EvolDir

February 1, 2026

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.

—— / ——

Conferences

Bern MolecularMechanismsOfSelfishElements Feb8-11

Dear all,

This is a final reminder to register for the EMBO workshop “Molecular Mechanisms of Selfish Elements and Strategies,” which will take place from Sunday 8 to Wednesday 11 February 2026 in Bern, Switzerland.

Registration remains open until the end of the month. The workshop covers topics of broad interest to the evolutionary genetics community.

More information and registration details are available on the workshop website: https://meetings.embo.org/event/26-selfish-elements Best wishes,

Luca Soldini

PhD Student - Schwander Group Selfish genetic elements and atypical reproductive modes Department of Ecology and Evolution University of Lausanne

Luca Soldini <luca.soldini@unil.ch>

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

Copenhagen AIinMolEvolPhylo Jun28-Jul02

Dear Colleagues:

I encourage you to submit abstracts for oral and poster presentations at SMBE 2026 on artificial intelligence (AI) and machine learning (ML) in molecular evolution and phylogenetics.

The symposium title is “Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics.” You can find its description at https://smbe2026.org/programme Abstract submission deadline: February 3, 2026 (please specify symposium #S02).

Invited Speakers are: Anne-Florence Bitbol - EFPL (ï¿½cole Polytechnique Fï¿½dï¿½rale de Lausanne), Switzerland Sudhir Kumar - Institute for Genomics and Evolutionary Medicine, Temple University, USA

Symposium description Artificial intelligence (AI) is poised to reshape the landscape of molecular evolution and phylogenetics. A growing number of machine learning and deep learning methods are being developed for tasks ranging from inferring evolutionary trees and detecting selection to modeling sequence evolution and predicting protein structures. Yet many remain skeptical, as fundamental questions persist: What exactly do these models learn from biological data? How do their internal representations relate to established evolutionary principles? And crucially, what are their blind spots?

This symposium at the SMBE annual meetings in Copenhagen (Jun 28-Jul 02, 2026) will provide a timely forum for examining both the transformative potential and the critical limitations of AI and ML in evolutionary research. Speakers will explore how AI models capture patterns of evolutionary variation and divergence, and whether their learned representations and models genuinely reflect underlying evolutionary mechanisms. The session will also feature discussions of new methodological advances, emerging interpretability frameworks, and benchmark analyses testing the reliability and reproducibility of AI-driven inferences.

Sudhir Kumar <s.kumar@temple.edu>

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

Copenhagen AI MolEvolPhylo DeadlineFeb03

SMBE 2026: AI in Molecular Evolution and Phylogenetics

Abstract deadline is approaching (February 3) for oral and poster presentations at SMBE 2026 on artificial intelligence (AI) and machine learning (ML) in molecular evolution and phylogenetics.

The symposium title is “Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics.” Specify symposium #S02 when submitting the abstract. SMBE annual meetings in Copenhagen (Jun 28-Jul 02, 2026) https://smbe2026.org/programme Invited Speakers are: Anne-Florence Bitbol - EFPL (?cole Polytechnique F?d?rale de Lausanne), Switzerland Sudhir Kumar - Institute for Genomics and Evolutionary Medicine, Temple University, USA

Symposium description Artificial intelligence (AI) may reshape the landscape of molecular evolution and phylogenetic analysis. A growing number of machine learning and deep learning methods are being developed for tasks ranging from inferring evolutionary trees and detecting selection to modeling sequence evolution and predicting protein structures. Yet many remain skeptical, as fundamental questions persist: What exactly do these models learn from biological data? How do their internal representations relate to established evolutionary principles? And crucially, what are their blind spots? This symposium is a forum for discussing the transformative potential and the critical limitations of AI and ML in evolutionary research. Speakers will explore how AI models capture patterns of evolutionary variation and divergence, and whether their learned representations and models genuinely reflect underlying evolutionary mechanisms. The session will also feature discussions of new methodological advances, emerging interpretability frameworks, and benchmark analyses testing the reliability and reproducibility of AI-driven inferences.

Contact: s.kumar@temple.edu

s.kumar@temple.edu

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

Copenhagen AI-MolEvolPhylo DeadlineFeb03

SMBE 2026: AI in Molecular Evolution and Phylogenetics

Abstract deadline is approaching (February 3) for oral and poster presentations at SMBE 2026 on artificial intelligence (AI) and machine learning (ML) in molecular evolution and phylogenetics.

The symposium title is “Powers and pitfalls of artificial intelligence for molecular evolution and phylogenetics.”

Specify symposium #S02 when submitting the abstract.

SMBE annual meetings in Copenhagen (Jun 28-Jul 02, 2026) https://smbe2026.org/programme Invited Speakers are:

Anne-Florence Bitbol - EFPL (ï¿½cole Polytechnique Fï¿½dï¿½rale de Lausanne), Switzerland

Sudhir Kumar - Institute for Genomics and Evolutionary Medicine, Temple University, USA

Symposium description

Artificial intelligence (AI) may reshape the landscape of molecular evolution and phylogenetic analysis. A growing number of machine learning and deep learning methods are being developed for tasks ranging from inferring evolutionary trees and detecting selection to modeling sequence evolution and predicting protein structures. Yet many remain skeptical, as fundamental questions persist: What exactly do these models learn from biological data? How do their internal representations relate to established evolutionary principles? And crucially, what are their blind spots? This symposium is a forum for discussing the transformative potential and the critical limitations of AI and ML in evolutionary research. Speakers will explore how AI models capture patterns of evolutionary variation and divergence, and whether their learned representations and models genuinely reflect underlying evolutionary mechanisms. The session will also feature discussions of new methodological advances, emerging interpretability frameworks, and benchmark analyses testing the reliability and reproducibility of AI-driven inferences.

Contact: s.kumar@temple.edu

Sudhir Kumar <s.kumar@temple.edu>

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

Copenhagen EvolutionGeneRegulation Jun28-Jul2

Dear EvolDir members,

We are happy to invite you to participate in our symposium entitled “Evolution of gene regulation: insights from novel molecular and statistical approaches”, as part of the annual SMBE meeting that will take place in Copenhagen (June 28th - July 2nd). This symposium features Margarida Cardoso-Moreira (Francis Crick Institute, London) as an invited speaker. Abstract submissions close on February 3rd.

We are looking forward to meeting you in Copenhagen.

Symposium organizers :

Maï¿½lle Daunesse (Institut Pasteur, Paris, France)

Camille Berthelot (Institut Pasteur, Paris, France)

Anamaria Necsulea (LBBE, Lyon, France)

Symposium abstract:

Understanding how gene regulation evolves is central to explaining phenotypic diversity and adaptation across species. Over the past two decades, comparative genomics approaches at the transcriptomic and epigenomic level have revealed that changes in cis-regulatory elements, chromatin organisation, and transcription factor binding are key contributors to regulatory and expression divergence.

Recent methodological advances are transforming our ability to address these questions. High-resolution single-cell and spatial assays are providing unprecedented views of regulatory activity across cell types and developmental stages, while chromosome conformation capture methods such as Hi-C are offering new insights into how three-dimensional genome architecture constrains or facilitates regulatory evolution. In parallel, sophisticated statistical frameworks and deep learning approaches are enabling more accurate modelling of regulatory element activity, and inference of causal links between gene expression and regulatory shifts and complex traits.

This symposium will bring together researchers exploring regulatory evolution through a diversity of approaches, including functional genomics, single-cell and spatial technologies, comparative epigenomics, and computational modelling. The symposium will also highlight how new computational strategies, including but not limited to deep learning, enable the interpretation of increasingly complex regulatory data. The session will provide a platform for interdisciplinary exchange and will emphasise how novel approaches are opening new avenues for understanding the evolution of gene regulation. We welcome submissions presenting cross-species comparative analyses of novel functional genomics data, as well as dedicated computational modelling approaches.

NECSULEA ANAMARIA <anamaria.necsulea@univ-lyon1.fr>

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

Copenhagen EvolutionRecombinationLandscapes Jun28-Jul2

Dear all,

The next Annual Meeting of the Society for Molecular Biology & Evolution will take place in Copenhagen, 28 June - 2 July 2026.

We are organising a symposium on ’The evolution of recombination landscapes’ (see details below), with Aurora Ruiz-Herrera from UAB Barcelona as our invited speaker.

Don't hesitate to submit your abstract to our Symposium: https://smbe2026.org/ Abstract submission deadline: February 3 2026

Marie Raynaud, Laurent Duret & Susan Johnston

SMBE2026 Symposium 11 | The evolution of recombination landscapes

Organisers: Marie Raynaud Institute of Ecology and Evolution, University of Edinburgh, United Kingdom (Female) Laurent Duret Laboratoire de Biomi Â©trie et Biologie Evolutive (LBBE), Lyon, France (Male) Susan Johnston Institute of Ecology and Evolution, University of Edinburgh, United Kingdom (Female)

Invited Speaker: Aurora Ruiz-Herrera Moreno Institute of Biotechnology and Biomedicine, Universitat Autonoma de Barcelona, Spain (Female)

Meiotic recombination is a key evolutionary mechanism. It ensures proper chromosome segregation and accelerates responses to selection by generating novel haplotypes. At the same time, recombination is also mutagenic, can disrupt favourable allelic combinations, reducing the fitness of subsequent generations, and may interfere with selection via biased gene conversion. The genomic landscape of recombination rates shows striking variation within and between chromosomes, individuals, sexes, population and species, yet the causes and consequences of this variation remain poorly understood. Recent methodological advances now allow fine-scale resolution of recombination events and cross-species comparisons. Emerging approaches such as Hi-C, single-cell sequencing, and improved cytological methods (e.g., FACS) are also providing new insights into the functional basis of recombination regulation and its links to phenotypic traits. Together, these developments are opening new avenues to characterize the molecular mechanisms of recombination regulation, the evolutionary forces shaping variation, and the consequences of recombination for adaptation, genomic conflict, and genome architecture. This symposium aims to foster cross-disciplinary exchange, and identify new discoveries in the evolution of recombination landscapes. It will bring together biologists addressing the proximate and ultimate causes of recombination rate variation across the tree of life and its evolutionary consequences. We seek submissions spanning topics broadly related to recombination's role in evolution, including theoretical and simulation approaches, methodological advances, field and experimental systems and studies of recombination modifiers (e.g., genetic variants, chromosomal rearrangements).

