo.pereira@smns-bw.de

www.naturkundemuseum-bw.de Prof. Dr. Ricardo Pereira Abteilungsleitung Biodiversitï¿½tsmonitoring, Head of the Department of Biodiversity Monitoring

Naturkundemuseum Stuttgart | Natural History Museum Stuttgart

Rosenstein 1, 70191 Stuttgart, Germany

+49 711 8936-2814

ricardo.pereira@smns-bw.de

www.naturkundemuseum-bw.de Bleiben Sie informiert: Abonnieren Sie unseren Newsletter!

Unterstï¿½tzen Sie das Museum und werden Sie Mitglied im Fï¿½rderverein! Informationen zur Verarbeitung personenbezogener Daten nach der DSGVO durch das SMNS finden Sie hier.

“Pereira, Ricardo” <ricardo.pereira@smns-bw.de>

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## UArkansas 6mnthTechnician

The Siepielski Evolutionary Ecology lab (https://asiepielski.wordpress.com) is hiring a short-term, 6-month lab technician position in quantitative genetics. Job duties include rearing and maintenance of damselfly larvae and assisting with digestive physiology experiments, as well as care and maintenance of fish in an aquarium setting. Some local field work will also be required. The position requires a high attention to detail and record-keeping. The technician will work closely with the PI, a post-doctoral scholar, and undergraduates to complete the work. Work will be conducted on the main campus at the University of Arkansas in Fayetteville. Pay rate is 16-17$/hr, 40 hrs/week. Ideal start date is late May, but there is some flexibility. Applications should be received by April 25th, 2025.

If you have any questions about the position, please email: amsiepie@uark.edu

Application materials include a CV, letter of interest, and three references. Please apply here:

https://uasys.wd5.myworkdayjobs.com/UASYS/job/Fayetteville/Hourly-Research-Assistant_R0069858-1
Thank you,

Adam

Adam M. Siepielski Department of Biological Sciences University of Arkansas Fayetteville AR, 72701

Website: https://asiepielski.wordpress.com Adam Michael Siepielski <amsiepie@uark.edu>

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## UCyprus PlantBiodiversity

The University of Cyprus invites applications for one (1) tenure-track position at the rank of Lecturer or Assistant Professor in the Department of Biological Sciences, in the field of *'Plant biodiversity'. *

We are seeking a plant ecologist or evolutionary biologist, who can develop a strong research and teaching programme in plant ecology and/or diversity at the University of Cyprus. Preferred areas of expertise include but are not limited to ecological responses or evolutionary adaptations to environmental change. Research focusing on climate change impacts and/or plant conservation or plant-environment interactions and ecosystem services, will be viewed favorably. We particularly welcome candidates employing multidisciplinary approaches that integrate field ecology, experimental ecology, macroecology, biogeography, evolutionary ecology and/or evolutionary genetics and genomics. Applicants with expertise in remote sensing, GIS-based analyses, species distribution modelling or other computational approaches to plant ecology and diversity research are also encouraged to apply. The successful candidate will be expected to contribute to the teaching of the undergraduate Botany course and to the graduate program in Biodiversity Conservation.

For all academic ranks, a Doctoral degree from an accredited University is required. The minimum requirements for each academic rank are available at https://rb.gy/e9oi7 and include: previous academic experience, outstanding research achievements and notable scientific contributions, experience in developing and teaching of high quality undergraduate and graduate curricula.

Candidates do not need to be citizens of the Republic of Cyprus. The official languages of instruction are Greek and Turkish. For the above position, fluency in the Greek language is necessary. In case the selected candidate is not proficient in the Greek language, the candidate and the Department shall ensure that the former acquires sufficient knowledge of the Greek language within 3 years from the date of appointment.

In accordance with the applicable legislation, the annual gross salary (including the 13th salary) for full-time employment is:

Lecturer

(Scale Ã12-Ã13)

euro 50.101,73 - euro 81.526,71

Assistant Professor

(Scale Ã13-Ã14)

euro 65.916,84 - euro 88.897,16

Employee contributions to the various State funds will be deducted from the above amounts.

Candidates are invited to submit their applications electronically by uploading the following documents *in English* and in PDF format at the following link: https://applications.ucy.ac.cy/recruitment 1. Cover Letter

2. Curriculum Vitae

3. Copy of ID/Passport

4. Copy of a bachelor's degree from an accredited University is required

5. Copy of a PhD degree from an accredited University is required

6. Review of previous research work and a brief description of future research projects (up to 3 pages)

7. List of publications

8. Representative publications (up to 3 publications which should be submitted separately). While publications are not required for the rank of Lecturer, candidates applying for this rank are encouraged to submit representative publications if they have any.

9. The names and email addresses of three professors from whom confidential letters of recommendation (in English) will be automatically requested upon submission of the application. Letters of recommendation may be submitted up to 7 days following the deadline for submission of applications. It is the responsibility of each candidate to ensure that the references are submitted. In case the letters of recommendation are not submitted on time, the application will not be considered.

The above documents (1-8) must be uploaded as separate PDF documents.

*No change will be possible following the submission of your application.*

The deadline for applications is *Friday the 11th of July 2025*.

The University of Cyprus reserves the right to ask from the selected candidate(s), and prior the offering of any position, to have their degrees submitted and evaluated upon by the relevant authority within Cyprus Democracy, "The Cyprus Council for the Recognition of Higher Education Qualifications (KY.S.A.T.S.)". The selected applicants will be required to submit copies of degree certificates certified by the Ministry of Education (if the degrees were obtained from universities in Cyprus) or from the Issuing Authority (if the degrees were obtained from foreign universities). The selected candidate will be responsible for ensuring that the authenticity of the degrees, certificates, and other relevant documents submitted in his/her application is certified by the competent Institutions, by sending a relevant email to the Human Resources Services.

Applications, supporting documents and recommendation letters submitted in

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## UExeter FieldAssist SkaneRodents

We are seeking a highly motivated field assistant for the upcoming field season (mid July - end September 2025) to help with a project that aims at investigating how genetic variation in disease susceptibility is maintained in natural population, using the bank vole (Myodes glareolus) as a model. The field assistant will help with trapping voles, sample and data collection, field equipment maintenance, animal husbandry, and data management. The field work is carried out at a beautiful field site in SkÃ¥ne, southern Sweden.

The ideal candidate has a can-do attitude, is highly organized, pays attention to detail, and has excellent interpersonal, teamwork and communication skills (incl. the ability to work and live with a small team). The work is physically demanding (incl. carrying traps, lots of walking through forests) and involves long days. Previous fieldwork experience and a driving license are a plus.

We can offer the opportunity to gain extensive field work experience and insights into a research project on the evolutionary ecology of wildlife health and disease, and to spend time in beautiful SkÃ¥ne.

The salary is 680 / week, for a 10 week period. Travel to and accommodation in Sweden are provided. Right to work in the UK is required. The successful candidate will have to complete an online animal experimentation course before the start of the project.

Applications should include a motivation letter (1 page), a CV (which details relevant experience), and contact information of two references. Send the above as a single PDF to: b.tschirren@exeter.ac.uk by May 1st 2025.

For more information, please contact Barbara Tschirren b.tschirren@exeter.ac.uk

"Tschirren, Barbara" <B.Tschirren@exeter.ac.uk>

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## UOulu Finland FreshwaterBiodiversity

Tenure Track Assistant or Associate Professor in Freshwater Biodiversity

Please apply via: https://oulunyliopisto.varbi.com/-what:job/jobID:811771/ Multidisciplinary recruitment The University of Oulu is a multidisciplinary, international research university, with about 3,600 employees who produce new knowledge based on high-standards research and provide research-based education to build a more sustainable, smarter, and more humane world. The University of Oulu community has about 17,000 people in total. Our northern scientific community operates globally and creates conditions for the emergence of innovations.

We are now looking for a

Tenure Track Assistant or Associate Professor in Freshwater Biodiversity

to join us in the interdisciplinary research program "SAFIRE: Safeguarding Biodiversity through Interdisciplinary Research on Habitat Restoration" < https:/-/www.oulu.fi/en/research/biodiverse-arctic-and-global-resilience/safeguarding-biodiversity-through-interdisciplinary-research-habitat-restoration-safire > at the University of Oulu (Finland).

We are looking for a motivated and talented researcher with a strong background in freshwater biodiversity and research on or relevant to habitat/environmental restoration to join our interdisciplinary Research Council of Finland Profi8 programme. SAFIRE is a new strategic research programme which brings together the faculties of Sciences, Humanities, and Information Technology and Electrical 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 the University of Oulu 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, and the 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 As an Assistant/Associate Professor, you will:

ÂÂÂÂÂÂDevelop and sustain a distinctive program of research and creative scholarly initiatives leading to academic publications, research funding applications, and public-facing outreach initiatives;

ÂÂÂÂÂÂCollaborate with the relevant faculties at the University of Oulu to further the aims of SAFIRE;

ÂÂÂÂÂÂParticipate in national and international scientific organizations;

ÂÂÂÂÂÂCommunicate research results to academic community, user groups and general public;

ÂÂÂÂÂÂParticipate in administrative tasks related to the position at the faculties and the university;

ÂÂÂÂÂÂDesign and lead undergraduate and graduate level courses, especially in the fields of Aquatic Biodiversity and Ecosystem Restoration;

ÂÂÂÂÂÂSupervise graduate research students (MA and PhD levels) and postdocs;

ÂÂÂÂÂÂFinnish skills or the motivation to learn Finnish is an asset;

ÂÂÂÂÂÂSupport the strategic aim to renew the scientific profile of the university and to promote multi- and interdisciplinary research approaches;

ÂÂÂÂÂÂParticipate on funding calls and project management

Who are you? We invite applications from candidates with strong academic backgrounds in ecology, zoology, limnology and/or other related research fields, who have experience with freshwater biodiversity and preferentially applied ecosystem restoration or conduct research relevant to ecosystem restoration. The candidate will be working with an interdisciplinary research team and conduct research on freshwater biodiversity and how to make the restoration of freshwater habitats, with a special focus on

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## UReading UK Two InvertZoology FieldEcol

Join the UK's Sustainable University of the Year 2025. The University of Reading is home to a vibrant academic team of Biological Scientists, strengthened by several new appointments in the past five years, that has built on international expertise in phylogenetics, zoology and applied ecology. Underpinning this, the School of Biological Sciences occupies state of the art facilities, including the Health & Life Sciences building, housing the Cole Museum of Zoology, which enhances both our research and teaching. The School is ideally situated in a large species-rich green campus close to other academic Schools with interests in biodiversity and climate change research.

The Division of Ecology and Evolutionary Biology seeks to appoint: 1. a Lecturer in Invertebrate Zoology: a highly motivated and successful scientist working on aspects of invertebrate zoology with an interest in museum based research. Duties will include: contributions to research including applications for funding, teaching at undergraduate and postgraduate level, and to administrative duties as normally expected in a University environment. The appointee may have the opportunity to take on the curation of the Cole Museum of Zoology.

2. a Lecturer in Field Ecology: a successful scientist or practitioner working on aspects of field ecology including identification of animals and plants. Duties will include: contributions to research including applications for funding, teaching at undergraduate and postgraduate level, and to administrative duties as normally expected in a University environment.

For further details see: https://jobs.reading.ac.uk/Job/JobDetail?JobId=3D24301 (zoology) and https://jobs.reading.ac.uk/Job/JobDetail?JobId=3D24303 (ecology).

Applications must include a detailed CV, including a full publications list, a one-page appendix outlining the applicant's proposed future research including sources of funding and the names and contact details of two referees. Closing date for applications is 25th April 2025.

Contact Name Dr Alastair Culham Contact Job Title Head of Division, Ecology and Evolutionary Biology Contact Email address a.culham@reading.ac.uk

The University is committed to having a diverse and inclusive workforce, supports the gender equality Athena SWAN Charter and the Race Equality Charter, and champions LGBT+ equality. We are a Disability Confident Employer (Level 2). Applications for job-share, part-time and flexible working arrangements are welcomed and will be considered in line with business needs.

l.j.johnson@reading.ac.uk

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## YaleU GlobalChangeAdaptation

Assistant Professor, Global Change Ecology

The Department of Ecology and Evolutionary Biology at Yale University invites applications for an Assistant Professor in Global Change Ecology. We seek a colleague who studies the impacts of global change on aquatic or terrestrial populations, communities, ecosystems, and/or biomes, and who focuses on understanding the processes underlying these changes. We view global change as having a myriad of dimensions ranging from land use change to habitat fragmentation, climate change, pollution, urbanization, perturbations to global nutrient cycles, alien species invasions, etc., as well as novel types of synergistic and antagonistic interactions among these. We encourage applications from those who use any combination of laboratory, field, statistical or theoretical approaches, and are particularly interested in candidates with integrative research programs that complement the mission of the Department of Ecology and Evolutionary Biology. A record of outstanding achievement and a promising research program are more important than the specific research area or study system. A Ph.D. or equivalent degree at time of hire is required for this position, and the successful candidate will contribute to undergraduate and graduate mentoring and teaching.

Interested candidates should submit a cover letter, CV, three relevant publications or preprints, a research statement that is no more than three pages, a teaching statement that is no more than two pages, and contact information for three references at http://apply.interfolio.com/164677 .Applicants may contact the Department Chair, David Vasseur at david.vasseur@yale.edu with any questions regarding the position. The search will remain open until the position is filled. Review of applications will begin August 15, 2025. The anticipated appointment start date is July 1, 2026.

The University is committed to basing judgments concerning the admission, education, and employment of individuals upon their qualifications and abilities and seeks to attract to its faculty, staff, and student body qualified persons from a broad range of backgrounds and perspectives. In accordance with this policy and as delineated by federal and Connecticut law, Yale does not discriminate in admissions, educational programs, or employment against any individual on account of that individual's sex, sexual orientation, gender identity or expression, race, color, national or ethnic origin, religion, age, disability, status as a special disabled veteran, veteran of the Vietnam era or other covered veteran.

"Dvoracek, Mitchel" <mitchel.dvoracek@yale.edu>

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# Other

## RohlfMedal 2025 CallForNominations

The Rohlf Medal was established in 2006 by the family and friends of F. James Rohlf to mark his 70th birthday. He has been a longtime Stony Brook University faculty member and is currently Emeritus Distinguished Professor in the Department of Ecology and Evolution, and Research Professor in the Department of Anthropology.

Recipients of the Rohlf Medal will be recognized for excellence in their sustained body of work on the development of new morphometric methods and their applications in the biomedical sciences, including evolutionary biology, population biology, biological anthropology, developmental biology, molecular structure, molecular geometry and medicine. The term "morphometrics" is intended to include high-dimensional pattern analyses of biological shape, especially those that analyze shape in a comprehensive way, or of covariation of shape with other variables. The award can recognize a body of work that has significantly advanced the field, including: mathematical or statistical theory underlying morphometric methods, software that implements or visualizes new methods, or a body of biological findings that rely crucially on contemporary morphometric methods and represent major advances in approach.

Candidates for the Rohlf Medal may be self-nominated or nominated by others. They must possess a Ph.D. degree or the equivalent. Nominations (at this stage only name, email and a 25-50 word rationale) should be submitted here < https://docs.google.com/forms/d/e/1FAIpQLScx-P1sxtfdbO2QwM_QhSCa-9xMXAxqQz04zYsKBHUBhxzXDA/viewform?usp=sharing >.

The winning candidate must agree to attend the award ceremony in person in order to accept the Rohlf Medal and then deliver the award lecture.

Nomination packages will be requested by the Award Committee and should include:

1. a description of the body of work (not to exceed two pages) on which the candidacy is based, 2. pdf versions of up to 3 relevant papers and/or software products, 3. a curriculum vitae, and 4. the names and emails of two potential references (letters are not needed yet).

Nominating packages should be submitted to the Rohlf Medal committee by 5 pm, EDT, 1 July of 2025 to be assured of full consideration. Note that upon request nominations from prior years can be retained (although updates of some of the information will likely be needed).

The successful candidate will receive the Rohlf Medal and a cash prize at Stony Brook University, planned for October 22nd, 2025. She or he will deliver a lecture that is appropriate for a broad audience, ranging from the exact sciences to the humanities, concerning the morphometric methodology, software, or findings for which the Rohlf Medal was awarded.

If you have questions about this nomination or need other information, please contact Committee Chair Dr. Eric Delson <mailto:eric.delson@lehman.cuny.edu?subject=>.