Laurent Duret <Laurent.Duret@univ-lyon1.fr>

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

Copenhagen GeneticBasisOfEvolutionaryRescue Jun28-Jul2

Dear evoldir,

We are excited to be hosting a symposium on "The genetic basis of evolutionary rescue" at SMBE 2026 (June 28 - July 2, Copenhagen). We encourage those of you working on relevant topics to submit an abstract, due Feb 3 (smbe2026.org).

Invited speaker:—Julia Kreiner (University of Chicago)

Symposium organizers: Matthew Osmond (University of Toronto) and Hildegard Uecker (Max Planck Institute for Evolutionary Biology)

Symposium abstract:

Rapid evolution can rescue populations from extinction. How often it does is of fundamental importance for the evolution of species' niches and geographic ranges. It is also of great applied relevance in conservation, where rescue is desired, and in agriculture and medicine, where resistance is unwanted rescue.

To better understand and manipulate population persistence there is now a large body of research on "evolutionary rescue" ("resistance evolution" in applied contexts) ranging from mathematical models to experimental tests to observations in the wild. The increasing threats of climate change and drug resistance are only accelerating these efforts. In an attempt to unite and propel the growing field of evolutionary rescue, this symposium aims to bring together theoreticians and empiricists with interests across evolutionary biology, conservation, agriculture, and medicine.

More specifically, this symposium aims to highlight recent work on the genetic basis of evolutionary rescue. Early models commonly assumed single mutations of large effect or an effectively infinite number of infinitely small effect alleles. Experiments and natural observations have now shown that the genetic basis of rescue can be much more complex (involving, for example, epistasis, gene amplifications, and hybridization) and theory has begun to explore the consequences of some of these complexities. To highlight these obstacles and advances this symposium will address questions such as: what genetic bases of rescue do we observe, what genetic bases do we predict, how does the genetic basis affect the probability of rescue, and what are the genetic signatures of evolutionary rescue?

Matthew Osmond <mm.osmond@utoronto.ca>

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

Copenhagen SMBE community role Jun28-Jul2

Dear all,

For the next Annual Meeting of the Society for Molecular Biology & Evolution taking place in Copenhagen from 28 June to 2 July 2026, we are organising a symposium on 'The role and responsibilities of the SMBE community in facing the polycrisis'. Anne Urai as our guest speaker will share her views on the academic system and potential ways to rethink and transform the norms of scientific practices to face the climate, ecological and political crises.

We are looking forward to hearing more about other initiatives and actions in the community to foster an academic system just and sustainable for all, so don't hesitate to submit your abstract to our symposium: https://smbe2026.org/programme/ The abstract submission deadline is February 3 2026 and submitting an abstract to our symposium does not prevent you to submit another one to a second symposium.

The organisers, Diego A. Hartasánchez, Fernando Racimo & Audrey Bras

—- L05 - The role and responsibilities of the SMBE community in facing the polycrisis

Across our community, researchers are producing data and knowledge helping us understand patterns of adaptation and selection. This understanding is essential to allow for species and societal adaptations to the climate breakdown and to reverse the biodiversity crisis. Yet, we are not taking enough time to reflect on our own activities and practices while academia itself is also in crisis across many fronts. From the reproducibility crisis to the publishing crisis, from increasing labor precarity to decreasing funding and increasing pressure to produce ever larger amounts of outputs -all these factors are putting a strain on its members and affecting their ability to practice science. What is the role of us, molecular and evolutionary biologists, in the face of a distressed academic system and collapsing ecosystems? How can the SMBE community participate in transforming academia into an institution that contributes to a just and sustainable future for all? Academia is already an environment that can foster transformation through collective action: much research in academia is itself the result of collective work. Increasingly, collective action initiatives have been gaining traction: from alternatives to the current publishing system, to alternative university structures; from demands to make universities divest from fossil fuels, to direct action groups fighting for ecological justice. In this symposium we invite the SMBE community to share their work and views related to initiatives addressing the climate, biodiversity and academic crises, with a focus on transformation through collective action.

Invited speaker: Anne E. Urai, Assistant Professor, Leiden University

—

Dr. Audrey Bras

Postdoctoral researcher

@AudreyBras@ecoevo.social < https://ecoevo.social/-@AudreyBras >

audreyb061992@gmail.com

audrey.bras@helsinki.fi

"Bras, Audrey" <audrey.bras@helsinki.fi>

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

Copenhagen SMBE IDEA symposium

It is our greatest pleasure to share with the evoldir community that we are organizing our annual IDEA symposium at the SMBE 2026 (June 28- July 2) Meeting in Copenhagen, Denmark. This symposium celebrates SMBE's commitment to fostering an inclusive, equitable, and diverse scientific community by addressing systemic inequities and empowering underrepresented groups in molecular biology and evolution. Please join us if you'd like to share your efforts that:

Highlight community-driven efforts to increase participation and dismantle barriers.Share strategies for creating inclusive scientific environments. Advance diversity, equity, and accessibility in molecular biology and related fields.Explore education-focused initiatives. The symposium will close with an interactive discussion to share practices, celebrate achievements, and inspire change. Submission Deadline:The deadline is soon, February 3rd Link:https://smbe2026.org/symposia/ We look forward to your contributions!

SMBEIDEA Taskforce

SMBE IDEA taskforce <smbe.idea@gmail.com>

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

Crete MathCompEvolutionaryBiology May4-8

Mathematical and Computational Evolutionary Biology (MCEB) Heraklion (Crete, Greece), 4-8 May, 2026

https://mceb2026.sciencesconf.org For its 2026 installment, MCEB will take place in Heraklion, Crete. This edition of the meeting will put an emphasis on computational methods in evolutionary genomics.

It will focus on recent algorithmic and statistical advances in comparative analysis of genomic data, but also present significant biological results obtained with these new techniques.

Beyond this year's themes, general concepts, models, methods and algorithms will be presented and discussed, just as in the previous editions of MCEB.

As usual, the meeting will bring together researchers from various disciplines: mathematics, statistics, computer science, phylogenetics, population genetics, molecular epidemiology, biodiversity and macroevolution...

Our keynote speakers will introduce a field of research and discuss their own work in this field.

The afternoons will be available for short presentations and posters, with plenty of time for discussions.

We will be stopping early every day, thus leaving time for other activities.

KEYNOTES:

Rosa Fernandez http://www.metazomics.com/ Nick Goldman https://www.ebi.ac.uk/people/person/nick-goldman/ Laura Kubatko https://www.asc.ohio-state.edu/kubatko.2/ Dimitris Paraskevis https://academicmedicaleducation.com/people/dimitrios-paraskevis-phd David Posada https://dposada.webs.uvigo.es/ PRACTICAL INFORMATION

Accommodation: Astir Beach hotel - https://www.astirbeach.gr Conference: Hellenic Centre for Marine Research - https://www.hcmr.gr/en/ Dates: 4-8 May, 2026. The conference will begin on Monday evening and will end on Friday morning.

Fees: Between 560 euro to 660 euro . Fees will vary depending on the type of room, shared (for students) or individual. They include accommodation for four nights with breakfasts, lunches, coffee breaks, and dinners, from Monday evening until Friday morning.

Abstract submission deadline: January 31st, 2026

Notification of acceptance: February 15, 2026

Registration deadline: March 15, 2026

Olivier GASCUEL <olivier.gascuel@mnhn.fr>

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

Glasgow Amphioxus Jun8-9

Dear colleagues,

We are pleased to announce the Amphioxus and Beyond Satellite Meeting < https://amphioxus.unige.it/ > at the EURO EVO DEVO Biennial Conference < https://www.evodevoconference26.com/satellite-meetings >, continuing the tradition of the Amphioxus Satellite Meeting.

The meeting will take place on 8-9 June 2026, immediately before EURO EVO DEVO 2026 in Glasgow.

This satellite meeting aims to bring together researchers working on cephalochordates, echinoderms, hemichordates, tunicates, and vertebrates, with a strong focus on comparative and cross-lineage perspectives in deuterostome development, genomics, and evolution.

We are delighted to announce three invited speakers: Guang Li (Xiamen University, China) Maria Ina Arnone (Stazione Zoologica Anton Dohrn, Italy) Cristian Cañestro (University of Barcelona, Spain) We invite abstracts (title + short abstract) by 31 March 2026 to amphioxusmeeting@unige.it.

Please note that registration < https://www.evodevoconference26.com/registration > is required for both the satellite meeting and the main EURO EVO DEVO conference (early-bird deadline: 9 February 2026).

For info: https://amphioxus.unige.it/ We hope to see you in Glasgow! Best regards, Marina Brasó-Vives (marina.brasovives@unil.ch) Matteo Bozzo (matteo.bozzo@unige.it)

“amphioxusmeeting@unige.it”
<amphioxusmeeting@unige.it>

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

Glasgow EuroEvoDevo Jun9-12 Registration

Dear Evo Devo Researchers,

Registration is open! We are excited to let you know that abstract submission and registration for the *10th European Society for Evolutionary Developmental Biology Meeting 2026 *(Euro Evo Devo 2026) is now live. The meeting will take place at the* University of Glasgow* *from 9**th - 12th June 2026*.

The conference will cover the panoply of topics and fields that are encapsulated by modern Evo-Devo, with satellite meetings and focused symposia alongside plenary speakers. This meeting marks a significant milestone in the life of this society, and the history, facilities, community and beauty of Glasgow will help us mark this milestone in a fitting manner.

Come together in Glasgow to share ideas, build collaborations, and celebrate the field of Evolutionary Developmental Biology.

*Please **click here* < https://registrations.hg3conferences.co.uk/hg3/335/register >* to register.*

*Please **click here* < https://hg3.co.uk/eed/ >* to submit an abstract. *(Note that registration is required for your abstract to be considered)

The deadline for submitting an abstract is Thursday 5th March 2026.

Please visit the conference website page for updates and further information; https://www.evodevoconference26.com/ Should you have any questions at all about the meeting, please email events@hg3.co.uk

Best wishes,

Organisers of the 10th European Society for Evolutionary Developmental Biology Meeting 2026

EED Society <eed.soc@gmail.com>

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

KewGardens PlantFungi Jun29-Jul1 TravelBursaries

Royal Botanic Gardens, Kew

Dear friends and colleagues of Kew,

We are pleased to announce a fantastic opportunity for delegates from low-income countries to attend the State of the World’s Plants and Fungi Symposium at Kew Gardens from 29 June to 1 July 2026.

Travel bursaries - applications now open

Kew is offering three travel bursaries to support in-person attendance at the symposium for delegates from low-income countries. These bursaries aim to remove financial barriers and encourage wider participation from the global science and policy community.

Each bursary covers:

* The symposium registration fee * Attendance at the symposium dinner on the evening of 30 June * Up to 3,000 towards travel and accommodation costs.

Application deadline: 16 March 2026

Full details regarding eligibility criteria and the application process can be found on the symposium web page.

Apply for a bursary

Early bird tickets - available until 28 February

Don’t miss your chance to book a discounted early bird ticket for in-person attendance by 28 February.

Tickets for online only participation are free. Visit the symposium web page for full ticket pricing and booking information.

Book now Poster abstracts and prizes

In-person attendees are invited to submit an abstract for a poster presentation accompanied by a one-minute flash talk. Prizes will be awarded for the best student and early career researcher posters.

Deadline for abstracts: 24 April 2026

Submit an abstract

For more information, visit the symposium web page.

We look forward to welcoming you to the symposium.

Best wishes,

The State of the World's Plants and Fungi Steering Committee

kew.org/sotwpf-symposium

Select unsubscribe to stop getting any marketing emails

The Board of Trustees of the Royal Botanic Gardens Kew

A non-departmental public body with exempt charitable status, established under the National Heritage Act 1983

Principal place of business: Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB

Kew Science <email@enews.kew.org>

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

Kiel ISEMPH EvolMedicine Jul28-31

2026 ISEMPH Meeting in Kiel, Germany

We would like to invite everyone interested in Evolutionary Medicine to the 2026 ISEMPH Meeting in Kiel!

Where? - Kiel, Northern Germany (directly on the coast of the Baltic Sea) When? - July 28-31, 2026 What? - The annual meeting of the International Society of Evolutionary Medicine and Public Health (ISEMPH)

Registration and abstract submission are now open! Please find all information on the meeting website: https://isemph.org/page-18356 . As usual we will offer talks, symposia, panel discussions, and plenty of opportunities to network and meet friends. A number of travel awards will be available to students that submit an abstract. We will update the website regularly with information about the program and the keynote speakers, so please stay tuned!

Important dates:

February 1, 2026: Travel award application deadline March 1, 2026: Abstract submission deadline and travel award decision announcement April 1, 2026: Abstract decision announcement April 15, 2026: Early-bird registration deadline June 15, 2026: Regular registration deadline

Please join us in Kiel, Northern Germany, to hear and discuss your work and other most recent findings of our field! Please also spread the above information to everyone who works on or is generally interested in Evolutionary Medicine!

We are looking forward to seeing you all in Kiel! Charles Nunn (ISEMPH president), Nicole Bender (ISEMPH manager) Misty Thomas, Michelle Blyth (Program committee) John Baines, Barbara Cania, Hinrich Schulenburg (Local committee Kiel)

Hinrich Schulenburg (he/him)

Evolutionary Ecology and Genetics Christian-Albrechts-Universitaet zu Kiel Am Botanischen Garten 9 24118 Kiel Germany Tel: +49-431-880-4143/4141 Email: hschulenburg@zoologie.uni-kiel.de Web: www.evoecogen-kiel.de/ Hinrich Schulenburg <hschulenburg@zoologie.uni-kiel.de>

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

LinnaeanSociety DarwinsFinchs Mar4

Joint Linnaean Society - Centre for Life's Origin and Evolution, UCL evening lecture: The Evolution of Darwin's Finch's - Peter and Rosemary Grant

The Linnean Society, Burlington House, LondonWednesday, Mar 4 from 6 pm to 8 pm GMT

https://www.eventbrite.com/e/the-evolution-of-darwins-finches-tickets-1978400378790?aff=-oddtdtcreator Prof. Julia J. Day Editor -Evolutionary Journal of theLinnean Society Department of Genetics, Evolution &Environment, Darwin Building, University College London, London, WC1E 6BT +44 (0)20 7679 0159 - internal 30159

"Day, Julia" <j.day@ucl.ac.uk>

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

Montpellier DrosEUDsuzukiiMeeting Apr13-17

Dear collegues,

Deadline for registration to the DrosEU/D. suzukii meetings is extended to January 30th 2026!

It is our pleasure to announce that the 16th DrosEU meeting will be held on April 13-14, followed by a 3-day D. suzukii satellite meeting on April 15-17 2026.

The European Drosophila Population Genomics Consortium (DrosEU) is a collaborative consortium of scientists and laboratories interested in evolutionary genetics and genomics of Drosophila species. Its main objective is to cooperate closely in collecting, generating and analysing genomic and environmental data for several Drosophila populations across the globe.

For the next meeting, a special focus will be put on the insect pest Drosophila suzukii: after the general DroEU meeting on April 13- 14 2026, we will organize a 3-day satellite meeting dedicated to D. suzukii on April 15-17 2026. A wide range of topics will be covered during this conference, including: - Population genetics - Molecular Genetics - Host-Microbiota Interactions - Physiology - Ecology and Population Dynamics - Integrated Pest Management.

Non DrosEU members are welcome to register to the DrosEU meeting, the D. suzukii meeting or both events. Registration is open until December 19th 2025 via the registration page. Abstract submission is not required for registration to either the DrosEU or the D. suzukii meeting.

Online attendance People can select the option to attend the meeting online when registering via the registration page. A Zoom link will be sent the week before the meeting. Please note that abstract submission will only be possible for in-person attendees.

To make both meetings accessible to the widest audience,registration is free of charge.

Registration website is now open:https://droseusuz.sciencesconf.org Both meetings will be held at the Genopolys amphitheater in Montpellier, France.

Please note that only titles (but not abstracts) are required for contributed talks for the DrosEU meeting. Registration and title (DrosEU meeting) or abstract (D. suzukii meeting) submission occur in two separate steps: upon acceptance of your registration, you will be able to submit a title/abstract via the "Title/abstract submission" page until January 30th 2026.

On behalf of the organizing committee, Svitlana Serga and Nicolas Rode,

Svitlana Serga, PhD MSCA Fellow UMR CBGP, INRAE 755 avenue du Campus Agropolis 34980 Montferrier-sur-Lez France

Associate Professor,

V.N. Karazin Kharkiv National University,

Kharkiv, Ukraine

Svitlana Serga <luchiksveta05@gmail.com>

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

Online AmericanSocietyNaturalists Proposals Feb3

The American Society of Naturalists Proposals for Virtual Symposia at the ASN, SSB, SSE Joint Meeting Deadline Extended: Now due February 3, 2026

The American Society of Naturalists will be participating in a joint meeting with the Society of the Study of Evolution and the Society of Systematic Biologists in May and June 2026! This includes hosting a special symposium during a virtual conference of the three societies on May 20-22.

Have an idea for this special symposium? We want to hear it!

The ASN Symposium Committee invites you to submit proposals for a special symposium. Proposed symposium topics should support the Society's goal to advance the conceptual unification of the biological sciences and to further knowledge in evolution, ecology, behavior, and organismal biology. Topics could center around important emerging issues in evolution, ecology, or behavior or focus on a pivotal historical paper, tracing its impact and exploring current cutting-edge research inspired by this work.

Proposals should include (1) a title; (2) a description of the symposium topic (up to one page); (3) a list of six speakers, including institutional affiliations, who have agreed to participate in the symposium; (4) a justification for the symposium, explaining why the topic and speakers are appropriate for an ASN symposium (up to one page).

Please submit proposals by email (cas383@miami.edu) no later than midnight Eastern Time on February 3, 2026. Send your proposal as a single pdf attachment, under subject heading “ASN 2026 Virtual Symposium Proposal”.

In line with the ASN’s commitment to diversity, we encourage including speakers from groups who have been historically excluded from STEM. Therefore, proposals that include a diverse list of speakers from a range of backgrounds, institutions, career stages, geography, gender, race, etc. are especially encouraged. Further, we especially encourage early career researchers to propose sessions as organizing symposia can advance their careers through building broader scientific networks and a record of scientific leadership.

Additionally, the Society’s selection committee will evaluate proposals based on their potential to attract a substantial audience and stimulate discussion, the significance and timeliness of the topic, and on the topic differing substantively from recent symposia hosted by the Society. Applicants will be notified of the decision before the end of February 2026.

Christopher Searcy ASN Symposium Committee Chair Department of Biology University of Miami cas383@miami.edu

---

Online ESEB InternalConflictsSTN Jan21

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 January 21st, 9:00 UTC. Our speakers for this seminar are:

Emily Hornett & Greg Hurst (both University of Liverpool) - Male-killing bacteria and the evolution of sex determination systems.

We expect the meeting to take approximately 1.5 hours.

Meeting details: Date: January 21, 2026. Time: 9:00 UTC <https://www.timeanddate.com/worldclock/fixedtime.html?msg=STN+seminar+17+-+Emily+Hornett+%26+Greg+Hurst&iso 260121T09&p1=%3A&ah=1&am0> . Meeting link: https://georgetown.zoom.us/j/99509526675?jst=2 . If you would like to get on our mailing list and take part in our upcoming events, please visit our website (https://internalconflictsstn.wordpress.com/) for more information.