Dr. Dean C. Adams Distinguished Professor Department of Ecology, Evolution, and Organismal Biology Iowa State University www.public.iastate.edu/~dcadams/ phone: 515-294-3834

“Adams, Dean [EEOB]” <dcadams@iastate.edu>

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## Software DAMBE UpdateOnNewMacComputers

Dear All,

Responding to popular requests, I have added instructions on how to install and run DAMBE on new MAC computers (with Apple Silicon M1, M2, ..., processors):

https://dambe.bio.uottawa.ca/DAMBE/dambe_install_mac.aspx Please let me know if you encounter any problems.

(DAMBE is a comprehensive software workbench in molecular biology and evolution.)

Best. Xuhua Xa Professor, Department of Biology University of Ottawa https://scholar.google.ca/citations?hl=en&user=fbAS_FcAAAAJ&view_op=list_works Xuhua Xia <Xuhua.Xia@uottawa.ca>

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## UKonstanz FieldAssistant SwedishLaplandJays

We are recruiting a fieldwork assistant to help run a social learning project in Siberian Jays (Perisoreus infaustus), in Arvidjaur, Sweden in the months of September-October 2025. Siberian Jays are territorial, group living corvids. In the field, the fieldwork assistant will help with running a social learning experiment, to test whether juvenile birds socially learn how to solve a two action puzzle from adults in the group.

You will primarily work with PhD student Alex Chan (University of Konstanz, Germany), supervised by Dr. Fumihiro Kano (University of Konstanz, Germany). The field site is run and managed by Dr. Michael Griesser (University of Konstanz, Germany) and Dr. Miya Warrington (Oxford Brookes University, UK)

Job description -Run cognition experiments in the wild -Operate cameras, microphones and field equipment -Observe behaviour of animals during experiments and narration

Required skills -Driver’s license and good driving skills -Available throughout the whole field work period (exact dates negotiable, ~8 weeks from start of Sept to end of Oct 2025) -Fluent in English -No colour blindness, work requires reading colour rings -Good physical health -Good interpersonal skills

Desired skills -Interest in animal cognition, social learning and animal experimentation -Happy to spend 2 months in the forest in the Swedish Laplands!

What is covered -Travel costs to and from Arvidsjaur, Sweden -Rent during the stay -All food and consumables throughout the stay

Contact -If you are interested in the position, please send a CV, short cover letter in body of the email and name + email of 2 referees to Alex Chan (hoi-hang.chan@uni-konstanz.de). Feel free to reach out to Alex for any questions! -Deadline for application is end of May (31st of May, 2025)

Alex Chan <hoi-hang.chan@uni-konstanz.de>

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# PostDocs

## CityUNewYork InvasionGenomics

Postdoctoral Fellow: Widow spider and parasitoid invasion genomics City University of New York, York College PI Monica Mowery < https://monicamowery.wordpress.com/ > at the City University of New York (York College < https://www.york.cuny.edu/ > and the CUNY Graduate Center < https://www.gc.cuny.edu/biology/subprograms/ecology-evolutionary-biology-and-behavior >) < https://www.gc.cuny.edu/ > has an opening for a postdoctoral researcher to begin in October 2025. This position will be for one year. Our lab investigates the ecology, evolution, behavior, and genomics of urban and invasive species, focusing on insects and spiders. Funded by the Binational Science Foundation, the postdoctoral fellow will work on a project to sequence and annotate a reference genome for a widow spider (genus Latrodectus) egg sac parasitoid wasp, Philolema latrodecti. The postdoctoral fellow will additionally analyze nuclear genomic data using ddRAD sequencing and mitochondrial sequencing for the invasive brown widow spider, Latrodectus geometricus, and the associated parasitoid wasp sampled globally to identify the native and invasive ranges of L. geometricus and P. latrodecti by comparing the nucleotide diversity and phylogeographic structure across populations. There will be opportunities to analyze sequenced libraries from museum specimens of the parasitoid wasp. The postdoctoral fellow will be on a collaborative team with Dr. Jessica Garb at University of Massachusetts Lowell and Dr. Michal Segoli and Dr. Yael Lubin at Ben-Gurion University.

Applications will be accepted until May 25, 2025, and will be evaluated on a rolling basis. Applicants must submit the following materials electronically through the Research Foundation website: https://www.rfcuny.org/careers/postings?pvnID=YC-2503-006772 * a resume/CV that documents all applicable required and preferred qualifications, * a cover letter (1-2 pages) that briefly (1) describes their relevant training and research accomplishments, (2) explains their reasons for applying for this specific position, (3) describes their career aspirations and how this position will advance their goals, and (4) clarifies any of the required or preferred job qualifications listed on the official posting that the candidate may meet but are not clearly indicated on their CV. * Three names and contact information for references

Queries regarding this position can be made by email to: mmowery@york.cuny.edu Required Qualifications:

* Ph.D. by the time of the start date in integrative biology, evolutionary biology, population genetics, or a closely related field. * A record of publishing research in peer-reviewed scientific journals

Preferred Qualifications:

* Experience generating, analyzing, and/or integrating

large datasets - whole genome sequencing, RAD sequencing, and/or transcriptome sequencing. * Experience sequencing and assembling reference genomes * Experience in programming in R, Python, or a similar programming language * Experience using computational methods to assess historical population and invasion dynamics * A demonstrated commitment to fostering an inclusive and equitable research environment

Monica Mowery <mmowery@york.cuny.edu>

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## DeakinU EvolutionAvianBehaviour

Associate Research Fellow in Avian Behaviour

Exciting opportunity to work with an accomplished and supportive team conducting field-based research into behaviour, evolution, and conservation management of threatened birds.

Deakin University, School of Life and Environmental Sciences, Burwood campus, Melbourne, Australia

Full-time and fixed-term for 2.5 years. AUD $80,065 - $107,633 (dependent on experience) + 17% superannuation

Full details and how to apply: https://careers.pageuppeople.com/949/cw/en/job/571425/associate-research-fellow-avian-behaviour The Associate Research Fellow in Avian Behaviour will initiate and conduct research into bird behavioural ecology and evolution: specifically the escape behaviour of two threatened bird species (the hooded plover, and helmeted honeyeater). The appointee will be responsible for conducting and coordinating field-based studies of escape behaviours in relation to management. They will also collect survival and reproductive data and perform evolutionary analyses. Other aspects will include working with the team to facilitate genetic analyses. The Fellow with work collaboratively as part of a research team led by Prof Matthew Symonds, A/Prof Mike Weston and Prof Lee Ann Rollins to conduct high-quality research on bird behaviour and evolution. The position is part of an ARC Discovery Grant: Evolving escape: anti-predator adaptations in threatened bird species, a collaboration between Deakin University and University of New South Wales. This position is suited to an emerging researcher keen to explore research questions at the interface of behaviour, evolution and conservation biology. It would be ideal for an early-career researcher who seeks to have real-world impact and is eager to be part of dynamic, enthusiastic and supportive research team. As an Associate Research Fellow, Avian Behaviour, you will:

* Carry out an extensive field-based research programme in bird behaviour * Engage collaboratively to produce novel and high-quality research outputs in high-impact international journals * Utilise knowledge of the latest literature and methods relevant to the avian behaviour, ecology and evolution * Develop and employ skills in the analysis of biological data * Exhibit excellent stakeholder engagement and relationship- management skills (e.g., with BirdLife Australia, Victorian State Government, Zoos Victoria)

To be successful, you'll have:

* A PhD in a relevant discipline * A clean, current driving licence * Demonstrated ability to conduct and publish high-quality research * Experience, skills and capacity to conduct independent field studies of bird behaviour in remote locations and for extended periods of time * Proven capacity to design and manage a research project

For inquiries and/or confidential discussion, please contact Prof Matthew Symonds - matthew.symonds@deakin.edu.au. Please do not send applications to this email (use the link above for the job selection criteria and application portal). Applications for this position close on 14 May 2025

matthew.symonds@deakin.edu.au

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## DTU Denmark eDNA AquaticBiodiversity

We are seeking two postdocs to work on funded projects on marine eDNA.

To apply for the positions, please follow the link below:

Job Description The application of Environmental DNA (eDNA) for aquatic biodiversity assessment and fisheries management is progressing rapidly. If you see yourself at the forefront of this development and are interested in innovative solutions for eDNA collection as well as practical implementation of eDNA for the detection and management of fisheries resources and aquatic biodiversity, these positions may be of interest to you.

The main tasks of the two positions are:

1. To investigate biodiversity at offshore wind farms using eDNA to monitor spatial and temporal biodiversity variation, and to develop eDNA into a robust cost-efficient tool for marine environmental impact assessment. The scholarship is partly funded of the "WINDNA" project, financed by the Independent Research Fund Denmark and the Velux Foundations. The project includes collaboration with partners from the wind energy sector (Ãrsted, Total Energies), private research and advice (DHI) and national authorities (Danish Environment Agency) as well as NGOs.

2. To develop eDNA based methods to estimate bycatch of non-targeted fish species in fisheries catches. The aim of the project is to develop a high quality, cost-effective pipeline for eDNA based catch composition assessment using DNA from samples of production water surrounding the catch. The scholarship is partly funded by of the DNACATCH project supported by the Ministry of Food Agriculture and Fisheries through the Green Development and Demonstration Programme (GUDP). The project includes collaboration with the Danish pelagic fishing fleet (DPPO), fishmeal and fish oil producers (MID) and a private genetics/genomics company (Eurofins Genomics).

You will be responsible for:

* Collecting field samples from marine areas (1) or fishing vessels (2) * Generating and analyzing qPCR/dPCR and metabarcoding data * Collaborate with the other postdocs and assist in PhD and Masters student supervision.

* Collaborating with industry partners to implement eDNA in fisheries and biodiversity management.

* Publishing the methods and data in peer reviewed scientific journals.

* Communicating with the scientific community, stakeholders and the general public.

* Participating in project meetings, communication and collective output.

The primary workplace will be at DTU Aqua, Silkeborg Campus, where you will join an enthusiastic team of researchers, postdocs, PhD, and Master's students who focus on all aspects of cutting-edge aquatic eDNA analysis. The ideal candidate will have strong interpersonal skills and a proven ability to work well within a team toward common goals.

As a formal qualification, you must hold a PhD degree (or equivalent). It will be an advantage if you have previous experience in (e)DNA analysis.

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 period of employment is 2 years. The start date is 1 August 2025 or as soon as possible thereafter.

You can read more about career paths at DTU here

Further information May be obtained from Professor Einar Eg Nielsen een@aqua.dtu.dk, +4540210231 who is the coordinator for the genetics group at DTU Aqua and Head of Section for Marine Living Resources Carsten Hvingel, carhv@aqua.dtu.dk, +4593511196.

You can read more about the Section at www.aqua.dtu.dk and about the genetics group at https://www.aqua.dtu.dk/english/research/population_genetics 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 1 May 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", 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 * Description of relevant experience and qualifications regarding eDNA analysis

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## France EvolOysterImmunity

Hello,

We are offering a postdoctoral research position focused on the role of epigenetics in immune priming in the Pacific oyster /Magallana gigas/. Please feel free to share this opportunity with any potential candidates.

Details about the position can be found at the following link: https://ihpe.fr/recrutements/ Applications must be submitted through the CNRS job portal at the following link: https://emploi.cnrs.fr/Offres/CDD/UMR5244-CELCOS-001/Default.aspx?lang=EN Best regards,

Cï¿½line Cosseau

Cï¿½line Cosseau Professeure des Universitï¿½s, CNU67 IHPE UMR 5244 Universitï¿½ de Perpignan Via Domitia 58 Avenue Paul Alduy Bï¿½t R F-66860ï¿½ Perpignan Cedex,ï¿½ France Tel 33 (0)4.68.66.22.81 http://ihpe.univ-perp.fr/ Eve Toulza <eve.toulza@univ-perp.fr>

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## FredHutch ViralEvolutionaryForecasting

We have an opening for a postdoc in the Bedford Lab at the Fred Hutch Cancer Center to work on developing and applying DNA and protein language models to understand and forecast viral evolution.

The Bedford Lab has worked extensively in the field of viral evolutionary forecasting. In this context, we've developed models to estimate fitness of seasonal influenza variants from genetic sequence data and to then use fitness estimates to forecast variant frequencies (Huddleston et al., eLife, 2020). We've taken a similar approach to forecasting SARS-CoV-2 variants in applying multinomial logistic regression (MLR) to estimate variant fitness and to project frequencies forward in time (Abousamra et al., PLoS Comput Biol, 2024). This approach underlies our live SARS-CoV-2 evolutionary forecasts at < http://nextstrain.org/sars-cov-2/forecasts >. Our influenza forecasts are directly utilized by the World Health Organization in the twice yearly vaccine strain selection meetings for seasonal influenza.

Recent advances in deep learning, especially transformer-based language models for protein sequences (see ESM3) and DNA sequences (see Evo2), present exciting new avenues to enhance evolutionary predictions. These models, trained to predict residues or nucleotides based on sequence context, have potential to significantly improve predictions of variant fitness and evolution.

In this role, you'll initially focus on incorporating state-of-the-art language models to assess and predict the fitness of influenza and SARS-CoV-2 variants, comparing these predictions to our established statistical models. A key aim is to leverage these advanced models to provide deeper insights than traditional "mutational load" metrics, which simply count the number of amino acid changes. Additionally, you will explore how embedding spaces derived from these language models could offer new perspectives on evolutionary processes (see Hie et al for an example of looking at semantic change via embedding). Beyond applying existing language model frameworks, you'll have opportunities to design novel model architectures to describe the process of sequence evolution.

The ideal candidate will have experience working with deep learning models via PyTorch or other frameworks. However, candidates with more traditional experience in sequence data and phylogenetic approaches who are excited to dive into deep learning models are also strongly encouraged to apply. Candidates should have experience in at least one programming language and a proven track-record of peer reviewed publications. A quantitative background is essential, though PhDs from diverse fields including biology, mathematics, statistics, physics and computer science are welcome. The Fred Hutch is an equal opportunity employer committed to workforce diversity. Applicants of diverse backgrounds are particularly encouraged to apply.

The position is available immediately with flexible starting dates. Informal inquires are welcome. Applications will be accepted until the position is filled. Fred Hutch offers competitive compensation and benefits packages.

To apply please submit 1. cover letter that includes the names and contacts for three references and a short statement of research interests 2. a current CV 3. code samples or links to code on GitHub

Send application materials or inquiries to tb@bedford.io.

Trevor Bedford Professor, Vaccine and Infectious Disease, Human Biology and Public Health Sciences Divisions, Fred Hutchinson Cancer Center Investigator, Howard Hughes Medical Institute Affiliate Professor, Department of Genome Sciences and Department of Epidemiology, University of Washington

https://bedford.io/blog/postdoc-sequence-language-models/ trevor@bedford.io

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## GeorgiaTech Speciation

The Anderson Lab at Georgia Tech is seeking a postdoctoral researcher interested in the process of speciation. The expected focus of the successful candidate's work will be questions related to evolutionary divergence in allopatry and to the genomic, demographic, and/or eco-evolutionary consequences of secondary contact.

Our Group & Interests:Research in the lab is focused on understanding the processes that generate biodiversity and that explain its biased distribution across the globe. Our work blends evolutionary genetics with evolutionary ecology and computational biology with field biology to shed light on speciation and the evolution of coexistence between close relatives.

Our understanding of speciation is currently in a period of historic transformation due to insights that have emerged from genomic data. It is now clear that basic questions we thought were answered just 20 years ago are in fact anything but. This means that researchers today have the rare opportunity to make progress on questions that are genuinely fundamental, which makes this an exceptionally exciting time for speciation research. We're looking for a researcher keen to tackling these big unanswered questions.

Skills Required:Our group is question-driven and works with a variety of organisms and data types. One component of our research involves the fine-grained investigation of speciation in individual lineage pairs, another involves large-scale data syntheses and comparative analyses, and yet another component is purely theoretical. As such, researchers with a variety of taxonomic interests and methodological skill sets are encouraged to apply. The most important criteria are that the applicant is enthusiastic about the research question(s) and has a proven record of seeing projects through to completion.

Start Date:The ideal start date is summer 2025. This is negotiable.

Salary:Salary starts at $60,000 and includes a health care package.

Term Length:Funding for the position is available for two years, pending a mutual performance review after year one. Extension beyond two years may be possible. Candidates will be encouraged to apply for external funding.

The Place:The School of Biological Sciences at Georgia Tech is a large and supportive biology department home to enthusiastic and highly productive researchers. Our group is part of a growing core of labs focused on eco-evolutionary research; you will find a great group of top-flight biologists here with whom to discuss your work. Atlanta is also a vibrant and diverse city that leads the Lower 48 in green space per capita.

Application Timeline:Applications will be considered until May 15th and are evaluated on a rolling basis. Short-listed candidates will be notified.

Relevant Websites:

Lab webpage: seanasanderson.github.io

Georgia Tech School of Biological Sciences: https://biosciences.gatech.edu/ To apply:please submit a single pdf file containing a letter of interest, a CV, and the names and contact information for 2-3 references to sean.anderson@gatech.edu.

Sean A. S. Anderson

sean.anderson@gatech.edu

Assistant Professor

School of Biological Sciences

Georgia Institute of Technology

"Anderson, Sean" <sanderson353@gatech.edu>

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## Krakow EvolMammalogy

A fully funded 3-year postdoctoral position is available in evolutionary ecology at the Institute of Nature Conservation, Polish Academy of Sciences (INC PAS), Kraków, Poland. The position is part of the OPUS project "Global Wind Regimes in Ecogeographical Rules of Evolution," funded by the National Science Centre Poland. We are seeking an independent researcher to explore how wind and climate drive global mammalian adaptations in body size and appendage length.

Position Details: - Start date: April/May 2025 - Salary: ~7000 PLN net/month (140,000 PLN gross gross per year) - Location: INC PAS, al. Adama Mickiewicza 33, Kraków, Poland - Duration: 3 years, with a 6-month trial period - Additional funding: travel to conferences, research stays abroad, support for independent research

Responsibilities: - Literature review on mammalian phenotypes and wind adaptation - Assemble and manage global datasets - Conduct phylogenetic and spatial analyses (R) - Publish high-impact papers - Participate in conferences, workshops, and outreach

Requirements: - PhD in evolutionary biology, zoology, computational ecology, or a related field (obtained within the past 7 years) - Experience with large-scale data, R, and phylogenetic comparative methods - Strong knowledge of mammalian diversity and evolutionary biology - Good spoken and written English

Additional advantages: - Experience with Brownian Motion and Ornstein-Uhlenbeck models - Publications in high-impact journals - Familiarity with ecogeographical rules and thermal biology

Application: Send a single PDF including: - 2-page cover letter - PhD diploma (recognized in Poland or nostrified) - CV with publication list and referees - Signed consent for data processing

Email: sekretariat@iop.krakow.pl (Cc: frohlich@iop.krakow.pl) Deadline: April 17, 2025

Full announcement: https://panel.iop.krakow.pl/uploads/232/postdoc_position_within_OPUS_2.pdf For questions, contact Dr. Arkadiusz Fröhlich at frohlich@iop.krakow.pl

Arkadiusz Fröhlich <frohlich@iop.krakow.pl>

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## NorthCarolinaStateU PlantPopulationEvolution

Postdoctoral position in Plant Population Ecology

Department of Plant and Microbial Biology

North Carolina State University

The Sheth plant evolutionary ecology lab < https://seemasheth.weebly.com/ > in the Department of Plant and Microbial Biology at North Carolina State University (Raleigh, NC; USA) and the Angert Lab < https://angert.github.io/index.html > in the Departments of Botany and Zoology at the University of British Columbia (Vancouver, BC; Canada) are currently seeking a highly motivated postdoctoral associate to participate in an NSF-funded study of range-wide demography in the riparian plant, scarlet monkeyflower. The project aims to understand how plant population dynamics vary along latitudinal and elevational gradients; how populations recover from extreme climatic events; and how rapid evolution increases population persistence under climate change. We strive to foster an environment where people from all backgrounds are respected.

Position summary: The successful candidate will contribute to studies of population dynamics across the geographic range of the scarlet monkeyflower, Mimulus cardinalis, a perennial herb that grows in riparian habitats in western North America. The postdoctoral scholar's primary responsibilities involve:

- Migrating the existing demographic database to a format that can be queried directly in R and accessed remotely - Contributing to demographic data collection and training technicians in the field - Training and managing personnel - Managing and analyzing data - Leading the dissemination of results through manuscripts and presentations - Participating in outreach activities

The position is based out of NCSU and requires travel to California and Oregon in August/September each year to train field technicians and help collect data during demographic surveys. The postdoctoral scholar will also have opportunities to analyze existing datasets, develop additional research programs related to the overall objectives of the project, and gain experience mentoring undergraduate and graduate students. The postdoc will be co-mentored by Dr. Amy Angert at the University of British Columbia.

Qualifications: Candidates must have a Ph.D. in Ecology, Evolutionary Biology, Botany, or a related discipline, and experience with demographic modeling and simulations in R. Candidates are also expected to have a background in statistical methods, a strong work ethic, and excellent problem-solving, interpersonal, communication, and time management skills. A clear track record of publications, independent research experience, and a commitment to mentoring post-bacs and undergraduates is also required. A valid driver's US license at the time of hire, and the candidate must be available to work away from home at field sites for a minimum of two weeks per year. Experience conducting field work with plants, along with knowledge of database management, are strongly desired.

Salary and appointment term: $62,000 per year with benefits < https://benefits.hr.ncsu.edu/postdoc-health-insurance/ >. At present, we anticipate this position to be initially for 1 year, with possible extension for an additional year. Start date is flexible, but ideally between October of 2025 and May of 2026.

Commitment to wellbeing and career development: The Sheth and Angert Labs are committed to fostering an environment where people from all backgrounds are respected. In addition, Drs. Sheth and Angert will develop a mentoring and professional development plan with the postdoc to identify priorities and needs that would help the postdoc achieve their professional goals and desired work-life balance. We are open to providing other accommodations (e.g., if there are barriers to participation in field work) as needed.

Commitment to field safety: We are committed to providing a safe field work experience for all members of the collaborative team. In the context of this position, safety measures we have in place include always having a second person along during all field work, pre-planned schedules and routes with work sites in protected areas whenever possible, a clear plan for daily check-ins and a mode of continuous communication while in the field, a checklist to ensure that appropriate personal protective equipment are included on each trip, and an agreed upon emergency plan. We are happy to discuss and address any other safety-related concerns you have.

About NC State and the Raleigh area: NC State's Department of Plant and Microbial Biology offers a highly-rated research environment and is situated in a collaborative and scientifically stimulating atmosphere in the Research Triangle, with both UNC Chapel Hill and Duke University nearby. There is a vibrant and growing community of ecologists and

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## Philadelphia BiodiversityAnalysis

Postdoctoral position in biodiversity analysis and extinction risk, Temple University, Philadelphia, USA

A postdoctoral position in biodiversity forecasting and extinction risk is available in the laboratory of Blair Hedges in the Center for Biodiversity at Temple University, Philadelphia. Funding for the position comes from the NSF program "Biodiversity on a Changing Planet" (BoCP). The research project tests hypotheses of global change and extinction risk across landscapes and through time using animal and plant species.

A PhD in a relevant field and fluency in English are required, as well as proven expertise in spatial modelling and scripting languages (e.g. R, Python). The ideal candidate will have experience with large biodiversity datasets including climate and landcover layers, cluster computing, be able to develop new ideas independently, and be an excellent team worker. The successful candidate will join a team of researchers from several institutions with expertise in organismal and evolutionary biology, satellite remote sensing, and extinction risk.

The Center for Biodiversity is located within Temple's Science, Education, and Research Center (SERC) on the main campus. It is affiliated with the Department of Biology and College of Science and Technology. Temple University is located in the heart of historic Philadelphia, home to many academic and research institutions as well as numerous cultural attractions.

Interested persons should send an e-mail to Prof. S. Blair Hedges (sbh@temple.edu) briefly stating their previous research, future career goals, and motivation for this project. Also, attach a full curriculum vitae that contains contact information for three academic references. Review of applications will begin immediately and continue until the position is filled.

The successful candidate could start immediately (preferred) or later in 2025. Temple University is an equal opportunity and equal access employer committed to achieving a diverse workforce (AA, EOE, m/f/d/v).

Hedges Lab https://www.hedgeslab.org Center for Biodiversity https://www.biodiversitycenter.org sbh@temple.edu

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## PurdueU EpigeneticClocks

Postdoc on Epigenetic Clocks at Purdue University (West Lafayette, IN, USA) — Closing date: 20th May 2025 or until the position is filled — A postdoc position is available immediately in Andrew DeWoody's lab at Purdue University (West Lafayette, Indiana, USA).

The successful applicant will develop, calibrate, and employ epigenetic clocks for use in demographic and evolutionary studies pertaining to wildlife and/or fisheries management. Requisite skills include DNA extractions (ideally from noninvasive sources), PCR, sequencing and basic statistical modeling (e.g., simple regression). Desired skills include qPCR, ddPCR, and/or bisulfite sequencing as well as elastic net regression or other statistical techniques suitable for use with high-dimensionality data. The initial appointment is for 12 months with the possibility of an extension.

Prospective applicants should first review this out-of-date webpage (https://www.purdue.edu/fnr/sites/-dewoody/lab-members/potential-students/), then contact Andrew DeWoody via email (please attach a current CV) to see if a video chat is warranted.

"Purdue University is a public research institution demonstrating excellence at scale. Ranked among top 10 public universities and with two colleges in the top four in the United States, Purdue discovers and disseminates knowledge with a quality and at a scale second to none. More than 105,000 students study at Purdue across modalities and locations, including nearly 50,000 in person on the West Lafayette campus. Committed to affordability and accessibility, Purdue's main campus has frozen tuition 13 years in a row. See how Purdue never stops in the persistent pursuit of the next giant leap including its first comprehensive urban campus in Indianapolis, the new Mitchell E. Daniels, Jr. School of Business, and Purdue Computes."

"DeWoody, James Andrew" <dewoody@purdue.edu>

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## SLU Sweden MicrobialResistance

Postdoctoral position in Chemical Ecology at SLU Alnarp, Sweden

Reference number SLU.ua.2025.2.5.1-1118

We are offering a Postdoctoral Position on Consequences of Microbial Induced Resistance on Trophic Plant-Microbe-Insect Interactions

We seek a motivated postdoctoral researcher for a new project on trophic interactions in systems of microbial induced plant resistance. The postdoc will be part of a collaborative research project entitled 'Mechanisms and consequences of microbial induced resistance on trophic interactions and biocontrol efficacy' funded by the Novo Nordisk Foundation.

Beneficial microorganisms can be used to colonize the rhizosphere of plants and modulate plant defence mechanisms against insect pests. The project aims to quantify the short- and long-term effects of microbial induced resistance (MIR) on aphid populations feeding for multiple generations on sweet pepper plants inoculated with root-colonizing fungi. The project will moreover investigate how aphid endosymbionts influence aphids in relation to MIR and natural enemies.

About the position: The project will bridge plant-microbe-insect interactions with chemical ecology in a trophic network approach, thereby contributing to our understanding of the full potential of beneficial microbes in plant production. Specifically, the project will investigate the interactive effect of MIR and aphid endosymbiont communities on the emission of volatile organic compounds (VOCs) of plants. Analyses of VOCs will be aligned with behavioural assays using aphidophagous hoverflies to evaluate how MIR affects plant-insect communication at higher trophic levels.

The main duties of the postdoc will be to carry out an independent research project under supervision. Specifically, the postdoc must develop and conduct behavioural experiments with hoverflies and chemical analyses of VOCs. Other duties include cultivation of plants, insects and microorganisms, writing scientific manuscripts, presenting project outcomes, and to supervise students at basic and advanced level.

The research project will be coordinated by Paul Becher at the Swedish University of Agricultural Sciences, Department of Plant Protection Biology, Alnarp, Sweden in partnership with Dr. Nicolai V. Meyling at Copenhagen University, Denmark. The postdoc will collaborate with a PhD student at Copenhagen University, where parts of the project will be carried out. The distance between Alnarp campus and the institute at Copenhagen is about 1.5 h travel by public transport.

Your profile: As a person you are enthusiastic and responsible, and have excellent collaborative skills. In addition, you should meet the following requirements:

- Hold a PhD degree in biology, ecology, analytical chemistry or equivalent - Educational and professional qualifications relating to the scientific area of the position - Experience with independent planning, execution and evaluation of experiments, including statistical analysis - Familiarity with theory and techniques of chemical ecology, chemical analyses, entomology, microbiology, plant science, biological control is meriting - Interest in contributing to an international research environment and interdisciplinary research - Curious mind-set and an interest in experimental biological systems - A proven record of English speaking, reading and writing skills - As postdoctoral appointments are career-developing positions for junior researchers, we are primarily looking for candidates with a doctoral degree that is three years old at most.

About us: At the Department of Plant Protection Biology we conduct interdisciplinary research, encompassing Chemical Ecology, Resistance Biology and Integrated Plant Protection research, providing excellent opportunities for strong research collaboration within and outside the departmental area. Research efforts at the department are directed towards both fundamental and applied research. Applied plant protection research is carried out in collaboration with industry and focuses primarily on the development of environmentally sustainable pest and disease control strategies for agriculture and horticulture, both in Sweden and internationally.

For more information about the department: Department of Plant Protection Biology https://www.slu.se/en/departments/plant-protection-biology/research/ Read more about our benefits and working at SLU by visiting: https://www.slu.se/en/about-slu/work-at-slu/ Location: This position is based in the Chemical Ecology unit at the Department of Plant Protection Biology at SLU Alnarp, one of SLU's main campuses.

Form of employment: Temporary employment 24 months, with the possibility of extension.

Scope: 100%

Start date: As agreed. Preferably September 2025.

Application: Please submit your application before

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## StateUNewYork Syracuse ComparativeImmunology

Title: Postdoctoral Associate in Comparative Immunology

Unit: Research Foundation

Duration: 1 year with potential for reappointment for up to 2 additional years

Location: SUNY College of Environmental Science and Forestry, Syracuse, NY

Salary: $59,000 annually plus benefits (https://benefits.rfsuny.org/regular–postdoctoral-employees/)

Position Description

The lab of Dr. Cynthia Downs (https://www.esf.edu/faculty/downs/index.php) at SUNY College of Environmental Science and Forestry (ESF) seeks to hire one Postdoctoral Associate to perform comparative immunology work. The individual will work on an NSF-funded research project in collaboration with Dr. Andreas Koenig at SUNY Upstate Medical University (Syracuse) and Dr. Jessica Brinkworth at the University of Illinois Urbana-Champaign. The successful candidate will be part of an interdisciplinary team investigating the comparative immunology of neutrophil functions across various mammalian species. Projects will involve quantifying neutrophil antibacterial functions and neutrophil cellular energetics during immune challenges ex vivo to test hypotheses about how body mass shapes investment in immune defenses.

Primary Responsibilities Include (but are not limited to):

The postdoc will be involved with isolating neutrophils from whole blood samples, conducting assays to antibacterial functions in neutrophils, quantifying cellular bioenergetics of neutrophils, and quantifying signaling pathways of neutrophils during an immune challenge using comparative transcriptomic approaches, and managing student technicians. The postdoc will also be encouraged to write new grants in an area related to the main project and to contribute to theory-based work in the workgroup. Mentoring and opportunities related to career development will be provided. This position requires travel to animal care facilities for lab work for up to two weeks at a time and may require relocation to the University of Illinois for three months for training in techniques, depending on prior experience. Candidates must be highly motivated, think independently, and work as part of integrated multidisciplinary research teams.

Please contact Cynthia Downs at cjdowns@esf.edu for additional information.

Required Qualifications:

A PhD in immunology, microbiology, integrative organismal biology, or another related field and experience with immunological and/or molecular techniques. Candidates must be willing to travel for training and sample collection.

Preferred qualifications:

Experience with aseptic and immunological lab techniques, including cell isolation from whole blood and cell culture.

Experience raising microbial populations in and outside of eukaryotic cells, culturing a broad range of microorganisms, and infection protocols.

Familiarity with comparative evolutionary methods and allometric theory or a willingness to learn.

Expertise with metabolic assays, metabolomic techniques, or both.

Experience with transcriptomics lab work and analytical workflows and analyses.

Experience with large datasets and Linux environments and proficiency in Program R. Experience with comparative analyses is a plus.

Record of academic and research achievements.

Application Procedure: To apply, send a cover letter, CV, and contact information for three employment references (as a single attachment) to Dr. Cynthia Downs at cjdowns@esf.edu.

Application Deadline: Applications will be accepted until the position is filled, but the first review will begin on May 5, 2025. A start date of June or July is preferred, but the start date is negotiable.

SUNY-ESF and the Broader Community

ESF is a specialized college within the 64-campus SUNY system, and a Carnegie R2 "High Research Activity" Institution that consistently earns high rankings in US News and World Report, Forbes, Princeton Review, and other national college guidebooks. With a total enrollment of about 2,200 undergraduates and 400 graduate students, combined with the immediate proximity of Syracuse University and Upstate Medical University, ESF provides an intimate, small-college atmosphere within a vibrant, large-university setting. ESF's extended campuses include more than 25,000 acres of forest properties, both close to Syracuse and across the Adirondack Park, which provide numerous opportunities for experiential coursework, research, and public outreach.