Sincerely,

The Internal Conflicts and Organismal Adaptation STN

Martijn Schenkel, Arvid Sgren, Thomas Hitchcock, Manus Patten, and Nina Wedell

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>

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

Online EvolAtypicalReproductiveModes

Dear all,

We are continuing our online series on the evolution and mechanisms of atypical reproductive modes and other types of non-mendelian inheritance systems. This series features talk between once and twice per month, on Tuesdays at 3:00 p.m. (CET time, UTC+1), via Zoom.

More information (description, calendar, how to sign-up) here :https://tinyurl.com/EvoRepro You can sign-up to our mailing list here : https://sympa.unil.ch/sympa/sigrequest/evo_repro_mailing_list Best wishes,

Caroline S. Blanc, Morgane Massy, Luca Soldini Schwander Group Department of Ecology and Evolution University of Lausanne

Luca Soldini <luca.soldini@unil.ch>

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

luca.soldini@unil.ch

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

QuebecCity NAFGS Jun15-19

We are pleased to announce the 2026 North American Forest Genetics Society (NAFGS) Conference, to be held June 15-19, 2026 in Quebec City, Canada. The meeting will bring together researchers, practitioners, and trainees working across forest genetics, genomics, ecology, and management.

Conference Theme: Connecting Research Across Scales & Disciplines to Uncover Species' Evolutionary Potential & Strengthen Forest Resilience NAFGS 2026 aims to highlight integrative research that links molecular to landscape scales, bridges basic and applied science, and advances our understanding of how forest tree species evolve, adapt, and persist under rapid environmental change.

A Brief History of NAFGS: The North American Forest Genetics Society was established to serve as a unifying forum for forest genetics and genomics research and practice. The biennial conference is a relatively new but rapidly growing meeting for our community, beginning with the inaugural NAFGS conference in 2022 and continuing to expand in scope and participation. .

Important Dates Conference dates: June 15-19, 2026 (Quebec City, Canada) Conference registration opens: January 26, 2026 Abstract submission: Now open Abstract submission deadline: March 13, 2026

Call for Abstracts We invite abstract submissions across the following topic areas:

(1) Forest Genomics & Bioinformatics: Research on the structure, function, and evolution of tree genomes, supported by computational tools for analyzing large-scale genomic, transcriptomic, and epigenomic data. (2) Tree Breeding & Phenotyping: Development of improved tree varieties using breeding strategies and precision phenotyping to measure traits such as growth, form, and stress responses. (3) Adaptation & Resilience: Studies of how tree species respond to environmental change, including climate adaptation, stress tolerance, and interactions with pests, pathogens, and symbionts. (4) Conservation & Restoration Genetics: Applications of genetic tools to protect biodiversity, maintain adaptive potential, and guide restoration strategies for vulnerable or declining tree populations. (5) Population & Quantitative Genetics: Analyses of genetic diversity, gene flow, and trait variation within and among populations to understand evolutionary processes and predict responses to selection.

Additional details, including conference logistics, abstract submission guidelines, and registration information, are available on the conference website: www.nafgs.org/conference2026 Jill Wegrzyn (on behalf of the NAFGS 2026 Organizing Committee)

Jill L. Wegrzyn Associate Professor Computational Biology Core Director

Department of Ecology and Evolutionary Biology Institute for Systems Genomics: Computational Biology Core University of Connecticut Storrs CT 06269-3214

jill.wegrzyn@uconn.edu +1 860-486-8742

Research: http://plantcompgenomics.com CBC Core: http://bioinformatics.uconn.edu Office (Gant West 419) / Lab (Gant West 401)

“Wegrzyn, Jill” <jill.wegrzyn@uconn.edu>

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

RickMichod ReorganizationOfFitness Jan28

Richard Michod (University of Arizona, USA) (Virtual)Reorganization of fitness during evolutionary transitions in individuality *PhilInBioMed Seminar, organized by Thomas Pradeu*

January 28th, 2026, 5pm French time (UTC+1)

Richard Michod < https://michodlab.arizona.edu/ > is Professor of Ecology and Evolutionary Biology, at the University of Arizona, USA. He is a world-leading expert on evolutionary biology, evolutionary transitions, and multicellularity. His favorite experimental model is the volvocine green algae. Rick is an excellent biologist with deep conceptual and philosophical thinking, as illustrated by his book Darwinian Dynamics: evolutionary transitions in fitness and individuality and by his many papers published in major journals in biology and philosophy of biology.

Zoom link:

https://u-bordeaux-fr.zoom.us/j/81626413626?pwd=-rakvxrTrTmCjPZVuQYl4xgbVp4YSeg.1 *Detailed information:*

https://philinbiomed.cnrs.fr/event/richard-michod-reorganization-fitness/ *Abstract*

The central question of this talk is: *How do groups of individuals become new kinds of individuals?* I approach evolutionary transitions in individuality (ETIs) as dynamic multilevel selection (MLS) processes in which cooperation, conflict, and conflict mediation reorganize fitness from lower to higher levels. Using mathematical models and the volvocine green algae as a model system, I show how cooperation arises from ancestral survival-reproduction trade–offs, and that cooperation inevitably generates conflict through mutations that increase cell-level replication at the expense of the group.

The key evolutionary and developmental innovations are *conflict modifiers*â–line sequestration, policing, programmed cell death, mutation–rate reduction, and determinate size control. These modifiers do more than stabilize cooperation: they *alter the structure of selection*, suppressing within–group selection while amplifying between–group covariance in fitness, thereby permitting complex adaptations to emerge at the new level.

Two–locus modifier models and Price–equation partitions reveal how conflict mediators reduce within–group change and increase group–level heritable variance in fitness. When between–group covariance dominates, selection favors alleles that enhance group-level heritability, enabling *fitness transfer* and *fitness decoupling* between cells and the collective.

At this point, the stabilized group becomes a *new focus level of complex adaptation*, capable of coordinated development, group level reproduction, and life cycles integrated at the group level. ETIs thus build new evolutionary individuals, opening new adaptive possibilities not accessible at the lower level. Multicellular individuality emerges as the cumulative outcome of MLS dynamics, not as a predefined endpoint.

Positions and Education

- Professor, Ecology and Evolutionary Biology, University of Arizona, 1987 - present. - Associate Professor, Ecology and Evolutionary Biology, University of Arizona, 1982 - 1987. - Assistant Professor, Ecology and Evolutionary Biology, University of Arizona, 1978-1982. - Ph.D., Genetics, Zoology, University of Georgia, 1978 - M.A., Mathematics, University of Georgia, 1978. - B.S., Zoology, Duke University, 1973

Research Interests

The Michod Lab < https://michodlab.arizona.edu/ > is studying the evolution of multicellularity and sex in the volvocine green algae as examples of evolutionary transitions in individuality. How groups of individuals become new kinds of individuals is the basic question that motivates us. Understanding evolutionary transitions in individuality is key to understanding one of the most familiar features of the living world, its hierarchical organization. We use methods from theoretical population biology, molecular biology, genomics, ecology, and philosophy.

Selected Publications

1. Solari, C.A., J. O. Kessler, and R. E. Michod. 2006. A hydrodynamics approach to the evolution of multicellularity: Flagellar motility and cell differentiation in volvocalean green algae. *American Naturalist*. 167:537-554. (PDF < https://eeb.arizona.edu/sites/default/-files/2022-11/Swimming%20paper%20draft.pdf >). Receipient of the President's Award Paper of the Year in American Naturalist for 2006. 2. Solari, C. A., S. Ganguly, J. O. Kessler, R. E. Michod, and R. E. Goldstein. 2006. Multicellularity and the functional interdependence of

— / —

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

---

Roscoff HostParasiteCoevolution Nov2-6

Dear colleagues ,

We are pleased to announce a new edition of the Jacques Monod Conference on the ecology and evolution of host-parasite interactions.

The conference, entitled Ecology and evolution of host-parasite interactions in a changing world , will take place in Roscoff (Brittany , France) , from 2- 6 November 2026.

Contributions will be organised around three main themes:

(1) Abiotic stressors and the evolution of host and parasite ecological niches ,

(2) Predicting disease emergence: Epidemics, connectivity and evolution ,

(3) Evolution in multi-species interactions and ecological networks.

More information about the conference, invited speakers and instructions on how to apply can be found under this link : [https://cjm.sb-roscoff.fr/-en/conference/ecology-and-evolution-host-parasite-interactions-changing-world]

The registration site is open and the deadline for applications is 6 June, 2026 . There are 7 5 slots available for participants , who will either give a short talk or present a poster.

Don't hesitate to contact us if you any questions (Oliver.kaltz@umontpellier.fr, bkoskella@berkeley.edu).

Looking forward to seeing you in Roscoff!

Britt Koskella & Oliver Kaltz

oliver.kaltz@umontpellier.fr

Oliver Kaltz Directeur de Recherche CNRS Institut des Sciences de l'Evolution (ISEM) UMR 5554 (CC065) Université de Montpellier Place Eugène Bataillon 34095 Montpellier Cedex 05 France

Tel. 33 (0)4 67 14 40 63 Fax 33 (0)4 67 14 40 61

Singapore EvolOrnithology Nov14-17 RegisterFeb1

Dear friends and colleagues,

We are happy to announce that the registrations for the Third Asian Ornithological Conference (AOC) will open on 1st February 2026 in Singapore.

Taking place from 14 to 17 November 2026, the conference brings together ornithological experts across the world to facilitate knowledge sharing and productive regional collaborations on Asian ornithology. The conference will be hosted at the National University of Singapore and will feature exciting plenary talks and presentations across different disciplines of ornithology.