Located on the eastern edge of the Finger Lakes region, Syracuse is a small city in a rural region offering a diversity of natural and cultural amenities, a low cost of living, and a high quality of life - ranking among the top 10 percent of "Best Places to Live" in "The Places Rated Almanac." Syracuse is situated with easy access to New York City, the Adirondack Park, Lake Ontario, and many other points of interest in

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## StockholmMuseum AdaptiveRadiationTheory

*All info* *What* Computational biologist/theoretical eco-evolutionary biologist for a two-year postdoc. The project focuses on developing trait-based models of adaptive radiation, exploring how ecological and evolutionary processes such as niche divergence, hybridization, and genomic structure may influence ecological diversification and speciation.

*Who/Where* Stockholm at the Swedish Museum of Natural History with JosïÂ¿Â½ Cerca and with strong links with Mikael Pontarp (Lund University)

*Some more info* 2-year position Supportive environment (possibility to co-supervise PhD students, write own grants)

(In)formal inquires are welcome - JosïÂ¿Â½

islandevolution.github.io

Google Scholar < https://scholar.google.pt/citations?user=ZI1vWPEAAAAJ&hl=en >

Evolutionary Biologist Swedish Museum of Natural History (20% @ the University of Oslo)

JosïÂ¿Â½ Cerca <jose.cerca@gmail.com>

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## StockholmMuseum PlantHybridGenomes

*All info* https://recruit.visma.com/spa/public/apply?guidAssignment=643055ec-ea42-4b85-928b-e93d4f7092cc&description=True *What* We will focus on sequencing the genome of an Argyranthemum species in the Canary Islands and investigate the evolution of two independent homoploid hybrid lineages. This work will integrate comparative genomics (including the production of reference genomes, annotation, and characterization of transposable elements) with population genomics (such as variant calling and analyses of hybridization), and simulation-based approaches.

You will explore questions such as:

Do different homoploid hybrid lineages exhibit signatures of hybridization in distinct genomic regions? Are homoploid hybrid lineages interbreeding with each other or with parental species? To what extent are these lineages genetically differentiated?

*Who/Where* Swedish Museum of Natural History with Josï¿½ Cerca with strong links with Rike Stelkens (Stockholm University)

*Some more info* 2-year position Supportive environment (possibility to co-supervise PhD students, write own grants)

(In)formal inquires are welcome - Josï¿½ –

islandevolution.github.io

Google Scholar < https://scholar.google.pt/citations?user=ZI1vWPEAAAAJ&hl=en >

Evolutionary Biologist

Swedish Museum of Natural History

(20% @ the University of Oslo)

Josï¿½ Cerca <jose.cerca@gmail.com>

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

## TechnicalU Denmark EvolutionGenetics

Postdoc in Building Development, Evolution and Genetics - DTU Construct, Technical University of Denmark (DTU)

Reference: 4440

Closing date: 12th May 2025

If a biologist had never seen a building before, how might they think it had grown and evolved? Could they find a âcode' for buildings?

We seek an evolutionary & / developmental / computational biologist for a Postdoc position in an interdisciplinary group applying biological analysis methods to building models to identify new methods to analyse and design better, more sustainable buildings.

The post is available for 21 months in the first instance, starting as soon as possible, with the possibility of an extension.

We encourage you to contact Tim McGinley with any questions about the position and discuss how the position and its aims could co-evolve with your own interests and ambitions. Tim's email is timmc@dtu.dk (please send CV to start an informal chat) and also possible to connect and chat on Linkedin - https://www.linkedin.com/in/timmcginley/ For further details and information on how to apply, please see here:

https://www.nature.com/naturecareers/job/12838548/postdoc-in-building-development-evolution-and-genetics-dtu-construct/ Postdoc in Building Development, Evolution and Genetics - DTU Construct job with Technical University of Denmark (DTU) | 12838548 - Nature Postdoc in Building Development, Evolution and Genetics - DTU Construct job in Copenhagen, Hovedstaden (DK) with Technical University of Denmark (DTU). Apply Today. www.nature.com î

Tim Pat McGinley <timmc@dtu.dk>

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## UBritishColumbia ModellingInfectiousDisease

The King Lab in the Department of Zoology at the University of British Columbia (UBC), in collaboration with Ben Ashby in the Department of Mathematics at Simon Fraser University, is seeking an enthusiastic and self-motivated Postdoctoral Fellow. The goal of the project would be to use mathematical modelling to understand the impact of biodiversity across species and populations on infectious disease emergence and evolution.

Dr. Kayla King leads a diverse team with an interdisciplinary approach to studying the evolution and ecology of host-pathogen interactions. This position is part of a larger Canada Excellence Research Chair program understanding infectious disease evolution amidst global change. The successful applicant will have the opportunity to develop mathematical models of relevance to zoonoses and conservation biology. In addition, there are several opportunities to contribute to ongoing studies linking models with empirical data in animal-pathogen systems.

We are looking for a recent PhD with experience in developing mathematical theory in the fields of evolutionary biology, ecology, and infectious disease. Start date is negotiable, but ideally summer 2025. Funding for this position is available for 2 years with possibility of extension. Salary will start at $60,000 CAD with a generous extended health benefits package. Salary will be commensurate with qualifications, experience, and any independent funding secured. Only shortlisted candidates will be notified. Contact Dr. Kayla King (kayla.king@ubc.ca) for more information or to apply. To apply, please send a CV, a letter of interest, and names/contact information for 2-3 references in one file (Last Name, First Name: PDF.BiodiversityInfection)

For more details about the two lab groups, please see: www.zoology.ubc.ca/kinglab (King Lab) and https://-ecoevotheory.com/ (Ashby Group).

Equity and diversity are essential to academic excellence. An open and diverse community fosters the inclusion of voices that have been underrepresented or discouraged. We encourage applications from members of groups that have been marginalized on any grounds enumerated under the B.C. Human Rights Code, including sex, sexual orientation, gender identity or expression, racialization, disability, political belief, religion, marital or family status, age, and/or status as a First Nation, Metis, Inuit, or Indigenous person. We understand that career paths vary. Legitimate career interruptions will in no way prejudice the assessment process, and their impact will be carefully considered.

Kayla C King (She, Her, Hers) Professor and Canada Excellence Research Chair Co-Director, PrePARE Research Cluster Department of Zoology and Department of Microbiology & Immunology University of British Columbia | Musqueam Traditional Territory

Professorial Fellow University of Oxford

www.zoology.ubc.ca/kinglab https://prepare.ubc.ca/ kayla.king@ubc.ca

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## UC London GeneticsEvolutionEcol

The Research Department of Genetics, Evolution and Environment, (GEE) at University College London (UCL) is organised into six Centres, with cross-cutting research interests, and close links with other organisations, including the Francis Crick Institute, the Natural History Museum, and The Zoological Society of London. The department has a long and rich history across many biological topics, a summary of which can be found here.

GEE is grouped into six centres that are especially interested in the following research areas:

Institute of Healthy Aging: Ageing, age-related disease; interventions improving late-life health in model systems (e.g. cellular senescence); applying computational approaches to ageing and late-life disease (AI, big data, medical genomics).

Centre for Biodiversity and Environment Research: Evolution in response to environmental change; theoretical ecology/evolution; community or behavioural ecology (especially in plants, insects, fungi or microbes); biodiversity and its contributions to human health and well-being.

Centre for Life's Origins and Evolution: Centre for Life's Origins and Evolution: Origins and diversification of major groups of life; comparative genomics; evolution of cells and cell types; invertebrate palaeontology, plant and fungal evolutionary genomics, experimental evolution.

UCL Centre for Computational Biology: Big data and computation; computational genomics; computational phylogenomics.

UCL Genetics Institute: Computational approaches to biology or medicine; computational tool development and applying them to genomic data; high-throughput bioinformatics, statistical genetics; metagenomics.

UCL East People and Nature Lab: Cross-disciplinary solutions hub bringing together expertise from ecology, computer science, public health, built environment and social science to gather evidence on how we can best manage our natural resources for a sustainable and resilient future.

About the role GEE invites Expressions of Interest from Early Career Researchers (ECRs) who wish to be sponsored to apply for external fellowships to establish an independent research group. GEE offers a world-class, interactive and supportive research environment within the Division of Biosciences at UCL. We are strongly committed to recruiting and supporting the most promising ECRs who choose to secure a Group Leader Fellowship as their route to becoming a Principal Investigator. This policy applies to senior fellowships such as Wellcome Trust Henry Dale, MRC CDA, BBSRC David Phillips, NERC IRF, Royal Society URF, CRUK, ERC Starting Grants and equivalent fellowships.

The deadline for this round is 25 April 2025.

Applications need to be submitted via this link https://www.ucl.ac.uk/work-at-ucl/search-ucl-jobs/details?jobId=32520&jobTitle=Research+Career+Development+Fellowships+in+the+Department+of+Genetics,+Evolution+and+Environment,+UCL:+Expre *Important* Salary is provided by the external award that is secured in future applications to the relevant fellowship schemes. UCL will not provide salary whilst the supported fellows apply for the fellowship schemes.

About you

We are looking for candidates of the highest calibre, able to demonstrate an exceptional track record in relation to their career stage, and have the potential to submit competitive fellowship applications and secure external funding. Your initial application will be pre-assessed by several members of staff. We will also identify the researcher in GEE closest to your field, who will act as your sponsor and guide you through the selection process.

If selected as a suitable candidate following pre-assessment, you will be invited to deliver a research talk to present your recent work and fellowship plans. This is planned to occur in early June 2025. You will get the chance to meet our staff and students and view our facilities. In addition, you will get the opportunity to meet current GEE fellows, including those who have progressed to permanent positions within the department, and learn about the supportive and stimulating environment we offer. Where a visit is not possible, the discussion will be conducted online. Following a positive outcome of the visit, we will identify a sponsor(s) to support your fellowship application.

Eligibility:

Candidates should confirm their eligibility for specific fellowship schemes and will be required to provide evidence of eligibility to work in the UK before commencing any fellowship offered.

To apply, please ensure to attach the following:

1. Your CV (3 pages maximum).
2. A brief (2 pages maximum) document outlining your research proposal

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## UCopenhagen 2yr NarwhalPopulationGenomics

Postdoc in narwhal population genomics and demography at Globe Institute, Faculty of Health and Medical Sciences, University of Copenhagen

We are looking for a highly motivated, competent, independent, and dynamic researcher for a 2-year Postdoctoral fellowship, with demonstrated experience in relevant areas of population genomic research. The position will commence on 1 October 2025, or as soon as possible hereafter.

The full-time postdoc position is funded by the Danish Independent Research Fund (DFF) 'BRIDGE – bridging fundamental science and applied conservation in polar research', as part of their 2024 thematic research call in 'Arctic research - Climate change and sustainable arctic communities'.

Our research and work environment This postdoc position is a joint project between the Globe Institute at University of Copenhagen and Pinngortitaleriffik (Greenland Institute of Natural Resources). The successful candidate will thus be part of both research environments.

The Molecular Ecology and Global Climate Change group at the Globe Institute is led by Professor Eline Lorenzen. The Lorenzen group integrates biomolecular data to understand patterns and drivers of eco-evolutionary change in mammal populations. We are an international group of PhD students and postdocs - currently from - China, Denmark, New Zealand, South Africa, and the US. Our work is interdisciplinary and highly collaborative, and we value a diverse, inclusive, supportive, and team-oriented work environment that fosters creativity. We are based in the Section for Molecular Ecology and Evolution, one of six research sections at Globe Institute.

Professor Mads Peter Heide-Jørgensen from the Greenland Institute of Natural Resources has extensive experience in marine mammal studies in Greenland, including narwhals. Mads Peter is responsible for the biopsy sampling program for narwhals in Scoresby Sound, which has been conducted annually since 2005 and is the foundation of this postdoc.

Senior researcher Marie Louis at the Greenland Institute of Natural Resources has a background in population genomics, ecology and evolution, with a focus on marine mammals, and has worked extensively on narwhal populations around Greenland.

The Greenland Institute of Natural Resources conducts research into Arctic ecosystems, monitors the living resources and the environment in Greenland, and advises the Government of Greenland and other authorities on sustainable exploitation of living resources and safeguarding the environment and biodiversity.

Your job Your research will focus on investigating patterns of demographic change in narwhals in Scoresby Sound, across the past 20 years, based on genetic analysis of a unique time series of 200 tissue samples collected by the Greenland Institute of Natural Resources since 2005.

Narwhals are considered the most sensitive Arctic marine mammal to climate change, due to their adaptations to a narrow sea-temperature niche, dependence on sea ice, specialised feeding habits, restricted range, and low plasticity in migratory patterns. They are the first Arctic marine mammals that at a population level show clear signs of the effects of habitat loss. A recent letter in the journal Science by Heide-Jørgensen et al. (2020) served as a clarion call that narwhals require targeted conservation to ensure the survival of individual subpopulations, each of which has its own ecological niche, migratory routes, and exploitation history.

Over the past two decades in Scoresby Sound, a vital area for Inuit subsistence hunting, narwhals have experienced an alarming level of decline. Due to their extreme site fidelity and niche-conservative behaviour, the loss of sub-populations will likely be permanent, and recolonization is unlikely. The extirpation of this top predator from Scoresby Sound, one of the largest and longest fjord systems in the world, would widely affect the trophic cascades of the ecosystem, and in addition have major impacts on Inuit communities relying on them for subsistence and their cultural heritage.

This project will use genome-wide data to identify the demographic consequences of a rapidly decreasing population in this top predator. We hypothesise the decline has resulted in an increase in relatedness and a change in population composition in recent years. Hence, the project will (i) estimate changes in abundance since sampling of the narwhals in Scoresby Sound was initiated in 2005; (ii) identify individuals and their relatedness through time; (iii) infer changes in population composition and kinship using estimates of sex and relatedness.

Your findings will provide crucial insights into the status of not just this population, but also the food web and trophic cascades of which narwhals are an integral part, at timescales of direct relevance to conservation and management efforts.

Your work will include laboratory work for DNA data generation, and

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## ULaReunion France Ecohydrology

I think this post doc offer at the University of La Réunion (France) could be of the interest of the EVOLDIR community.

Post Doc in Ecohydrology offer (36 months):

In a context of climate change, understanding the effect of environment on plants is a major challenge. In particular, it is important to characterise rainfall and its effect on plants. Spatial and temporal patterns of rainfall are highly heterogeneous and vary according to rain regimes and local terrain, while raindrop characteristics (distributions of size, terminal fall velocity, kinetic energy) can be modified by orographic effects (altitude and local slope) that affect the microphysical processes at play. Furthermore, raindrop characteristics are disrupted by canopy which can make drops explode into smaller drops or allow the generation of larger drops, while elevation of the canopy above ground may modify the associated fall speed.

To address the effect of rainfall on plants, we identified a suitable system: the splash-cup of the basal plant Marchantia globosa. Splash-cups are organs involved in dispersal: progenies are dispersed away from the parent plant by raindrops bouncing off splash-cups. This dispersal should depend on local raindrop characteristics. The fall velocity and volume of the raindrop determine the kinetic energy available for dispersal. Our preliminary results raise the question of whether plants adjust, directly or indirectly, splash-cup geometry to the local impacting raindrops in order to maximise dispersal.

To our knowledge, no such study has been reported in the literature, despite its ecological importance We are seeking for a postdoctoral researcher for a 36 month position as part of a collaborative project, the HYDROPOP ANR project, at PVBMT (Peuplements végétaux et bioagresseurs en milieu tropical) UMR in collaboration with LaCy (Laboratoire de l'atmosphère et des cyclones) UMR in La Réunion Island. This project is being carried out in collaboration with the Ecole Polytechnique (Palaiseau) and the Muséum National d'Histoire Naturelle (Paris).

S.he will be responsible for the following tasks:

1) Local characterization of raindrops in a tropical mountain forest on Reunion Island (Mascareignes archipelago), as well as forest microclimates, using optical disdrometers deployed within the experimental setup of the Observatoire de la zone critique de La Réunion.

2) Investigation of the "under-canopy" rain characteristics with respect to "free" precipitations at the different sites investigated

3) Identification of the environmental parameters influencing the morphology of splash-cup

4) testing phenotypic plasticity of splash cups of M. globosa in the island of la Réunion by performing reciprocal transplantation experiments along an elevational gradient.

Knowledge:

- In-depth knowledge (PhD level) in ecohydrology (PhD level) with good knowledge in climate data processing or of atmospheric physics with general knowledge of ecology or ecohydrology or ecophysiology.
- Good analysis skills.

Know-how:

- Participation in project team meetings and production of project deliverables
- Good writing skills
- Proficiency in oral and written presentation techniques
- Fluent in scientific English.

Soft skills:

- Communicate and manage relations with internal and external contacts
- Scientific rigor
- Ability to work as part of a team
- Adaptability to work in tropical field environments
- Demonstrate conscientiousness and scientific integrity.

The post doc will be based on the Northern campus of the University of la Réunion at the UMR PVBMT, on the Northern campus, in Saint-Denis and will be interacted with colleagues from the Observatory of the critical zone of Réunion (OZC-R) and from the Laboratory of the atmosphere and cyclones (LaCY).

For questions and formal applications (curriculum vitÃ including contact information of two references, a one-page letter describing your motivation), please send all the information in a single pdf with the subject "HYDROPOP Postdoc application_your name" to both Dr. Claudine Ah-Peng (claudine.ahpeng@univ-reunion.fr) and Pr. Joël van Baelen (joel.van-baelen@univ-reunion.fr).

Deadline of application: May 31st 2025 - 23:59 (Europe/Paris)

Dr. Claudine Ah-Peng Université de La Réunion, UMR PVBMT Pôle de protection des plantes 7 chemin de l'IRAT 97410 Saint-Pierre La Réunion T: +262 (0) 262 49 27 13 GSM: 06 92 68 79 93

Claudine Ahpeng <claudine.ahpeng@univ-reunion.fr>

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## ULausanne EvolQuantGenetics

Subject header: Postdoc in evolutionary quantitative genetics

TEXT OF POSTING:

***Postdoc in evolutionary quantitative genetics, Department of Ecology and Evolution, University of Lausanne, Switzerland

A postdoctoral position in evolutionary quantitative genetics is available in the research group of John Pannell in the Department of Ecology and Evolution, University of Lausanne. The postdoc would contribute to one or both of two projects funded by the Swiss National Science Foundation: (1) the evolution of sex allocation, sexual antagonism and sex chromosomes during transitions between hermaphroditism and dioecy; and (2) the evolution of plant populations at and beyond species range margins. The first project will involve the quantitative genetic analysis of a rapid transition from hermaphroditism to dioecy in experimental populations that have been evolving for approximately 15 years. We aim to understand the quantitative genetic architecture of the breakdown of dioecy and the subsequent ongoing evolution of an increased separation of the sexes in some of the experimental populations. The second project will involve the quantitative genetic and genomic analyses of experimental populations that have been established at multiple sites in Europe, including beyond the current range limits, under various admixture treatments. Both projects are using the annual dioecious plant species Mercurialis annua as an experimental model, for which we have substantial genetic resources including a good genome assembly.

***Research scope and skills sought While there are clearly defined goals in both projects, the postdoc's research direction can be tailored to his/her specific interests and expertise. He/she should have a PhD in evolutionary biology and/or population genetics/genomics and a skill set that would ideally include the statistical and quantitative genetic analysis of phenotypic and underlying genomic variation in natural eukaryote populations. Experience or an interest in working on sexual systems, sex chromosomes, sex allocation, and life histories would be an advantage, as would experience of research on plants (though this is not essential). The successful candidate should also have good communication and interpersonal skills, and an ability to work in a team. Although not a requirement, some knowledge of French would be an asset for living in French-speaking Switzerland.

***Host Department and University Information on the Pannell lab and its recent publications can be found here: https://www.unil.ch/dee/pannell-group . The lab is part of the Department of Ecology and Evolution of the University of Lausanne. The department hosts a broad range of research groups, with a particular strength in evolutionary biology, and its members enjoy a lively intellectual and social life, with weekly seminars and discussion groups. Although the University of Lausanne is francophone, the department is highly international, and all its research activity and seminars are conducted in English. The University has seven faculties and approximately 14,300 students and 3,900 researchers from over 120 countries. It is situated on a beautiful campus on the shore of Lake Geneva, and is close to the Swiss and French Alps.

***Contract details

The position is envisaged at 100% for an initial period of one year, with a possible (and desirable) renewal of a further two years. Most of the postdoc's time will be dedicated to research, but a contribution to teaching is expected, including the possibility of supervising master students. The starting date is flexible but would ideally be between September and the end of 2025.

***Applications Informal enquiries should be sent to John Pannell (john.pannell@unil.ch). Formal applications should include a cover letter detailing your research interests, experience and motivation for applying, a CV, and the names of two or three referees. Applications should be uploaded through the University of Lausanne platform (link given below). All applications received by 31 May will receive full consideration, but review of applications will begin immediately.

***Application link: https://tinyurl.com/4e7jhpu3
***University equality policy

The University of Lausanne promotes an equitable representation of men and women among its staff and encourages applications from women and minority groups.

John Pannell <john.pannell@unil.ch>

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## UMinnesota EvolBehavioralGenomics

Post-doctoral associate position in evolution and genomic of mating preferences

Mingzi Xu is seeking a post-doctoral associates to work on a NSF funded project about genomics of mating preferences using crickets as a model system in the Xu lab (https://mingzixu.weebly.com) at Department of Ecology, Evolution and Behavior at University of Minnesota-Twin Cities. The Xu lab conducts research to answer fundamental questions about sexual selection and evolution of behavior. We combine diverse research approaches, including behavioral ecology, genetics, neurogenomics, bioacoustics, and physiology, offering a rich context for lab members to learn and grow.

Successful candidates will lead the project that aims to quantify individual variation and heritability in mating preference and use genomic tools to identify candidate genes underlying variation in choosiness. Successful candidate will also conduct data analysis, prepare manuscript for publication, communicate findings at conference, assist in broader impact activities that explores the use of dance as an alternative teaching tool for animal behavior in classroom and outreach.

The position is expected to start in fall in 2025. The exact start date is negotiable. The position is initially for two years, pending satisfactory review at the end of the first year. Continuation of the positions beyond two years depends on funding availability.

Required qualifications:

ï¿½Ph.D. degree in evolution, genetics, genomics, or related fields or degree expected before the start date

ï¿½Experience working with genomic data

ï¿½Familiarity with behavioral research

ï¿½Strong writing skills and experience in peer-reviewed publication

ï¿½Demonstrated ability to work independently and strong communication skills

Preferred qualifications:

ï¿½Experience in both behavioral ecology and genomics

ï¿½Collaborative nature, ability to lead projects and work in teams

ï¿½Demonstrated bioinformatic skills

ï¿½Proficiency in genomic wet lab skills

ï¿½Manual dexterity to work with small, delicate insects and conduct micro-dissections

Applicants should submit the following through UMN application system https://hr.umn.edu/Jobs/Find-Job (Job ID:367720) and email me at xu000574@umn.edu to alert me to your submission.

1.A cover letter

2.CV

3.A research statement no more than 3 pages specifying:

ï¿½Your research interests

ï¿½Past research experience and what you can bring to the project

ï¿½What you are looking for in the postdoc experience

ï¿½How this postdoc can help you with your future career

4.Name, email address, and phone number of three references

5.One representative publication (published papers and preprints are both acceptable)

Review of application begins on April 30th 2025 and will continue until the position is filled.

Mingzi Xu Assistant professor Department of Ecology, Evolution and Behavior University of Minnesota https://mingzixu.weebly.com (she/her/hers)

Mingzi Xu <xu000574@umn.edu>

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## UNottingham ParentalCareEvolution

Research Associate/Fellow in Behaviour & Evolution University of Nottingham - School of Life Sciences

Location: Nottingham, U.K. Salary: 31,387 to 46,485 per annum Hours: Full Time Contract Type: 48 months Closes: 11th April 2025 Job Ref: MEDLS1295

For further details see: https://jobs.nottingham.ac.uk/Vacancy.aspx?ref=MEDLS1295 An exciting opportunity for a Research Associate in Behaviour and Evolution is available to work with Andrew MacColl at the University of Nottingham on a 48 month Leverhulme Trust funded project: "Don't put your eggs in one basket: evolution of emancipation from parental care". The primary aim of the project is to quantify the ecological causes and genomic basis of loss of parental care in three-spined stickleback fish, using a mixture of field work, field and behavioural experiments, classical genetics and bioinformatics.

The role holder will investigate the loss of male parental care in sympatric ecotypes of three-spined stickleback on the Scottish island of North Uist. The post will involve substantial fieldwork on North Uist, including conducting aquatic habitat surveys, carrying out large experiments to quantify behaviour and performing field experiments. The role holder will also investigate the genomic basis of parental care loss using genomic analyses of QTL experiments and tissue-specific expression data. They will lead on publishing the results of this work.

Essential or desirable skills and experience (see role profile) include ecological fieldwork (especially in aquatic systems/with fish), behavioural experimentation and analysis, statistical data analysis (e.g. in R), molecular biology lab skills and familiarity with relevant scientific literature.

Applicants must have, or be very near to completing, a PhD in a relevant subject (e.g. behaviour, evolutionary biology, genetics, ecology) and a track record of publishing their research in relevant journals, appropriate to career stage.

The position will be based in the School of Life Sciences, a large, diverse and supportive unit at the University of Nottingham, with diverse opportunities to interact with a wider group of evolutionary biologists and ecologists locally, in the UK, and with European research labs. You will work closely with other postdoctoral research associates studying ecological and genomic divergence between the ecotypes.

Potential applicants are encouraged to contact Andrew MacColl (andrew.maccoll@nottingham.ac.uk) with informal questions, in advance of applying. Applications to this email address cannot be accepted. All applications must be submitted at: https://jobs.nottingham.ac.uk/Vacancy.aspx?ref=MEDLS1295 Best wishes Andrew MacColl

Professor of Evolutionary Ecology School of Life Sciences University of Nottingham University Park Nottingham NG7 2RD, U.K. Tel: +44 115 951 3410 http://ecology.nottingham.ac.uk/AndrewMacColl/index.php Andrew Maccoll <Andrew.Maccoll@nottingham.ac.uk>

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## UOklahoma EvolutionBehaviorDrosophila

Postdoctoral Researcher in the School of Biological Sciences - Everman Lab University of Oklahoma, Norman Campus

General Description:

The Everman Lab at the University of Oklahoma seeks applicants for a full-time postdoctoral researcher to study the effects of heavy metal exposure on gene expression and behavior in the Drosophila melanogaster model system with a starting date of July 1, 2025.

Research in the Everman Lab is focused on dissecting and characterizing the genetic relationship between physiological and behavioral responses to heavy metal stress. Our work leverages a combination of large mapping populations (such as the Drosophila Synthetic Population Resource and Drosophila Genetic Reference Panel) as well as D. melanogaster collected from wild populations from diverse habitats that have been undergoing continuous artificial selection for copper resistance using an experimental evolution approach.

The primary research focus for this position is on characterizing the transcriptomic response to copper throughout development and the persistence of the transcriptomic response through adulthood in genetically diverse D. melanogaster strains. These patterns will be examined using inbred strains as well as populations that have undergone artificial selection. Researchers with a background or interest in RNA sequencing and evolutionary genomics are particularly encouraged to apply.

Additional research topics are open for discussion but should align with the general focus outlined above and of the lab, and the researcher will have the opportunity to develop independent projects. The start date is flexible, and starting salary will be consistent with NIH guidelines (~$61,008 per year).

Required and Preferred Qualifications:

Required:

PhD in Biology, Genomics, or similar field Proficiency in working with Drosophila melanogaster Experience working with DNA and RNA Demonstrated ability to publish Proficiency in an analytical coding language (e.g. R or Python) Preferred:

Experience with next generation sequencing molecular techniques Bioinformatics experience Aligned interests in heavy metal toxicology, environmental stressors, and evolutionary genetics Experience working as a collaborator with other lab members

Application Instructions:

Applicants are invited to submit a letter detailing graduate research and research interests (not to exceed 2 pages), current CV, preprints of 2 papers, and contact information for three references. Additional materials may be requested at a later date. The search will remain open until filled.

Contact Person: Contact: Elizabeth Everman, Assistant Professor, School of Biological Sciences; e.everman@ou.edu

Dr. Elizabeth Everman (she/her) Assistant Professor of Biology School of Biological Sciences University of Oklahoma Norman, OK 73019

“Everman, Elizabeth R.” <e.everman@ou.edu>

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## UppsalaU FungalGenomeEvolution

Uppsala University, Department of Organismal Biology Are you interested in working with systematic biology, with the support of competent and friendly colleagues in an international environment? Are you looking for an employer that invests in sustainable employeeship and offers safe, favourable working conditions? We welcome you to apply for a postdoctoral position at Uppsala University.

The lab focuses on understanding the evolution of genomes and the genetic basis of adaptation in fungi. We recently discovered that many fungi harbour massive transposable elements, named Starships, that mobilize a vast diversity of fungal genes. We have now deciphered how the Starships move within genomes, but a growing amount of evidence suggests that they are also capable of moving between genomes. The main goal of the position is to demonstrate in a laboratory setting the horizontal transfer of a Starship between different fungi. This will be done by genetically modifying model strains so that successful transfers can be screened at high throughput on selective media.

Duties The applicant will be expected to be largely based in the wet lab. Focussing on transformations of the fungus Aspergillus fumigatus and potentially related species. This will also include vector construction using yeast and/or bacterial transformations. Methods may also employ CRISPR/Cas9. They are also expected to analyse data that they generate, including some minor bioinformatic work. Applicants are expected to communicate findings both at international conferences and through writing scientific articles for publication.

Requirements PhD degree in molecular biology/evolutionary biology or a foreign degree equivalent to a PhD degree in molecular biology/evolutionary biology . The degree needs to be obtained by the time of the decision of employment. Those who have obtained a PhD degree three years prior to the application deadline are primarily considered for the employment. The starting point of the three-year frame period is the application deadline. Due to special circumstances, the degree may have been obtained earlier. The three-year period can be extended due to circumstances such as sick leave, parental leave, duties in labour unions, etc.

Experience with molecular techniques is a necessity. Additional assets include microbial culturing of fungi, and fungal transformations. Previous experience with Aspergillus fumigatus is especially desired. Knowledge on presenting data and on conducting statistical analyses is also a plus. Candidates who demonstrate strengths in organization, problem solving, communication, and collaboration will be preferred. The applicant must have documented experience and proficiency in oral and written presentation in English.

About the employment The employment is a temporary position of 2 years according to central collective agreement. Full time position. Starting date 2025-05-01 or as agreed. Placement: Uppsala

For further information about the position, please contact: Aaron Vogan, aaron.vogan@ebc.uu.se

Please submit your application by 18th April 2025, UFV-PA 2025/909.

Are you considering moving to Sweden to work at Uppsala University? Find out more about what itÂs like to work and live in Sweden.

Uppsala University is a broad research university with a strong international position. The ultimate goal is to conduct education and research of the highest quality and relevance to make a difference in society. Our most important asset is all of our 7,600 employees and 53,000 students who, with curiosity and commitment, make Uppsala University one of Sweden's most exciting workplaces.

Read more about our benefits and what it is like to work at Uppsala University https://uu.se/om-uu/jobba-hos-oss/ The position may be subject to security vetting. If security vetting is conducted, the applicant must pass the vetting process to be eligible for employment.

Please do not send offers of recruitment or advertising services.

Submit your application through Uppsala University's recruitment system.

Type of employment Temporary position Contract type Full time First day of employment 2025-05-01 or as agreed Salary Individual salary Number of positions 1 Full-time equivalent 100% City Uppsala County Uppsala län Country Sweden Reference number UFV-PA 2025/909 Union representative Seko Universitetsklubben, seko@uadm.uu.se ST/TCO, tco@fackorg.uu.se Saco-rÃ¥det, saco@uadm.uu.se Published 25.Mar.2025 Last application date 18.Apr.2025 11:59 PM CEST

Dr. Aaron Vogan, Ph.D. Associate Professor Uppsala University Norbyvägen 18D Uppsala, Sweden 752 36

När du har kontakt med oss pÃ¥ Uppsala universitet med e-post sÃ¥ innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gör det kan du läsa här:

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## USaoPaulo Brazil MHCgenomics

**Two postdoctoral opportunities in population genetics and bioinformatics**

Two postdoctoral positions are open for researchers interested in human evolutionary and population genetics, at the University of Sao Paulo, in Brazil

One position will be supervised by Diogo Meyer, at the University of Sao Paulo, and will focus on the development of population genetic models of strong balancing selection, as is the case of MHC genes. Using genomic data, the project aims to explore the interactions between selection and demographic history, with particular attention to admixed populations, such as that of Brazil.

Current projects address adaptive introgression in the MHC region, distinguishing between selective regimes shaping MHC diversity, understanding the role of selection in maintaining common haplotypes, and relating variation in MHC diversity across continental ancestries to equitable access to transplantation.

The second position will be co-supervised with Erick Castelli, at the Universidade Estadual Paulista, with a focus on the development of computational tools for the analysis of highly polymorphic genes related to the immune system (HLA and KIR).