We are accepting abstracts from a wide range of topics which may be linked to evolutionary and molecular biology, namely:

Anatomy, Physiology & Morphology Behavioural Studies Bioacoustics & Communication Biogeography, Diversity & Distribution Bird Trade Birdwatching & Citizen Science Comparative Genomics & Macro-Evolution Conservation, Restoration & Threatened Species Disease, Microbiota & Health General Ecology (e.g. Breeding, Feeding, Behaviour, etc.) Habitat, Environment & Global Change Invasion, Colonisation & Pestilence Methods, Technology & Tools Migration & Flyways (Ecology, Methods, & Conservation) Phylogenetics, Population-Genetics, Diversification & Introgression Policy, Human Dimensions & Outreach Taxon-Specific Themes (i.e. Cranes, Hornbills, Spoon-billed Sandpiper, Straw-headed Bulbul, Vultures) Urban Ecology

The registration portal and more details can be found on our website at www.aoc2026.sg. Early bird registration ends on 30 April 2026. Sign up now and be a part of one of Asia's most impactful biodiversity and conservation gatherings in 2026! See you there!

For information unavailable on our website, contact Ms Sng Chen Xi Email: sng.chenxi@nus.edu.sg

Sng Chen Xi <sng.chenxi@nus.edu.sg>

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

SMBE Copenhagen AbstractsOnGeneEditing

Call for Abstracts - gene editing symposium S23 SMBE 2026

Dear all, A quick reminder that the abstract submission deadline for SMBE is February 2nd, and that we are organizing a symposium at SMBE 2026 titled “Gene editing as a driver of evolution: advances, challenges, consequences and frontiers” (S23).

Our aim is to create a forum for ideas and discussion on gene editing as a conservation tool. If you have work you would like to share, even at an early stage, on gene technologies for safeguarding species' genetic diversity or on the ethical questions surrounding editing evolution, we warmly encourage you to submit an abstract.

The symposium program will feature opportunities for extended presentations, flash talks, and a poster session, offering multiple formats for sharing your research and ideas.

Abstract submissions are open until February 2nd at: https://smbe2026.org/abstracts/ We very much look forward to reading your abstracts! B. Parreira and C. van Oosterhout

Bárbara Parreira

Department of Cellular and Molecular Medicine Blegdamsvej 3 1353 Copenhagen

Denmark

Bárbara Ribeiro Parreira <bparreira@sund.ku.dk>

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

SMBE Copenhagen Jun28-Jul2 DueFeb3

The 2026 Society for Molecular Biology and Evolution (SMBE) Conference will be held in Copenhagen between 28th June and 2ndJuly

If you are considering attending, please note that the deadline for abstract submission and award application is 3 February 2026.

Abstracts may be submitted for oral presentations, flash talks, or posters, and presenting authors are also encouraged to apply for relevant awards

Full guidelines and submission details are available at: https://smbe2026.org/abstracts/ On behalf of the organising committee

Tom Gilbert

Tom Gilbert <tgilbert@sund.ku.dk>

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

SmithsonianInst MidSEC Jun13-19

Abstract submission is now open for the inaugural meeting of MidSEC (Midwater Science and Engineering Conference) 13-19 June 2026.

We are doing things a bit differently so please read instructions carefully. There are multiple ways to present/participate and these are outlined in the online form where you indicate your preferences for each.

Abstract submission is a 2-step process < http://midsec.info/register >. 1. Complete the online form, and 2. Use the template provided to create a single page pdf containing your bio and abstract/position statement using the template provided. Email your pdf to the organizers. Both steps are required to participate in the conference.

We are asking everyone who would like to attend to submit a short BIO explaining your background, connection to, and interests in midwater. This helps everyone understand where you are coming from, which will lead to more meaningful conversations throughout the conference.

We ask for an abstract/position statement even if you do not want to present a standard research talk, lightening talk, or poster, but would be willing to participate in a panel discussion or tech showcase. A position statement explains what you would like to represent at the conference - a resource, a cause, a policy, whatever?

If more than 120 people would like to attend, the abstracts/position statements and bios will help the advisory panel select participants.

We are in the process of fundraising to assist early career and underrepresented nations participants with the costs of attending (lodging, meals, registration), so please don't let cost deter you from submitting an abstract.

Please let us know if you have questions, Karen, Jan, Bronwyn and Sam

Link to registration < http://midsec.info/register >

–

Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 osbornk@si.edu http://orcid.org/0000-0002-4226-9257 Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012, Washington, D.C. 20013-7012 USA

Courier Address: Smithsonian Institution, MR 0163, Natural History, West Loading Dock, 10th and Constitution Ave NW, Washington, D.C. 20560

OsbornK@si.edu

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

Taipei Taiwan EvolvingTogether Apr24-27

Dear EvolDir community,

We are pleased to announce the EMBO Workshop "Evolving together: from genomics to biological interactions," which will take place from April 24-27, 2026, at Academia Sinica in Taipei, Taiwan.

This workshop will integrate perspectives from molecular evolution, population genomics, ecology, and systems biology to explore how interactions between organismsâwith their environmentsâadaptation and innovation.

Key Themes: Symbiosis Host-pathogen interactions Predators and prey Competition and cooperation Environmental and anthropogenic interactions

Confirmed Speakers: Deepa Agashe (NCBS, India) Aileen Berasategui (Vrije Universiteit Amsterdam, Netherlands) Aude Bernheim (Institut Pasteur, France) Ko-Hsuan Chen (Academia Sinica, Taiwan) Stephen R. Doyle (Wellcome Sanger Institute, UK) Kenji Fukushima (National Institute of Genetics, Japan) Raphael M. Gutaker (Royal Botanic Gardens, Kew, UK) Yu-Ying Phoebe Hsieh (Fred Hutchinson Cancer Research Center, USA) Yen-Ping Hsueh (Max Planck Institute for Biology Tübingen, Germany) Asano Ishikawa (University of Tokyo, Japan) Laura A. Katz (Smith College, USA) Britt Koskella (University of California, Berkeley, USA) Cheng-Ruei Lee (National Taiwan University, Taiwan) Gianni Liti (Université Côte d'Azur, CNRS, France) Yi-Jyun Luo (Academia Sinica, Taiwan) Wenbo Ma (The Sainsbury Laboratory, UK) Michael McDonald (Monash University, Australia) Frederik Schulz (DOE Joint Genome Institute, USA) Gregory J. Velicer (ETH Zürich, Switzerland) Michelle M. Leger (OIST, Japan)

Venue: Academia Sinica, Taipei, Taiwan Dates: April 24 - 27, 2026 Registration Deadline: February 28, 2026

For the full program, list of speakers, and registration details, please visit our website: https://meetings.embo.org/event/26-bio-interactions Taiwan's unique biodiversity and vibrant research community provide an ideal setting for these discussions. We look forward to welcoming you to Taipei in 2026.

Best regards, Isheng Jason Tsai (On behalf of the Organizing Committee) Academia Sinica, Taiwan

èæ€éISHENG-JASON TSAI <ijtsai@as.edu.tw>

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

UHamburg DZGGraduateMeetingEvolBio Mar25-27

We are excited to announce the DZG Graduate Meeting in Evolutionary Biology, which will take place at the University of Hamburg, Germany, from March 25 to 27, 2026.

Theme: Interactions and Coevolution: from Molecules to Species

The meeting is organized by the Evolutionary Immunogenomics Research Group and will include invited talks, student presentations, poster sessions, a workshop, and networking opportunities.

PhD students, early postdocs, and advanced Master's students in evolutionary biology are warmly invited to register and submit abstracts.

Website and registration information: https://www.biologie.uni-hamburg.de/en/forschung/evolutionaere-immungenomik/dzg-meeting.html Contact: diyar.hamidi@uni-hamburg.de tobias.lenz@uni-hamburg.de

"Hamidi, Diyar" <diyar.hamidi@uni-hamburg.de>

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

GradStudentPositions

AMU Poznan ConservationGenomics

We invite applications for a PhD position within the project “Genetic load and adaptive potential of European bison”, funded by the Polish National Science Centre (NCN) OPUS grant.

ABOUT THE PROJECT: Demographic history can impose long-lasting genetic threats on populations, persisting even after apparent demographic recovery. Assessing these legacy effects requires detailed genomic analyses. In this project, we will investigate the dynamics of genomic erosion in the European bison, a species that survived both the late Pleistocene megafaunal extinction and extinction in the wild at the beginning of the 20th century. To quantify the impact of these events on genomic health, we will develop analytical pipelines to estimate genetic load and compare it between historical and contemporary samples. We will further annotate and analyze genes involved in pathogen response, exploring patterns of genetic variation and genetic load within these functionally important regions. Finally, we will move beyond classical genetic markers to characterize structural variation in contemporary populations. To achieve these objectives, we are assembling an interdisciplinary team that will apply state-of-the-art genomic and bioinformatic approaches.

ABOUT THE POSITION: The position is funded for 48 months. The successful candidate will work in the ancient DNA (aDNA) laboratory, extracting DNA and sequencing genomes from available specimens. The resulting data will be used to quantify the dynamics of genomic erosion over time, using bioinformatic tools developed by other members of the team. The research will involve both wet-lab work and statistical and population genomic analyses of ancient and contemporary samples, and may also include museum-based work to collect additional material. The PhD student will be supervised by Mateusz Konczal (evolutionary genomics) and co-supervised by Maciej Chyleñski and Anna Juras (archaeogeneticists) from ancient DNA laboratory. The student will gain extensive experience in handling and interpreting historical and ancient samples, as well as in large-scale genomic analyses.

HOST INSTITUTION, LOCATION AND PARTNERS: The PhD student will be based at the Evolutionary Biology Group, Adam Mickiewicz University (AMU) in Poznañ, Poland one of the leading research groups in Ecology and Evolution in Europe (https://evobio.web.amu.edu.pl/) and will work in close collaboration with ancient DNA Laboratory AMU and Mammal Research Institute in BiaÂ³owieÂ¿a. Poznañ is a vibrant, safe and green city offering good balance between nature and culture. Several lakes located within the city along with green areas offer excellent access to outdoor activities such as swimming, sailing or cycling. The city offers modern museums, theaters, cinemas and restaurants, as well as fast connections to Warsaw and Berlin.