Both positions are funded by FAPESP (https://fapesp.br/en) postdoctoral scholarships, with initial appointment of 12 months, but renewable for up to 4 years.

Ideal start date is June 2025 but negotiable.

If you are interested in these positions or would like more information, please contact Diogo Meyer (diogo@ib.usp.br) or Erick Castelli ( erick.castelli@unesp.br)

More information on the positions can be found in the following links: Population genetics position - fapesp.br/oportunidades/7974 Bioinformatics position - fapesp.br/oportunidades/7975

Diogo Meyer <diogo@ib.usp.br>

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## UStAndrews Conservation

Post-doctoral Research Fellow / Project Manager, University of St Andrews, UK

Reference: AR3119LS Closing date: 09 May 2025

Are you interested in movement ecology, animal tracking, conservation science, environmental planning, and finding pathways towards sustainable human-wildlife coexistence? There is an exciting opportunity to join the team coordinating the Urban Exploration Project - a collaborative initiative developed in close partnership with the National Geographic Society.

The post is available for 2 years in the first instance, starting as soon as possible, with the possibility of an extension. For further details and information on how to apply, please see here:

https://www.vacancies.st-andrews.ac.uk/Vacancies/I/7169/0/449460/889/post-doctoral-research-fellow-ar3119ls Informal enquiries can be sent, with CV, to the Project Lead, Professor Christian Rutz (christian.rutz@st-andrews.ac.uk).

Christian Rutz <cr68@st-andrews.ac.uk>

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## UStockholm PredictionEvoDevo

1-2 Postdoctoral Researcher positions in Data-Driven and Predictive Evo-Devo Modeling at Stockholm University and SciLifeLab, Sweden

*Link with all info* https://su.varbi.com/en/what:job/jobID:813144/ *Contact* lisandro.milocco@zoologi.su.se

*What* We are seeking up to two highly motivated postdoctoral researchers for interdisciplinary projects at the intersection of evolutionary-developmental biology, dynamical systems, and machine learning.

These fully funded positions (2+1 years) are based in Assistant Professor Lisandro Milocco's group at SciLifeLab and the Department of Zoology, Stockholm University. The group is part of the National Program for Data-Driven Life Science (DDLS), funded by the Knut and Alice Wallenberg Foundation.

Our research centers on evolvability the capacity of organisms to evolve. This project leverages the rise of data-driven dynamic modeling from fluid dynamics to ecosystem studies to uncover developmental rules underlying phenotypic variation. The candidate will develop and implement an empirical framework that utilizes data-driven algorithms to learn relationships between past and future developmental timepoints from time-series data.

The role further offers substantial freedom to develop research ideas that align with the group's overall vision. We are thus especially interested in candidates who demonstrate strong independence and a proactive approach to exploring innovative research directions.

*Keywords* evolution, prediction, systems biology, developmental biology, dynamical systems, nonlinear dynamics, biophysics, machine learning, evo-devo

*Desired qualifications* - Knowledge in the three key areas of evolutionary and developmental biology, dynamical systems and/or machine learning - Strong interest in evolutionary questions - Enthusiasm, dedication and an ability to work both independently and in a team

Please apply by 25 of May 2025 following the link to the official Stockholm University job portal:

https://su.varbi.com/en/what:job/jobID:813144/
Lisandro Milocco Asst. Professor and DDLS Fellow Department of Zoology, SciLifeLab Stockholm University Tomtebodavägen 23A, Gamma 7 SE-171 65 Stockholm, Sweden Email: lisandro.milocco@zoologi.su.se Website: https://lisandromilocco.github.io/ Lisandro Milocco <lisandro.milocco@zoologi.su.se>

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# WorkshopsCourses

## Barcelona InternalConflicts Aug17

Internal Conflicts STN Workshop at ESEB 2025 - Registration Open

We're happy to announce that registration is now open for the second workshop of the ESEB-funded Special Topic Network (STN) on *Internal Conflicts and Organismal Adaptation*. The workshop will be held in Barcelona, Spain on Sunday August 17th, 2025, just before the start of the ESEB 2025 meeting.

This one-day event will feature a morning of selected talks, followed by afternoon discussion sessions on key topics in the field. We'll also provide updates on ongoing STN activities and encourage participants to help shape new initiatives.

The workshop will run from 09:00 to 17:00 (UTC+2) at the Princess Hotel, close to the main ESEB conference venue. Registration is free and includes lunch and coffee breaks.

We aim to provide hybrid access to both the talks and the discussion sessions to enable participation by those who cannot attend in person. More information on virtual access will be made available as details are confirmed.

To register (in person or virtually), please fill out the form here: https://forms.gle/Nsh52Y7pBKbJqkQ18 More information is also available on our website: https://internalconflictsstn.wordpress.com/-workshop-ii/ For any questions, please contact us at: internalconflictsstn@gmail.com

Organizing Committee: Martijn Schenkel, Arvid ?gren, Manus Patten, Nina Wedell, and Thomas Hitchcock

ESEB-funded Special Topic Network: Internal Conflicts and Organismal Adaptation

thomas.hitchcock@riken.jp

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## Beijing TamingTheBEAST Jul14-18

Dear colleagues,

It is our great pleasure to announce the first "Taming the BEAST" summer school in China! It will take place in Beijing, July 14-18, 2025.

Phylogenetics and phylodynamics are central topics in modern biology. Phylogenetic inferences reconstruct the evolutionary relationships between organisms, whereas phylodynamic inferences reveal the dynamics that lead to the observed relationships. These two fields have many practical applications in disciplines such as epidemiology, developmental biology, paleontology, ecology and even linguistics. However, phylogenetics and phylodynamics are complex and fast-evolving fields. As such, inference tools are not easily accessible to researchers who are not from a computational background.

Taming the BEAST is a summer school focusing on the BEAST 2 software and consisting of a mix of invited talks, lectures and hands-on tutorials by leading and renowned experts in the field (including several of the core developers of BEAST 2). The aim of this summer school is to equip participants with the skills necessary to confidently perform their own phylogenetic and phylodynamic inferences in Bayesian settings, while providing them with a firm grasp of the theory behind those inferences. Participants are also highly encouraged to bring their own datasets along and to engage with the organisers and speakers to address any problems specific to their own datasets/analyses.

REGISTRATION IS NOW OPEN. We welcome applications from graduate students and early-career scientists in the life sciences. Preference will be given to applicants who are not from a computational background and applicants who have already collected/assembled a dataset that they need to analyse.

Organizing committee: Chi Zhang (Chinese Academy of Sciences) Rachel Warnock (Friedrich-Alexander Universit??t) Jo??lle Barido-Sottani (Ecole Normale Sup??rieure) Louis du Plessis (ETH Z??rich)

Instructors: Sasha Gavryushkina (University of Adelaide) Sophie Seidel (ETH Z??rich) Robert Yuan (ETH Z??rich) Arong Luo (Chinese Academy of Sciences) Xing Xu (Chinese Academy of Sciences) Simon Ho (University of Sydney) Rong Zhang (Duke-NUS Medical School) Walter Xie (University of Auckland)

Dates: July 14-18, 2025 (Deadline for registration is April 17).

Place: Beijing, China

Registration Fee: 1500 CNY (approx 200???) (Registration fee includes all meals during the workshop.)

For more information please visit the summer school webpage: https://taming-the-beast.org/workshops/-

Taming-the-BEAST-Beijing/ For information on previous workshop programs, tutorials etc. please visit https://taming-the-beast.org . We hope to see you there, the Taming the BEAST organising team

Tim Vaughan <timothy.vaughan@bsse.ethz.ch>

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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: 11/05/2025 Course dates: 7-11/09/2025

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. This five-day workshop explores cutting-edge developments in genomics, focusing on evolutionary and conservation applications from pangenomics to population genomics, with a mix of theory and hands-on training. It will be enriched with sessions on essential bioinformatics skills, best practices for coding, practical grant writing with special emphasis on funding sources such as ERC and MSCA grants. An evolutionary board game night will be hosted at a local pub!

Designed for a small number of participants, it is sponsored by the Italian Society for Evolutionary Biology and followed by the meeting of the society's Conservation Genetics and Genomics group.

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.

Full details, including the course programme, invited speakers and the application form, at: https://sites.google.com/view/sibesummerschool/home-page 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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## Florence Italy GenomeAssembly Sep8-12

Dear All,

EMBO Practical Course on Genome sequencing, assembly, curation, and downstream analyses

Location: Florence, Italy Dates: 8-12 September, 2025 Application deadline: 31 May, 2025 EMBO travel grants and registration fee waivers are available

This hands-on course, supported by the European Molecular Biology Organization, will guide participants through main sequencing techniques and latest bioinformatic tools to produce high-quality genome assemblies of interest for downstream analysis and publication.

The course offers practical training in the use of computational tools for genome assembly such as HiFiasm, Verkko, Flye and NextDeNovo for PacBio HiFi reads or Flye, Canu, Raven and NextDeNovo for ONT reads, with troubleshooting sessions highlighting strengths and weaknesses of each methodology. Training and learning tools include a user-friendly dedicated Galaxy instance (https://usegalaxy.eu) through the Galaxy Training Infrastructure as a Service (TIaaS, https://usegalaxy.org/tiaas), which provides a GUI to run and analyse complex workflow. Students will be also trained in the use and interpretation of tools to perform Quality Control at each step of the genome assembly process and will participate in discussion on the quality of the results and possible strategies to improve the accuracy of assemblies. The course is aimed at graduate students and postdoctoral researchers as well as scientists at any stage of their careers.

Speakers and Instructors:

Astrid Bï¿½hne, Museum Koenig Bonn, DE Aureliano Bombarely, CSIC Institute for Plant Molecular and Cellular Biology, ES Tom Brown, Leibniz Institute for Zoo and Wildlife Research, DE Claudio Ciofi, University of Florence, IT Jean-Franï¿½ois Flot, Universitï¿½ libre de Bruxelles, BE Giulio Formenti, The Rockefeller University, USA Bjï¿½rn Grï¿½ning, University of Freiburg, DE Nadï¿½ge Guiglielmoni, University of Cologne, DE Silvia Manrique, Polytechnic University of Valencia, ES Kirsty McCaffrey, The Rockefeller University, USA Alice Mouton, University of Liï¿½ge, BE Marco Sollitto, University of Florence, IT

***General information can be found on the EMBO course website: https://meetings.embo.org/event/25-genome-seq ***Online applications can be submitted here: https://coms.app/pc25-33/welcome.html On behalf of the coordination team Claudio Ciofi

Claudio Ciofi Professor of Ecology and Molecular Ecology Associate Head Department of Biology University of Florence Via Madonna del Piano 6, Sesto Fiorentino (FI) 50019, ITALY Tel: +39 055 457 4740

Claudio CIofi <claudio.ciofi@unifi.it>

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## France GenomeAcquisition Dec8

Hello everyone,

As part of the PEPR ATLASea program, we are organizing a thematic school to bring together students and researchers from various backgrounds (taxonomists, bioinformaticians, evolutionary biologists) interested in generating reference genomes of marine organisms. The school will take place the week of December 8, 2025 at the Banyuls-sur-Mer marine station. For full details (program, registration), click here:

https://www.atlasea.fr/atlasea-winter-school-2025/

The school is free, but places are limited. The deadline for applications is May 31. Don't hesitate to spread the word around!

Stefano Mona

Stefano MONA <stefano.mona@mnhn.fr>

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## FUBerlin ProgrammingEvolBiol Feb17-Mar6

Course on Programming for Evolutionary Biology

When: February 17th - March 6th 2026

Location: Berlin, Germany

Application deadline: May 13th 2025

Detailed information about the course content and how to apply: http://evop.bioinf.uni-leipzig.de/ Founded in 2012, our well established course is back with novel content! In this intensive 16 days course, students will learn how to survive in a Linux environment, get hands-on experience in two widely used programming languages (Python and R), and statistical data analysis. The classes will be given by experts in the field and consist of lectures and exercises with the computer. The aim of the course is to provide the students with the necessary background and skills to perform computational analyses with a focus on solving research questions related to genomics and evolution. The philosophy of the course will be "learning by doing", which means that the computational skills will be taught using examples and real data from evolutionary biology for the exercises. During the course, students will also propose projects of their own interest and perform them as final projects in small groups under the supervision of a teaching assistant. This course is open for students from all countries and targeted toward PhD students and postdocs of evolutionary biology or related research fields with no or little programming experience who want to become proficient in computational evolutionary biology in a couple of weeks.

The course takes place at the Free University of Berlin. For any questions related to the course, please send an email to: evop@bioinf.uni-leipzig.de

Katja Nowick <katja.nowick@fu-berlin.de>

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Katja Nowick Professorin für Humanbiologie Freie Universität Berlin Königin-Luise-Straße 1-3 14195 Berlin

http://www.nowick-lab.info/ My working hours may not be your working hours. Please do not feel obligated to reply outside of your normal work schedule.

Katja Nowick <katja.nowick@fu-berlin.de>

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## Krakow BioinformaticsComputationalGenomics Jul7-12

EEBG 2025 - Bioinformatics and Computational Genomics Workshop Dates & Location: July 7-12, 2025; MaÂ³opolska Centre of Biotechnology (MCB), Jagiellonian University, Gronostajowa 7, 30-387, Kraków, Poland

Application and Registration

Participation in EEBG 2025 is open to graduate students, young researchers, and industry professionals interested in bioinformatics, computational genomics, medicine, and biology.

Application is free;registration fees are due only after acceptance.

Important Dates:

Call for Application for Early Registration:April 2 - May 12, 2025

Application Deadline for Scholarship Consideration:May 12, 2025

Notification of Acceptance and Scholarship Awards:May 20, 2025

If you are qualified, you must respond with Confirmation of Participation to be accepted,Due by June 5, 2025

Early Registration Fee ( euro 450):Due by June 15, 2025

Call for Application for Regular Registration:May 12 - June 22, 2025 (subject to space availability)

Regular Registration Fee ( euro 550):Due to 10 days after receiving confirmation letter or July 1, 2025 - whichever comes first

Participation Options We offer two modes of participation:

In-Person Attendance: All lectures and workshops will be held at the state-of-the-art MCB facility, featuring interactive sessions and hands-on computational labs. Limited fellowships covering registration and accommodation are available for qualifying participants. You do not need to pay anything before you are qualified for the Workshop!

Remote Participation: For participants unable to travel, we offer comprehensive virtual access, including livestreamed lectures and interactive online workshops.

Scholarship Opportunities While the workshop is open to everyone, and acceptance is based on merit, to promote local participation, a limited number of scholarships covering registration fees and/or accommodation expenses are available for students from Central and Eastern Europe. To be eligible, your application must be submitted by May 20, 2025. Please clearly indicate your interest in scholarships within the application form.

Workshop Overview EEBG 2025 is dedicated to connecting Eastern and Central European students with leading international experts in bioinformatics and computational genomics.

Participants will engage in:

- Hands-on sessions using real-world genomic datasets - Training in variant calling, ancestry inference, and AI-driven biomedical methodologies - Opportunities for international networking and collaborative research - EEBG 2025 will prepare participants to advance their skills in genomic research, personalized medicine, and computational biology in a rapidly globalizing scientific community.

Exceptional International Faculty EEBG 2025 will feature renowned researchers and industry leaders from Western Europe, the USA, Japan, and beyond. Students will benefit from direct mentorship and exposure to diverse approaches and perspectives in genomic science.

Venue All activities will take place at the MaÂ$^3$opolska Centre of Biotechnology, a cutting-edge facility equipped to facilitate interactive lectures, workshops, and computational labs.

Contact Information For questions, sponsorship opportunities, or general inquiries: Local Organizing Committee: support@eebg2025.edu.pl Address: MaÂ$^3$opolska Centre of Biotechnology (MCB), Jagiellonian University, Gronostajowa 7, 30-387 Kraków, Poland

Important notes

The EEBG 2025 workshop will welcome approximately 40 in-person students, 100 online students, and about a dozen distinguished international faculty from leading institutions in genomics, bioinformatics, medicine, and biology. The workshop is directed and coordinated by a local organizing committee at Jagiellonian University, with sessions led by internationally recognized scientists and educators specialized in modern genomic methods, bioinformatics analyses, and their applications to medicine, biology, and interdisciplinary research. Participants will receive hands-on training in computational tools, pipelines, and modern approaches for genomic data analysis. The sessions will include interactive computational exercises, practical demonstrations, and insightful evening presentations by invited speakers sharing their cutting-edge research. While much of bioinformatics and genomic analysis is conducted digitally, the EEBG 2025 faculty will offer valuable real-world insights and personal experiences, engaging actively with students throughout the course. Students will gain exposure to ongoing research efforts and methodological advancements directly from prominent international experts. The cost of participation in EEBG 2025covers tuition, course materials, and access to all workshops and lectures, coffee breaks, and lunches during the workshop days. Limited fellowships for qualifying in-person attendees are available after their acceptance. Detailed cost information, including the final registration

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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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## LakeDistrict UK FreshwaterMeiofauna Aug27-Sep11

Dear all,

Applications are now open for the NERC funded “Field workshop on the taxonomy and natural history of freshwater and limno-terrestrial meiofauna”.

This is field workshop designed and run by the Natural History Museum, London, will take place in the iconic Lake District in the North of England.

Course dates: 27 August - 11 September 2025 Application deadline: 31 May 2025 Cost: Free Course website: https://www.nhm.ac.uk/our-science/study/training/taxonomy-and-natural-history-of-freshwater-and-limno-terrestrial-meiofauna.html This field workshop will cover field techniques for sampling meiofauna in soils and mosses in limno-terrestrial habitats, as well as standing and running waters and groundwater. It will also consider the impacts of human land and water use patterns and climate change on these organisms. It will be taught by 13 taxonomists and ecologists, many of whom represent globally prominent experts, teaching the fundamental biology and natural history of various meiofauna groups. Each will focus on the microscopical techniques and morphological characters needed for identification and review the most important literature and database resources. Participants will also receive training in

1. DNA taxonomy, including an in-field nanopore sequencing component targeting popular “barcoding” loci and species delimitation techniques. 2. taxonomic publication, including peer-review of student-drafted species descriptions targeted at an expert audience. 3. science communication, including recording a short-form video addressed to a public audience.

Applications are welcome from anyone who expects to practice research in meiofauna systematics or ecology, including staff in environmental NGOs and charities, public sector bodies, ecological consultancies and education.

Early-career scientists of any nationality are encouraged to apply, especially those recently enrolled or expecting to enrol in a PhD programme. But preference will be given to those in NERC-funded projects.

We seek a competitive, diverse applicant pool encompassing a balance of female and male students from all backgrounds.

Further information, together with links to the application form can be found on the course website:

https://www.nhm.ac.uk/our-science/study/training/-taxonomy-and-natural-history-of-freshwater-and-limno-terrestrial-meiofauna.html Dr Nick Crumpton (He/They) Graduate Training and Short Course Coordinator Natural History Museum Cromwell Road, London, SW7 5BD nick.crumpton@nhm.ac.uk

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## Lausanne NaturalAndDirectedEvolution Jun23-27

Summer school on Natural and Directed Evolution

Where: Lausanne, Switzerland, When: June 23 - June 27, 2025 Application deadline: May 1st

Detailed information: https://evolution-school25.epfl.ch/ Invitation: Are you a PhD student working on designing new biomolecules through directed evolution or analyzing the evolution of populations? Our summer school is designed to bring together researchers like you to explore the connections between these fields while also deepening your expertise in your own field. By combining experimental and computational approaches, this five-day program will give you a broader perspective on evolutionary processes at multiple scales - from biomolecular design and molecular evolution to genetic networks and microbial communities. Through talks, practical workshops, and poster sessions, you’ll gain fresh insights, expand your practical skill set, and connect with students working on similar challenges. Whether you’re studying evolution in nature or designing it in the lab, join us in Lausanne for an inspiring and interdisciplinary week!

Speakers include: Corina Tarnita (Princeton U.), Otto Cordero (MIT), Chang Liu (UC Irvine), Frances Arnold (Caltech, via live stream), Liedewij Laan (TU Delft), Calin Guet (ISTA), Dominik Niopek (Heidelberg), Juan Diaz-Colunga (Salamanca), Michael Nash (ETHZ), Adrian Bunzel (ETHZ), Yolanda Schaerli (UNIL), Sara Mitri (UNIL), Anne-Florence Bitbol (EPFL), Angela Steinauer (EPFL), Ana-Marija JakÂ¹iÃ (EPFL)

Organizers: Sahand Rahi lab (EPFL), Joerg Stelling lab (ETHZ)

Contact: evolution2025@epfl.ch.

Vojislav Gligorovski <vojislav.gligorovski@epfl.ch>

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## Madrid ForestGenetics 8months

Do you want to train in Forest Genetic Resources and Omic data analysis,including Machine Learning?

We offer a CSIC JAE Intro SCHOLARSHIP for graduate students and recent graduates at the Institute of Forest Sciences (ICIFOR-INIA-CSIC), Madrid (Spain).

8 months / €700 per month / 20 hours per week

APPLICATION DEADLINE: April 16, 2025

Omics Data Analysis for the Characterization of Mediterranean Forest Species, Including Machine Learning. PI: Dr. Irene Cobo Simón

Climate change and biotic and abiotic threats are severely affecting Mediterranean forest ecosystems, where key species such as pines play a fundamental role in ecological stability. Genomics and systems biology have opened new avenues for understanding the resilience of these species to stress factors. However, the integration of multi-omics data remains a challenge in predicting adaptive responses. This scholarship aims to provide the student with experience in the generation and analysis of omics data in Mediterranean forest species, combining experimental laboratory work with bioinformatics analysis and computational modeling.

Objectives - Familiarize the student with the main laboratory techniques for generating omics data. - Train them in bioinformatics tools for the analysis and/or integration of genomic, transcriptomic, and/or epigenomic (miRNAs) data. - Develop skills in applied statistics and machine learning for predicting adaptive traits in forest species. - Foster critical thinking in the interpretation of omics data and its application in forest management and conservation. - Transfer of results to the public-private sector (MITECO and TRAGSA).

The training plan is structured in two main blocks: 1. Generation and processing of data in the laboratory (40%): DNA and/or RNA extraction, library preparation for next-generation sequencing (NGS), Quality control and data preprocessing.

2. Data analysis and integration (60%): Processing omics data using bioinformatics tools, Multivariate statistical analysis and dimensionality reduction techniques, Application of models (e.g., Bayesian, machine learning) to predict functional traits, Data visualization and interpretation of results in the context of forest adaptation.

This training program will equip the student with key competencies in molecular biology, bioinformatics, and omics data analysis, highly sought after in biotechnology, genetic resource conservation, and forest improvement. Additionally, experience in machine learning and predictive modeling will provide tools applicable in other emerging fields of computational biology and systems ecology. The combination of experimental and computational training will ensure a versatile and competitive profile in both the academic and professional spheres.

Please, if you are interested, kindly send an email briefly explaining your background and motivation for the scholarship to: irene.cobo@inia.csic.es

More information: tinyurl.com/yv87j7cp https://sede.csic.gob.es/tramites/programa-jae/-convocatoria-jae-intro-icu-2025 Irene Cobo <irenecobo88@gmail.com>

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## NHM London FreshwaterTaxonomicSkills May19-23

Dear all,

Applications are now open for the NERC funded short course "Taxonomic skills and field techniques for freshwater ecology and quality".

This is a five-day course held onsite at the Natural History Museum, London, UK.

Course dates: 19-23 May 2025 Application deadline: 24 April 2025 Cost: Free Course website: https://www.nhm.ac.uk/our-science/study/training/-freshwater-ecology.html This five-day course combines a mixture of lectures, practicals and a one-day field excursion to the New Forest to introduce course delegates to the principles and applications of field technique skills, sample collection, microscopy and taxonomic identification of freshwater species relevant to water ecology and quality.

This course has been running for six years and has a capacity for 15 participants. It is suitable for PhD students, postdoctoral researchers, early career biology and environmental science researchers and individuals who work in the environment and ecology sectors. By working closely with Museum scientists, participants will gain expertise to meet the needs and challenges of their current and future careers.

Further information, together with links to the application form can be found on the course website:

https://www.nhm.ac.uk/our-science/study/training/-freshwater-ecology.html Dr Nick Crumpton Short Course Programme Coordinator The Natural History Museum Cromwell Road, London SW7 5BD UK nick.crumpton@nhm.ac.uk

Nick Crumpton <nick.crumpton@nhm.ac.uk>

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## Online AnalysisRNASeqData Apr17-May22

Hi everyone

Last chance to sign up for the new 6-day seminar, Analysis of RNA-Seq Data < https://instats.org/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 Professor and Director Institute for Statistical and Data Science *instats.org* Follow Instats: Bluesky < https://bsky.app/profile/instats.bsky.social > Linkedin < https://www.linkedin.com/company/81837504/admin/dashboard/ > Facebook < https://www.facebook.com/InstatsTraining/ >

Michael Zyphur <mzyphur@instats.org>

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## Online AncientMetageno

Dear all,

We are excited to announce the upcoming Ancient Metagenomics course, taking place online from 27-29 May.

Course website: ( https://www.physalia-courses.org/courses-workshops/adna-metagenomics/ )

This 3-day course will explore the unique challenges and bioinformatic approaches in analyzing ancient microbial and environmental DNA. Participants will gain hands-on experience with tools such as aMeta, Kraken, Bowtie2, mapDamage, and more.

Key topics include:

Ancient DNA quality control and decontamination

Taxonomic profiling and genome mapping

DNA damage authentication and metagenomic assembly

Full implementation of the aMeta workflow

For the full list of our courses and workshops, please visit: ( https://www.physalia-courses.org/courses-workshops/ )

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 BiodiversityData Jun9-13

Dear all,

We're excited to announce our upcoming online course: Analysing Biodiversity Through Time and Space Using R

Dates: 9-13 June 2025Course website: ( https://www.physalia-courses.org/courses-workshops/biodiversity-in-r/ )

This hands-on course will guide you through building reproducible workflows for acquiring, cleaning, and analysing biodiversity data from both modern and fossil records. You'll explore how diversity patterns vary across space and time, and learn to address common sampling challenges using powerful R tools and packages.

By the end of the course, participants will be able to:

Access and clean biodiversity occurrence data from major databases (GBIF, PBDB, IUCN).

Analyse biodiversity patterns across spatial and temporal scales.

Visualise biodiversity data and estimate diversification rates using appropriate R tools.

Integrate palaeontological and neontological datasets for comprehensive biodiversity analysis. For the full list of your courses and workshops, please visit: ( https://www.physalia-courses.org/courses-workshops/biodiversity-in-r/ )

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 DataInR Apr28-30

Dear colleagues,

I am happy to announce that registration is open for Transmitting Science course "Organise and manipulate your data in R", organized by Transmitting Science [1].

R language is one of the most standard tools for many analysis in evolutionary biology, this course will help you learn to organise and manipulate your data in R, saving time and making it reproducible.

Dates and schedule: Online live sessions on April 28th, 29th, and 30th, 2025, from 13:00 to 18:00 (Madrid time zone).

Course webpage: https://www.transmittingscience.com/courses/statistics-and-bioinformatics/data-manipulation-with-r-tidyverse/ Instructor: Dr Ashton Drew [2] (KDV Decision Analysis LLC, USA), Ashton is an R Studio Certified Tidyverse and Shiny instructor.

Course overview:

This course will highlight useful tools of data manipulation from R's Tidyverse suite of packages. The Tidyverse packages are built upon a philosophy of a tidy data structure: a rectangular (spreadsheet-like) data structure where each row is one observation, each column is one variable, and each cell contains one value. The Tidyverse packages follow a set of shared rules and share a typical syntax style, both designed to maximize code readability and reproducibility.

The emphasis of this short course will be on the core packages dplyr and tidyr in combination with packages specific to manipulating date-time data (lubridate), text data (stringr), and categorical data (forcats). Class exercises will provide practice restructuring data, value replacement, group operations, and row- and column-wise functions.

The course content assumes some prior basic R experience and will require a current installation of both R and RStudio.

If you have any doubts, do not hesitate to contact us at courses@transmittingscience.com

Feel free to share this information with anyone that can be interested :)

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses Bluesky @soledeesteban.bsky.social 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/courses/ [2] https://www.transmittingscience.com/instructors/ashton-drew/ Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

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## Online DataManipulationNGS May5-14

Dear colleagues,

There are a few slots available for the course “Manipulation of NGS Data for Genomic and Population Genetics Analyses”.

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/ Do not hesitate to contact us at courses@transmittingscience.com if you have any doubts or questions.

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 GenomeAnnotation May19-22

Dear all,

there are only a few seats left for our upcoming online course: Introduction to Genome Annotation

Dates: 19-22 MayFormat: Online (Live sessions from 13:00 to 19:00, Berlin time) Course website: ( https://www.physalia-courses.org/courses-workshops/-genome-annotation/ )

Genome annotation is a crucial component of genomics research, as the quality and biological relevance of a genome assembly depend heavily on accurate annotation. This course offers a practical and comprehensive introduction to genome annotation workflows and tools. Topics will include:

Sample quality requirements and sequencing platforms

Ab initio and de novo transcriptome assembly

Evidence-guided gene prediction (e.g., BRAKER, Augustus)

Gene model construction and evaluation

Addressing genome-specific challenges This course is intended for PhD students, postdoctoral researchers, and scientists working on genome annotation projects. Participants should be comfortable using the UNIX command line.

By the end of the course, participants will be able to:

Set up and run an annotation pipeline for their genome of interest

Handle common challenges in annotation projects

Use key tools for gene prediction and quality assessment More information and registration about our courses and workshops: ( https://www.physalia-courses.org/-courses-workshops/ )

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 GenomeAssembly Apr15-17

The Computational Biology Core at the University of Connecticut is hosting virtual bioinformatics workshops this month! We still have space available in our Genome Assembly Workshop (virtual but live instruction - April 15-17). This workshop will cover sequencing strategies, short-read and long-read assembly, hybrid approaches, and quality control. Participants will learn how to process raw sequencing data and generate high-quality genome assemblies.

Learn more & register here: bioinformatics.uconn.edu/cbc-workshops/ WHERE: Virtual (Zoom) WHEN: 10:00 AM - 2:00 PM EST COST: $400 (UConn affiliates) $500 (External participants) Registration is first come, first served. Questions? E-mail cbcsupport@helpspotmail.com

"Lambert, Karelyn" <zsc25001@uconn.edu>

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## Online InteractiveMapsWithR May13-14

Dear all,

there are only a few seat left for the online Physalia course Interactive Maps with R, taking place on 13-14 May.

More info & registration: ( https://www.physalia-courses.org/courses-workshops/interactive-maps-with-r/ This course provides a practical introduction to creating and customizing interactive maps using R and open-source packages such as leaflet and mapview. Participants will learn to integrate and display spatial data, design multi-layered and user-friendly visualizations, and publish interactive maps for collaboration or public access.

The course is ideal for students, researchers, and professionals with a basic knowledge of R and spatial data, looking to enhance their data communication and visualization skills.

For the full list of our courses and workshops, please visit: ( https://www.physalia-courses.org/courses-workshops/-interactive-maps-with-r/ 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 IntroAncientMetagenomics Aug4-8

Dear all,

The SPAAM Community in collaboration with Friedrich Schiller Universitï¿½t Jena (Germany) and Harvard University (USA) is happy to again offering a new 5 day virtual summer school course sponsored by the Werner Siemens Foundation and the NFDI4Microbiota: Introduction to Ancient Metagenomics.

DATE AND SCHEDULE ï¿½Online (Hybrid/MPI-EVA Leipzig) from Monday 4th to Friday 8th of August 2024 from 09:00 to 17:00 (CEST, Leipzig time zone).

ORGANISERS Prof. Dr. Christina Warinner (Harvard University, Max Planck Institute for Evolutionary Anthropology) and Dr. James Fellows Yates (Max Planck Institute for Evolutionary Anthropology, Leibniz Institute for Natural Product Research and Infection Biology Hans Knï¿½ll Institute).

INSTRUCTORS Dr. Aida Andrades Valtueï¿½a, Dr. Alexander Herbig, Dr. Alex Hï¿½bner, Clemens Schmid, Dina Memar Moshrefi, Freya Steinhagen, Dr. Giulia Zampirolo, Jasmin Frangenberg, Keri Burge, Dr. Megan Michel, Dr. Meriam Guellil, Dr. Nikolay Oskolkov, Dr. Remi Denise, Dr. Thiseas C. Lamnidis, Tessa Zeibig, and Dr. Vilma Pï¿½rez.

OVERVIEW: Ancient metagenomics applies cutting-edge metagenomic methods to the degraded DNA content of archaeological and paleontological specimens. The rapidly growing field is currently uncovering a wealth of novel information for both human and natural history, from identifying the causes of devastating pandemics such as the Black Death, to revealing how past ecosystems changed in response to long-term climatic and anthropogenic change, to reconstructing the microbiomes of extinct human relatives. However, as the field grows, the techniques, methods, and workflows used to analyse such data are rapidly changing and improving.