REQUIREMENTS: The successful candidate must hold (or expect to obtain by June 2026) a M.Sc. degree in relevant field. We seek applicants with: - A strong interest in Evolutionary and Conservation Genomics. - Experience in molecular laboratory, preferentially with interest in aDNA techniques - Strong English language, communication and organizational skills.

Previous experience in conservation genomics, museomics and/or aDNA analyses is an advantage, but not required.

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 Mateusz Konczal (mateusz.konczal@amu.edu.pl).

DEADLINE AND SELECTION PROCESS: Review of applications is ongoing. To ensure full consideration, please apply as early as possibly (but not later than 30th April 2026). The selected candidate will receive assistance with the formal application to the PhD school at AMU, with entrance exams scheduled for early July 2026. The PhD position starts on the 1st October 2026. We look forward to receiving your application!

Mateusz Konczal Institute of Environmental Biology Adam Mickiewicz University Uniwersytetu Poznanskiego 6 61-614 Poznañ tel. +48 61 829 5845 http://evobio.home.amu.edu.pl/?team=dr-mateusz-konczal Mateusz Konczal <mateusz.konczal@gmail.com>

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

AngeloStateU Texas BotanyPhylogenomicsAI

Master's position in Botany with paid Greenhouse Manager appointment I am recruiting motivated Master's students in Botany at Angelo State University (San Angelo, Texas, US), for a program that combines research independence with professional stability. The position includes a secure, paid part-time Greenhouse Manager role with high scheduling flexibility throughout the two-year program.

Students may develop their own research project in botany or join my ongoing research lines, including: - Phylogenomics - Population genetics and incipient speciation - Predictive modeling of plant traits using machine learning - Development of computational tools for biological applications

Financial support at Angelo State University may include Distinguished Graduate Scholarships to help cover tuition, as well as Graduate Research Fellowships and departmental funds to support thesis research.

Please email me if you are interested (carlos.maya-lastra@angelo.edu). Classes start in Fall 2026.

Carlos A. Maya-Lastra, Ph.D. Assistant Professor, Department of Biology Curator of the SAT herbarium, ASNHC Director of the Biology Greenhouse Angelo State University Member, Texas Tech University System San Angelo, TX, 76909 Phone: 325-486-6699 Email: carlos.maya-lastra@angelo.edu Web: https://www.angelo.edu/live/profiles/13544-carlos-maya-lastra Github: https://github.com/camayal Carlos Maya-Lastra <carlos.maya-lastra@angelo.edu>

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

BielefeldU Germany MutationLoadDynamics

PhD studentship: Mutation load dynamics in banded mongooses. Supervisors: Prof Joe Hoffman (Bielefeld University, Germany) and Dr Hazel Nichols (Swansea University, United Kingdom).

An outstanding opportunity is available for a PhD student to work on mutation load dynamics in a cooperatively breeding mammal, the banded mongoose. The position is available in Joe Hoffman's research group (www.thehoffmanlab.com) at the Department of Evolutionary Population Genetics at Bielefeld University and is co-supervised by Hazel Nichols at Swansea University. The position is fully funded for three years.

The PhD project Ever since Darwin, inbreeding depression has been recognized as a major evolutionary force affecting individual fitness and population viability. Consequently, in an era of unprecedented anthropogenic impacts on wild populations and global species declines, understanding the mechanisms underlying inbreeding depression is more pressing than ever. Traditional studies used genome-wide inbreeding as a proxy for the effects of deleterious mutations on fitness, but the specific contributions of these mutations remain poorly understood. Fortunately, advances in genome sequencing and bioinformatics now allow the prediction of deleterious mutations from whole-genome data, enabling investigation of their dynamics in wild populations. This project will explore how predicted deleterious mutations influence fitness in the banded mongoose (Mungos mungo), a cooperatively breeding African mammal. In this species, inbreeding occurs at unusually high rates, with around 9% of pups resulting from father-daughter or brother-sister matings, offering a rare opportunity to study the dynamics of deleterious mutations. The PhD student will analyse their contributions to inbreeding depression using a long-term dataset spanning three decades, which includes molecular data from ~2,000 individuals, a multigenerational pedigree, and detailed behavioural and life-history data. This PhD offers a unique opportunity to combine cutting-edge genomic approaches with rich ecological and behavioral data to uncover the genetic basis of fitness variation in a wild population.

Applicant's profile We seek a bright and highly motivated student with a good first degree and an M.Sc. or equivalent in a relevant topic (e.g. population genomics, bioinformatics, molecular ecology, behavioural ecology). The ideal candidate will have strong quantitative skills, including proficiency in working in R and experience of writing custom scripts. Practical experience of handling, analysing and interpreting next generation sequence (NGS) data is strongly preferred, although additional training will be provided as needed. The candidate should also be able to work both independently and as part of a multidisciplinary team, and must demonstrate a high standard of spoken and written English.

The working environment The PhD student will be based at the Department of Evolutionary Population Genetics at Bielefeld University, Germany (www.thehoffmanlab.com). Our group is located in the newly constructed Verhaltensforschung building, which features modern offices and state-of-the-art, fully equipped laboratories. The building currently hosts 11 principal investigators and more than 30 postdocs and PhD students. It offers a stimulating, supportive and highly international research environment. The working language of the department is English.

Bielefeld is a city of 325,000 inhabitants with an attractive historical centre and easy access to the Teutoberger Wald for hiking and other outdoor pursuits. It is an affordable and pleasant city to live in and is well connected to most major European cities.

This project will be mainly carried out at Bielefeld University, but the PhD student will also have the opportunity to spend some time at Swansea University (https://www.swansea.ac.uk/staff/h.j.nichols). The successful applicant will therefore benefit from excellent opportunities for international travel and collaboration, while receiving a rigorous integrative training that will prepare her/him very well for a scientific career in evolutionary genetics / population genomics / molecular ecology / behavioural ecology.

Remuneration This generous PhD studentship is funded by the German Science Foundation (DFG) for a period of three years and includes health insurance, pension contributions etc. The pay scale is TVL E13 (65%). Funding will also be available for the student to attend workshops and conferences.

Application procedure To apply for this position, please provide: (i) a letter of motivation; (ii) a CV; (iii) copies of relevant degree certificates, (iv) a maximum 2-page statement of your research interests, including your relevant skills and experiences; (v) a publication list, if applicable, (vi)

— / —

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

---

CharlesU Czechia ComputationalGeneticCodeEvol

* Two PhD positions in Computational Biology at Charles University, Prague *

We are recruiting two fully funded PhD student positions in computational biology at the Department of Cell Biology, Faculty of Science, Charles University (Prague, Czechia), in the group of Dr. Hana RozhoÃ²ová.

Our research asks a simple "what-if" question: if we rewired the genetic code, would evolution take different paths? Almost all organisms on Earth share the same genetic code a mapping from 64 three-letter codons to amino acids and stop signals. Because mutations typically change one nucleotide at a time, the genetic code makes some amino-acid changes easy to reach and others much harder potentially biasing evolution in predictable ways.

Two PhD projects are available:

1. Genetic-code bias in amino-acid substitution patterns. The student will quantify whether amino-acid pairs that are more "accessible" under the genetic code

(connected by more or shorter mutational paths) tend to substitute for each other more often in nature, and how this interacts with classical mutation bias. 2. Codon degeneracy as a source of evolutionary bias. Most amino acids are encoded by multiple synonymous codons (1-6 in the standard genetic code).

We will focus on two questions: 1. Do amino acids with more synonymous codons become more abundant because they are more “findable”? 2. Synonymous codons differ in their one-step mutational neighbors. Can these differences help explain why organisms prefer some synonymous codons over others?

Both projects are purely computational, combining evolutionary simulations with analysis of real biological data.

Applicants should hold (or soon obtain) a Master’s degree (or equivalent) in biology/computer science/math/physics/etc. Strong candidates will enjoy programming and data analysis and be curious about evolutionary questions; prior biology knowledge is helpful but not required.

Start date: October 1, 2026 Duration: 4 years Application deadline: March 31 2026

How to apply: email a single PDF (CV, transcript, motivation letter, and contact details for 1-2 referees) to hana.rozhonova@natur.cuni.cz

More information: https://natur.cuni.cz/en/biology/departments-and-work-places/department-of-cell-biology/research/rozhonovalab/opportunities Hana Rozhonova <hana.rozhonova@natur.cuni.cz>

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

Krakow InvasionGenomics

PHD POSITION IN INVASION GENOMICS

We invite applications for a PhD position within the project “Invasion success through genomic lens: insights from whole-genome diversity of invasive Hemiptera pests”, funded by the Polish National Science Centre (NCN) OPUS grant.

ABOUT THE PROJECT: The number of emerging alien species is growing worldwide, causing damage to natural ecosystems. A major focus in invasion ecology is to identify traits that contribute to invasion success. Genomic studies can be used to track the invasion process, reveal genomic regions involved in adaptation in the novel range and identify genome characteristics potentially facilitating invasions. In this project, we use two Hemipteran invasive insect species, Cinara curvipes and Leptoglossus occidentalis, as invasion models to unravel the genetic mechanisms behind invasion success. We will use whole genome data to get insight into population genomic differentiation of single nucleotide polymorphism (SNP), structural variants (SV) that can have strong and immediate phenotypic effects and are often related to traits that support range expansion. We will also identify evolutionary events, such as gene family expansions or transposable element (TE) activity, that can modulate invasion success.

ABOUT THE POSITION: The position is funded for 48 months. The successful candidate will be involved in de novo sequencing, assembly and annotation of C. curvipes genome. Further, the genomes of both species will be analysed in terms of structural variation, TE content and expansions of gene families potentially related to survival outside the native range. The presence of facultative bacterial endosymbionts of both species in their native and invasive populations will also be studied as a potential driver of invasiveness. The research will involve wet-lab work, but will be more skewed towards population genomic analyses. The PhD student will be supervised by Dr Aleksandra Biedrzycka, an evolutionary, conservation and invasion geneticist, at the Institute of Nature Conservation, Polish Academy of Sciences in Krakï¿½w. The candidate will work in collaboration with Dr Pierre Nouhaud, evolutionary geneticist of invasive pest arthropod populations, at INRAE - CBGP Marseilles, France.

REQUIREMENTS:

The successful candidate must hold a M.Sc. degree. We seek applicants with:

- a strong interest in evolutionary and population genomics.

- experience or interest in bioinformatic analyses

- good English language, communication and organizational skills.

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 Aleksandra Biedrzycka (Biedrzycka@iop.krakow.pl).

DEADLINE AND SELECTION PROCESS:

Review of applications is ongoing. To ensure full consideration, please apply as early as possible (but not later than August 2026). The PhD position may start between March and October 2026.

We look forward to receiving your application!

Aleksandra Biedrzycka

Instytut Ochrony Przyrody Polskiej Akademii Nauk Al. Mickiewicza 33 31-120 Krakï¿½w Tel. +48 12 370 35 53

Institute of Nature Conservation Polish Academy of Sciences Al. Mickiewicza 33 31-120 Krakï¿½w, Poland phone +48 12 370 35 53

Aleksandra Biedrzycka <biedrzycka@iop.krakow.pl>

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

LiverpoolJohnMooresU SoaySheepMatingClimateChange

PhD opportunity: Climate change and alternative mating tactics in Soay sheep APPLY BY 20/01/2026

See also: https://www.findaphd.com/phds/project/-climate-change-and-alternative-mating-tactics-in-soay-sheep/?p192085 This project offers a rare opportunity to use unique long-term data to explore how climate change is reshaping competition, behaviour, and reproduction in a wild mammal. Soay sheep males on St Kilda engage in intense fights as they compete for access to females. Yet about 10% of males lack functional horns to fight with and so cannot win. Instead, they adopt alternative tactics that can be highly successful - sneaking or disrupting guarded females to gain reproductive opportunities. Climate change is altering the timing and distribution of receptive females, and early analyses suggest that males may face shifting dynamics in the intensity and form of reproductive competition. It may also influence parasite pressures and energetic trade-offs during the rut, further affecting which tactics succeed. This PhD will investigate how climate-driven environmental and parasitic changes influence mating behaviour, hormones, and reproductive success in Soay sheep. The project will draw on nearly a decade of detailed behavioural observations from over 150 males, combined with 40 years of genetic, parasite, and environmental data. Fieldwork on St Kilda during the rut will provide opportunities to collect new behavioural, physiological, and parasite data.

The project will be supervised by Dr. Brian T. Preston (LJMU), Prof. Dan Nussey (University of Edinburgh), and Susanne Zajitschek (LJMU). Applicants should hold relevant BSc and MSc degrees and be comfortable with both fieldwork in challenging conditions and advanced quantitative analyses. We welcome motivated candidates with enthusiasm for behavioural ecology, evolution, and environmental change.

The Faculty of Health, Innovation, Technology and Science (HITS) and its Schools have dedicated Diversity and Inclusion (DI) Groups. The individual School Diversity & Inclusion Coordinators and the Faculty Associate Dean for Diversity & Inclusion lead collective action to promote and embed a culture of equality, diversity and inclusivity. Some Schools are awarded the Athena SWAN Bronze or Silver in recognition of their respective equality initiatives and action plans. Also, Schools have proactive diversity and inclusion groups that are aimed to support staff and students by addressing the inclusivity requirements that are unique to each School, in alignment with the LJMU Diversity & Inclusion policies. Applicants are invited to visit the Faculty of HITS website https://www.ljmu.ac.uk/about-us/faculties and follow the link to each School.

Funding Notes The successful student will be entered for the LJMU VC PhD Studentship competition. These awards cover three full years of funding including UKRI-standard student stipend and research support. The competition is open to UK home students and international students, and applications from candidates from under-represented ethnic minority backgrounds are encouraged.

References For an informal discussion about this opportunity please email Brian Preston b.t.preston@ljmu.ac.uk for more information.

Applicants should email a CV, covering letter detailing their suitability for the project and contact details of two referees to Brian Preston, b.t.preston@ljmu.ac.uk

We are committed to making scientific research more inclusive and are keen to support applicants from groups that have long been underrepresented and/or marginalised from the field. If you belong to such groups, we would like to offer dedicated pre-application advice and mentorship, so that you can prepare the strongest possible application.

Please contact b.t.preston@ljmu.ac.uk by 20/1/26 for this opportunity.

[Liverpool John Moores University] < https://www.ljmu.ac.uk/ > Susanne Zajitschek (FHEA Fellow)

School of Biological and Environmental Sciences James Parsons Building Byrom Street, Liverpool, L3 3AF t: 01519041061 e: S.R.Zajitschek@ljmu.ac.uk w: https://suszaj.github.io/ZajitschekLab/ Important Notice: Liverpool John Moores University was established as a Higher Education Corporation under section 121 of the Education Reform Act 1988. Further information about Liverpool John Moores University can be found at https://www.ljmu.ac.uk/about-us The information in this email and any attachments is for the sole use of the intended recipient(s). If you are not an intended recipient, or a person responsible for delivering it to an intended recipient, you should

— / —

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

---

MaxPlanckInst Konstanz Two NematodeBehaviourEvol

“Towering behavior and collective dispersal in nematode groups, PhD student (m/f/d), 100%:

The Max Planck Institute of Animal Behavior at its sites in Konstanz and Radolfzell offers an international, interdisciplinary, and collaborative environment that opens up unique research opportunities. The goal of our basic research is to develop a quantitative and predictive understanding of the decisions and movements of animals in their natural environment.

The Genes and Behavior Research Group at the Max Planck Institute of Animal Behavior would like to fill the following position with a starting date as soon as possible. This position is fully funded for a period of 3 years with the possibility of a 1-year extension. The workplace will be in Konstanz, Germany.

Our group The student will join the Genes and Behavior research group led by Dr. Serena Ding. The Max Planck Institute of Animal Behavior and the University of Konstanz together form a thriving research community representing a global hotspot for collective behavior, including the Centre for the Advanced Study of Collective Behavior. The student will join the International Max Planck Research School for Quantitative Behavior, Ecology and Evolution from lab to field (IMPRS-QBEE), a cooperative doctoral program between the Max Planck Institute of Animal Behavior and the University of Konstanz.

Project details How animals choose between individual versus collective behavioral strategies, how they execute the behavior from a mechanistic point of view, and how they navigate the cooperative versus competitive social dynamics when behaving together in a group are central questions to this PhD project.

Nematodes are the most abundant animals on Earth; many nematode species live a boom-bust lifestyle and disperse frequently. These tiny little worms often hitchhike on passing vectors to move great distances in search of new resources. Nematodes can disperse individually; we recently found that Caenorhabditis nematodes can also build worm towers to disperse collectively (Perez et al., Current Biology 2025). Moreover, we identified natural dispersal vectors for our local nematode species in southwestern Germany (Greenway et al., bioRxiv 2025). Together, these work pave way for combining the empirical tractability of our study system, including the model organism species C. elegans, with the relevant ecological context to investigate why and how nematodes behave collectively.

Research will involve designing, executing, and analysing experiments to address one or more of the questions we ask above. The student may also propose their own questions in addition. The student will develop their own research approach with the support and guidance from our international team of collaborators specialising in behavioral ecology, evolutionary biology, molecular biology, quantitative behavior, computer vision, and physics of behavior. We envision this project to primarily involve laboratory-based investigations, although the student will have the opportunity to join field work to gain insights into the study system.

Your qualifications Essential requirements: - MSc in biology, animal behavior, collective behavior, or a related field - Fundamental interest in biological phenomena and questions - Experimental and analytical capability, critical thinking, literature awareness - Excellent verbal and written communication skills in English. German language skills are not required Desirable experience: - Hypothesis-driven experimental design and implementation in animal behavior - Quantitative data analysis skills; proficiency in one or more programming languages (R, Matlab, Python) - Video-based approach to behavioral analysis is beneficial - Competence with C. elegans and/or fluorescence imaging techniques is beneficial but not necessary

Our offer The successful candidate will become part of the International Max Planck Research School for Quantitative Behavior, Ecology & Evolution (IMPRS-QBEE).

You will therefore work in a dynamic and highly international research environment. Our working language is English. The payment for the position is made in accordance with your experience and qualification of the collective agreement for the public service (TVï¿½D-Bund).

The Max Planck Society endeavors to employ more severely disabled people. Applications of severely disabled persons are expressly welcome. The Max Planck Society strives for gender and diversity equality. We welcome applications from all backgrounds.

How to apply Are you interested? Then we are looking forward to receiving your application until January 13, 2026 via the IMPRS application system: https://imprs-qbee.cloud.opencampus.net/ . To be considered for this position, applicants must include a CV and a research statement that addresses the following points:

— / —

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

---

Oldenburg Germany CoralPopulationGenetics

PhD position in population genetics and conservation genomics of corals (f/d/x/m) Background The Marine Conservation group < https://www.baumslab.org/ > of Prof. Dr. Iliana Baums at HIFMB is looking for a PhD student to study the population genetics and conservation genomics of reef building corals in the Caribbean. Populations of reef-building corals have declined dramatically and the Baums lab in collaboration with international restoration and academic partners in Belize, Honduras, the USA, Curacao, Mexico and the Dominican Republic are working together to develop population management tools for these species.

In the Marine Conservation group < https://www.baumslab.org/ > at the HIFMB in Oldenburg we use molecular techniques to answer fundamental questions about marine evolution and ecology to guide coral reef conservation efforts. The group currently has two focus areas: coral physiology and symbiosis and coral restoration genomics.