In this hands-on summer school (block praktikum) we will go through the main steps of ancient metagenomic bioinformatic workflows, familiarising students with the command line, demonstrating how to process next-generation-sequencing (NGS) data, and showing how to perform de novo metagenomic assembly. Focusing on host-associated ancient metagenomics, the course consists of a combination of lectures and hands-on exercises, allowing participants to become familiar with the types of questions and data researchers work with. Round table discussions with experts at each stage of the workflow will be held to allow participants to get advice on their own projects and research.

By the end of the course, participants will have an understanding of how to effectively carry out the major bioinformatic components of an ancient metagenomic project in an open and transparent manner. Attendees will be eligible for ECTS points (awarded by the JSMC Graduate School, Friedrich-Schiller University, Germany) or a certificate of completion (Max Planck -

Harvard Research Center, MHAAM).

ELIGIBILITY The course is aimed at masters students and early-stage PhD students, to a maximum of 40 participants. Course instruction will take place online. There are no fees.

APPLICATIONS Applications are now open until May 30 2025. To apply, please visit our website: https://spaam-community.org/wss-summer-school/ For questions or more information, contact James Fellows Yates (james_fellows_yates@eva.mpg.de) or Christina Warinner (christina_warinner@eva.mpg.de)

Kind regards

James and Christina

Dr. James A. Fellows Yates

Microbiome Sciences Group, Dept. of Archaeogenetics Max Planck Institute for Evolutionary Anthropology

Dept. of Paleobiotechology Leibniz Institute for Natural Product Research and Infection Biology Hans Knï¿½ll Institute

James Fellows Yates <james_fellows_yates@eva.mpg.de>

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## Online IntroPalaeogenomics May21-27

Dear colleagues,

Transmitting Science has opened registration for the online course “Introduction to Palaeogenomics”.

Date and schedule: Online live sessions on May 21st, 22nd, 23rd, 26th, and 27th, 2025; from 16:00 to 21:00 (Madrid time zone).

Course webpage: https://www.transmittingscience.com/courses/genetics-and-genomics/introduction-to-palaeogenomics-concepts-methods-and-applications-of-ancient-dna-data/ Course Overview:

Ancient DNA (aDNA) research, defined as the retrieval and analysis of DNA sequences from various degraded biological materials, has been evolving as a research field for four decades.

DNA extracted from archaeological samples, and museum specimens has proven useful to study species and life on earth from the genomic perspective. It has made it possible to measure changes in genetic diversity through time, test hypotheses about the association of environmental phenomena and genetic changes in natural populations, and to resolve long-standing questions about the evolutionary relationships between species.

In a combination of interactive lectures and hands-on practical sessions, this course will provide a theoretical overview of molecular biology laboratory techniques for the retrieval of aDNA from ancient samples from different species and an introduction to the bioinformatic pipelines for the analysis of palaeogenomic data.

Students will be introduced to the standard bioinformatic methods often used in palaeogenomic projects for the analysis of aDNA data from human and non-human samples.

We will also review the history and developments of the field to understand how it came to be what it is today and consider and discuss the practical problems of ancient DNA recovery, the theoretical problems associated with the interpretation of palaeogenomic data, and the ethical implications embedded in this type of research.

At the end of the course, students will have gained a general understanding of common key methods and tools used in palaeogenomics projects: from the basics in the field to the interpretation of the results, as well as ethical and responsibility aspects and implications of aDNA research.

If you have any questions, please do not hesitate to write to courses@transmittingscience.com

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses Bluesky @soledeesteban.bsky.social 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 MachineLearningWithChatGPT Apr30

Hi everyone

Instats is excited to offer a 1-day seminar, Machine Learning for Complex Datasets with ChatGPT < https://instats.org/seminar/machine-learning-for-complex-datasets-wi >, running April 30 with Professor Nikolay Oskolkov from Molecular Biosciences, Lund University. For evolutionary biologists and ecologists, effectively analyzing complex datasetsfrom genomic sequences and population dynamics to ecological monitoring datais essential for uncovering the hidden patterns that drive evolutionary processes and environmental change. In this workshop, you'll learn how to harness advanced machine learning techniques in R and Python, supported by AI tools like ChatGPT, to develop models that reveal intricate patterns and causal relationships in your data. Enhance your research toolkit with practical, hands-on coding sessions and real-world case studies tailored to the unique challenges of evolutionary biology and ecology.

https://instats.org/seminar/machine-learning-for-complex-datasets-wi 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 Professor and Director Institute for Statistical and Data Science *instats.org < http://instats.org >* Follow Instats: Bluesky < https://bsky.app/profile/instats.bsky.social > Linkedin < https://www.linkedin.com/company/81837504/admin/dashboard/ > Facebook < https://www.facebook.com/InstatsTraining/ >

Michael Zyphur <mzyphur@instats.org>

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## Online MultivariateDataInR May20-23

Dear all, We are pleased to announce our upcoming online course: GLLVMs: Advanced Multivariate Analysis of Ecological Communities in R Dates: 20-23 May Format: Online - ( https://www.physalia-courses.org/courses-workshops/gllvm/ )

This course introduces Generalized Linear Latent Variable Models (GLLVMs) as a powerful and unifying framework for multivariate analysis of ecological communities. Unlike traditional distance-based methods (e.g., NMDS, PCoA), GLLVMs provide a flexible statistical model formulation that allows for robust ordination, inference on species associations, and model diagnostics.

This course is ideal for PhD candidates, postdocs, and researchers with basic statistical knowledge looking to analyze multivariate ecological data appropriately. Prior experience with generalized linear models (GLMs) and basic R programming is required. Live sessions will run daily from 2-8 PM Berlin time, with practical demonstrations and opportunities to apply GLLVMs to your data.

After attending, attendees will be able to:

Fit GLLVMs using the gllvm R package

Select appropriate model distributions

Perform residual diagnostics and model selection

Visualize and interpret ordination results

For more information about our courses and workshops, please visit: ( https://www.physalia-courses.org/courses-workshops/gllvm/ )

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 NetworkAnalysisInSystemsBiology Jun2-5

Dear all,

Registration is now open for our upcoming online course: Network Analysis in Systems Biology with R/Bioconductor Dates: 2-5 June

Course website:( https://www.physalia-courses.org/courses-workshops/network-in-systems-biology/ )

This hands-on course will introduce participants to the inference and analysis of biological networks from RNA-seq data using R and Bioconductor. Topics include gene co-expression and regulatory networks (GCNs and GRNs), network comparison, and integration with genetic markers for gene prioritization.

The course is targeted to researchers and students that would like to learn how to use R and Bioconductor to infer and analyze networks for systems biology projects.Attendees need to have a working knowledge of R (R syntax, commonly used functions, basic data structures such as data frames, vectors, matrices and their manipulation).

For the full list of our courses and workshops, please visit: ( https://www.physalia-courses.org/courses-workshops/ )

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 Palaeogenomics May21-27

Dear colleagues,

Registration is now open for the Transmitting Science course: "Introduction to Palaeogenomics" (5th edition).

Max capacity: 16 participants Format: Live online sessions Dates: May 21st, 22nd, 23rd, 26th, and 27th Schedule: 16:00-20:30 (Madrid time)

Instructors: Dr. Marcela Sandoval Velasco (Smithsonian Institution, Museum of Natural History, USA & Centro de Ciencias Genï¿½micas UNAM, Mexico) Dr. Jazmï¿½n Ramos-Madrigal (University of Copenhagen, Denmark)

This course covers concepts, methods and applications of ancient human and non-human DNA data.

Learn more and register here: https://www.transmittingscience.com/courses/genetics-and-genomics/introduction-to-palaeogenomics-concepts-methods-and-applications-of-ancient-dna-data/ Course overview:

Ancient DNA (aDNA) research, defined as the retrieval and analysis of DNA sequences from various degraded biological materials, has been evolving as a research field for four decades. Through advances in DNA isolation and amplification techniques, sequencing technologies and data analysis pipelines, the field has been revolutionized and transitioned to what we now know as palaeogenomics. DNA extracted from archaeological samples, and museum specimens has proven useful to study species and life on earth from the genomic perspective. It has made it possible to measure changes in genetic diversity through time, test hypotheses about the association of environmental phenomena and genetic changes in natural populations, and to resolve long-standing questions about the evolutionary relationships between species.

In a combination of interactive lectures and hands-on practical sessions, the course will provide a theoretical overview of molecular biology laboratory techniques for the retrieval of aDNA from ancient samples from different species and an introduction to the bioinformatic pipelines for the analysis of palaeogenomic data. Students will be introduced to the standard bioinformatic methods often used in palaeogenomic projects for the analysis of aDNA data.

At the end of the course, students will have gained a general understanding of common key methods and tools used in palaeogenomics projects: from the basics in the field to the interpretation of the results, as well as ethical and responsibility aspects and implications of aDNA research.

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]

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 ##12646598990215736262##1##. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es [2]. 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 for any damages that such

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## Online PhylogeneticComparativeMethods My12-16

Dear all,

We would like to inform you that only a few seats remain for our upcoming online course: Phylogenetic Comparative Methods in R. Dates: 12-16 May Course website: ( https://www.physalia-courses.org/courses-workshops/course44/ )

This course provides a comprehensive introduction to the use of ultrametric phylogenies in trait evolution and lineage diversification studies. Designed for researchers and students with a background in molecular evolution and some familiarity with R, the course combines theoretical lectures with hands-on practical sessions.

For the full list of our courses and workshops, please visit: ( https://www.physalia-courses.org/courses-workshops/course44/ )

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>

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

## Online SpatialOmicsInR May19-21

Dear all,

We are excited to announce the 2nd edition of the Physalia online course "Spatial Omics in R/Bioconductor".

Dates: 19-21 May (9.30 AM - 1.30 PM Berlin time)

Course website: ( https://www.physalia-courses.org/courses-workshops/spatial-omics-1/ )

This course offers a comprehensive introduction to spatial omics, highlighting both imaging- and sequencing-based technologies, their experimental design considerations, and the unique challenges of data analysis in this emerging field. Through a combination of theory and hands-on sessions in R, participants will explore the application of tidy data principles using tools such as Bioconductor, Seurat, tidySpatialExperiment, and more.

For the full list of our courses and workshops, please visit: ( https://www.physalia-courses.org/courses-workshops/ )

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 SpeciesCommunityAnalysis Sep15-19

ONLINE COURSE - Multivariate Analysis Of Ecological Communities Using R With The VEGAN package (VGNR08) https://www.prstats.org/course/multivariate-analysis-of-ecological-communities-using-r-with-the-vegan-package-vgnr08/ 15th - 19th September 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.

Email oliverghooker@prstatistics.com with any questions. – Oliver Hooker PhD. PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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## Pantanal Brazil Metabarcoding Aug3-9 CallForApplications

* ** Call for Applications - Metabarcoding Course in the Pantanal, Brazil!*

We are excited to invite PhD students, postdocs, researchers, and professors especially from Latin America to apply for the *hands-on course: "Metabarcodes of e/iDNA for Biodiversity Analysis and Monitoring"*, which will take place *August 3-9, 2025*, at the *Pantanal Field Station (UFMS), Brazil*.

This intensive 5-day course combines theoretical and practical sessions, providing a comprehensive introduction to the use of environmental DNA (eDNA), ingested DNA (iDNA), and sedimentary DNA (sedaDNA) in biodiversity studies. Participants will extract DNA, prepare libraries, sequence real samples, and analyze data using bioinformatics pipelines guided by world-leading experts. This is a unique opportunity to build skills, strengthen your research, and connect with a global network of researchers working at the forefront of biodiversity monitoring.

*Topics include*:

- Experimental design and molecular lab techniques - Primer development and library preparation - Bioinformatics tools and pipelines (OBITools, MetabaR, R) - Applications in ecology, diet analysis, and conservation - One-on-one mentorship with instructors on your research project

*Instructors include international leaders* in the field such as Pierre Taberlet, Eric Coissac, Frédéric Boyer, Meng Yao, Philip Thomsen, Anthony Chariton, and Carla Lopes.

*Requirements*:

- *Fluency in English* (all lectures and activities will be in English) - *Personal laptop* for bioinformatics activities - Basic knowledge of molecular lab work and/or data analysis pipelines is desirable

*Important info*:

- The course is *free of charge* - Participants are responsible for their transportation to Campo Grande, as well as accommodation and meals at the Pantanal station (to be paid on site at a very accessible price) - Round-trip transportation between Campo Grande and the field station will be arranged by the organizers

*Location:* Pantanal Field Station, UFMS - a unique opportunity to study biodiversity in one of the world's most iconic ecosystems, with full infrastructure for practical and theoretical activities.

*How to Apply*: To apply, please send the following documents by *May 4, 2025*, to cmlopes82@gmail.com

- A copy of your CV - A motivation letter (max. 2 pages) describing your academic background, current research, and how this course will benefit your present and future projects - Selected candidates will be notified by email by May 11, 2025 - Spots are limited to 20 participants - don't miss out!

Best Regards,

Carla Lopes

Carla Lopes <cmlopes82@gmail.com>

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## Poznan Poland Bioinformatics Jul7-9

Dear Colleagues,

We are pleased to invite you to participate in the fifteenth edition of the Poznan Summer School of Bioinformatics. The course will be held July 7-9, 2025 at the Faculty of Biology, AMU. The title of this year's edition is Oxford Nanopore sequencing: data analysis and applications.

The course is suitable for beginners as well as for those with basic knowledge in the field of bioinformatics and will be held in English. The course will be largely hands-on, allowing you to familiarize yourself with the topics discussed and to practice the problems presented.

The participation fee for the Poznan Bioinformatics

Summer School is EUR 380 (or PLN 1,600). The fee includes participation in the course, materials, certificate of participation, catering (coffee breaks, breakfast and lunch) and participation in accompanying activities. Desktop computers with the necessary software will be provided during the course.

More information can be found at: https://pssb.amu.edu.pl/ . Looking forward to your participation,

dr hab. MichaÂ³ SzczeÂ, prof. UAM

Contact: genomics@amu.edu.pl

Joanna Ciomborowska-Basheer, PhD

Laboratory of Nature Education and Conservation Faculty of Biology Adam Mickiewicz University, Poznan Uniwersytetu Poznañskiego 6 Street, 61-614 Poznan e-mail: joannac@amu.edu.pl tel. +48 61 829 58 36

Joanna Ciomborowska <joanna.ciomborowska@amu.edu.pl>

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## StAndrews MLGenomics Jun24-27 AbstDeadlineMay13

*** Call for Participation and Abstracts***

We are 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. We have extended the deadline for abstract submission to * May 13th*.

***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 and Christoph Mayer (Research Museum Koenig Bonn) among others.

*** Important Dates ***

Registration opens: 17th March 2025 Abstract submission: 13th May 2025 (please send an email to: MLSpeciationGenomics@gmail.com)

Reduced rate accommodation: 24th April 2025 Registration closes: 2nd June 2025 Conference: 24th- 27th June 2025

For registration and more information see

https://www.eventsforce.net/standrews/264/home https://ckosiol.github.io/MLSpeciationGenomics/ Looking forward to seeing you in St Andrews!

Dr Carolin Kosiol Reader in Bioinformatics Centre for Biological Diversity School of Biology University of St Andrews St Andrews, Fife KY16 9TF, UK ck202@st-andrews.ac.uk

https://biology.st-andrews.ac.uk/kosiol-lab/ Carolin Kosiol <ck202@st-andrews.ac.uk>

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## ULausanne EvolutionaryModelling Sep1-6

UNIL Summer School on Modelling for Evolutionary Biology Lausanne, Switzerland - 1 to 6 September 2025

We are pleased to announce the second edition of the UNIL Summer School on Modelling for Evolutionary Biology. This one-week course is designed primarily for PhD students with an interest in applying formal modelling approaches to evolutionary questions.

The programme combines lectures, practical sessions, and collaborative work, focusing on population genetics, quantitative genetics, and invasion analysis. These tools will be used to explore problems in sexual selection, social evolution, senescence, and life history theory. The course is open to participants from any institution, and we particularly welcome international students.

Application deadline: 15 June 2025 Scholarship deadline: 15 May 2025 (covering travel and tuition for selected participants)

Full details and programme available at: https://www.unil.ch/unil/en/home/menuinst/etudier/programmes-courts/summer-winter-schools/modelisation-pour-la-biologie-de-l-evolution-1.html With best wishes, Charles Mullon Département d'Ãcologie et d'Ãvolution Université de Lausanne

Charles Mullon <charles.mullon@unil.ch>

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## Venice EvoSysBioMultiLevel Aug17-22

Dear all,

REGISTRATION DEADLINE EXTENDED by one week, to **Apr 7** !

*** 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.