Research at the HIFMB focuses on marine biodiversity and its importance for the functioning of marine ecosystems. We aim to develop sensitive strategies to measure and understand environmental and social processes that influence or influenced by the change in biodiversity in marine systems, and implement effective means to define a scientific basis for marine conservation, marine governance, and ecosystem management efforts. HIFMB is a highly interdisciplinary research environment that currently brings together experts from 18 countries who focus on contemporary yet distinct topics of research. Our growing research portfolio to understand marine systems at the HIFMB spans from molecular ecology to human geography, microbial metabolism to mathematical modeling and art. As a cooperation between the University of Oldenburg (UOL) and the Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research (AWI), the HIFMB benefits from its access to a diverse set of resources for cutting-edge research. The new building of the HIFMB offers state-of-the-art wet-lab and computational resources. The HIFMB is located in Oldenburg, a city in Northern Germany, which is a region that is home to a large number of institutions dedicated to environmental and marine research. In addition to the AWI and the ICBM, the institutions with which the HIFMB researchers regularly interact include the Max-Planck Institute for Marine Microbiology in Bremen, the Center for Marine Environmental Sciences (MARUM) at the University Bremen, and Leibniz Centre for Tropical Marine Research in Bremen.

Your Tasks You will..

* collect coral samples from both field and laboratory settings and prepare them for experimental and genetic analyses. * design, organize, and conduct experiments to investigate population genetic structure, genetic load, inbreeding levels, parentage, clonality, and adaptive signatures in corals and their algal symbionts. * generate and analyze physiological data, including growth and reproductive performance, under experimental conditions. * apply molecular and genomic approaches such as RNA sequencing and DNA sequencing to assess adaptive potential and stress responses. * integrate physiological and genomic datasets to develop alternative conservation genetics strategies aimed at maximizing adaptive capacity in threatened coral species. * work closely with international collaborators and contribute to interdisciplinary research projects. * disseminate research outcomes through peer-reviewed publications, conference presentations, and public data repositories.

More information is available under https://www.awi.de/en/work-study/out-of-university/as-phd-student.html . Your Profile

* Master's degree (or equivalent) in marine biology or

molecular ecology or related fields * Strong background in population genetic theory and experience in using molecular and bioinformatic tools * Proficiency in at least one coding language (Phyton), and proficiency in R

Preferred Qualifications and Skills

* A background in marine biology, experience with DNA/RNA extractions and amplification * Disposition to work in laboratory and field conditions * Very good English knowledge (approximately equivalent to CEFR < https://europass.europa.eu/en/common-european-framework-reference-language-skills > level C1)

Further Information

* Contact in day-to-day work: collaboration mainly with more than 5 people * Communication: predominantly internal (with colleagues and other departments) in the following ways

— / —

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

---

StockholmU BehaviouralEvolution

PhD student position at Stockholm University

We are recruiting a fully funded 4-year PhD student position for a project examining how sexual selection acts in females and using a small freshwater fish, the pygmy halfbeak (Dermogenys collettei), as a model.

Female halfbeaks express a conspicuous sexual ornament???an orange abdominal gravid spot that males use when making mate choice decisions. This trait allows experimental manipulation of female ornamentation, providing an exceptional opportunity to test key evolutionary hypotheses. The PhD project will combine laboratory experiments, fieldwork in Southeast Asia (Malaysia and Singapore), and AI-assisted behavioural tracking to examine the costs, benefits, and ecological drivers of female sexual ornaments in halfbeaks.

The project integrates evolutionary biology, behavioural ecology, and sensory ecology, and uses state-of-the-art automated tracking and phenotypic manipulation techniques. Therefore, we are looking for a person with a strong interest and training in evolutionary biology and behavioural research.

The PhD student will join the research group of Prof. John Fitzpatrick (www.su.se/english/profiles/j/jfrit) 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 behavioural ecologists. Overseas applications are encouraged.

The complete ad with information on qualification requirements and instructions on how to apply is at: https://su.varbi.com/en/what:job/jobID:893229/ Application deadline: February 15, 2026

For 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>

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

UAuckland MathematicalPhylogenetics

Two PhD Scholarships in Mathematical Phylogenetics

Two full-time PhD scholarships are available in the School of Computer Science at the University of Auckland, New Zealand. The successful applicants will work on combinatorial and algorithmic questions related to phylogenetic networks, which are used to analyse and represent the evolutionary histories of biological entities such as species, viruses, and populations. A particular focus of the two projects are phylogenetic networks with directed and undirected edges. The exact questions to be investigated will be discussed with the PhD students to suit their interests and skillsets.

Requirements. A successful applicant has a Masters or Honours degree in mathematics or computer science, and a strong background in at least one of graph theory, combinatorics, algorithms, and theoretical computer science. Some knowledge of phylogenetics would be helpful, but is not a strict requirement. Candidates must also be eligible for admission to the PhD program at the University of Auckland. For more information on postgraduate studies at the University of Auckland, see the following link: https://www.auckland.ac.nz/en/study/study-options/-find-a-study-option/doctor-of-philosophy-phd.html . Scholarship. The PhD scholarships are funded by the New Zealand Marsden Fund and available from March 2026 onwards. A starting date is negotiable. Each scholarship is for three years, and covers tuition fees and an annual tax free allowance of NZ$35,000. The successful candidates will be supervised by Dr Simone Linz.

Application. To apply, please email your CV and academic transcript, a short statement of research interests, and names and contact details of two referees to Simone Linz (s.linz@auckland.ac.nz). Informal inquiries can be directed to the same email address. Applications will be accepted until the positions are filled.

Dr Simone Linz School of Computer Science University of Auckland, New Zealand s.linz@auckland.ac.nz https://simonelinz.wordpress.com Simone Linz <s.linz@auckland.ac.nz>

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

UBonn BiodiversityMonitoring

We want you:PhD position (4 years) in the PhenoRob Cluster of Excellence!

In cooperation, we are looking for a part-time

Research Assistant (65%)

within the DFG-funded Cluster of Excellence “PhenoRob - Robotics and Phenotyping for Sustainable Crop Production” (EXC2070/2) in Core Project 5.

As a doctoral candidate, you will contribute to the technological development of novel approaches for automated biodiversity monitoring in the field and collect data on biodiversity and the effects of diversified cropping systems on ecosystem processes and interaction networks between organisms.

Your tasks:

- Conducting independent research as part of your dissertation project, including the design, planning and analysis of ecological field experiments

- Collecting and processing field and/or laboratory data using appropriate methods and quality standards

- Statistical evaluation of complex data sets and interpretation of the results in a scientific context

- Publishing research results in international journals and presenting them at national and international scientific conferences

- Collaborating in project organisation, including coordination with cooperation partners and co-supervision of theses

- Supporting research and teaching in the field of biodiversity monitoring

Your profile:

- University degree (master’s degree) in biology, ecology, agricultural sciences or related disciplines

- Knowledge of and interest in measurement technology, environmental technology or engineering sciences

- Species knowledge in at least one species group (plants, insects, birds)

- Excellent knowledge of the English language

- Committed, flexible, team-oriented and interested in further training.

We offer:

- A varied and challenging role with one of the largest employers in the region

- Opportunity to pursue a doctorate

- Company pension scheme (VBL),

- Numerous university sports activities

- Excellent public transport connections thanks to our central location in Bonn, as well as the opportunity to take advantage of affordable parking

- Flexible working hours and the opportunity to work from home

- Remuneration in accordance with remuneration group 13 TV-L.

The University of Bonn is committed to diversity and equal opportunities. It is certified as a family-friendly university. Its goal is to increase the proportion of women in areas where women are underrepresented and to promote their careers in particular. It therefore strongly encourages suitably qualified women to apply. Applications will be treated in accordance with the State Equality Act. Applications from suitable candidates with proven severe disabilities and persons of equal status are particularly welcome.

If you are interested in this position, please send your complete and informative application documents by 17 February 2026, quoting the reference number PhenoRob2/CP5, exclusively in a PDF file by email to c.scherber@leibniz-lib.de for technical reasons. For further information, please contact Prof. Dr. Christoph

Scherber (c.scherber@leibniz-lib.de).

The University of Bonn is an international research university offering a wide range of subjects. With 200 yearsof history, around 31,500 students, more than 6,000 employees and an excellent reputation both at home andabroad, the University of Bonn is one of Germany's most important universities and has been designated a University of Excellence.

The Leibniz Institute for the Analysis of Biodiversity Change (LIB) is one of the large, globally networked research museums of the Leibniz Association. In addition to excellent research on biological diversity and its change, we are driving forward the further development of our extensive scientific collections with an international team and state-of-the-art technology.

Stiftung Leibniz-Institut zur Analyse des Biodiversitätswandels Postanschrift: Adenauerallee 127, 53113 Bonn, Germany

Stiftung des öffentlichen Rechts; Generaldirektion: Prof. Dr. Bernhard Misof (Generaldirektor), Adrian Grüter (Kaufm. Geschäftsführer) Sitz der Stiftung: Adenauerallee 160 in Bonn Vorsitzender des Stiftungsrates: Dr. Michael H. Wappelhorst

Meusemann Karen <K.Meusemann@leibniz-lib.de>

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

UCork SalmonGenetics

PHD POSITION: GENETIC DIVERSITY OF ATLANTIC SALMON

The Fish Ecology and Evolution in Dynamic Ecosystems (FishEyE) group at University College Cork is offering a PhD position to work on genetic diversity in Atlantic salmon (Salmo salar), and its ecological and evolutionary drivers, across the island of Ireland. Salmon are iconic species of broad cultural, ecological and economic value, renowned for their precise homing to natal rivers. This behaviour, coupled with natural selection acting on heritable phenotypic traits across gradients of landscape heterogeneity, has produced a profusion of distinct, locally adapted, salmon populations. Yet salmon are in crisis and face a cocktail of anthropogenic stressors.

This project will examine spatiotemporal patterns in genetic diversity in salmon at different spatial and temporal scales and elucidate underlying environmental and anthropogenic drivers. The project will be embedded in a newly funded research programme titled LEGACY: Understanding the Origins and Vulnerability of Diversity within Atlantic Salmon to Safeguard our Natural Evolutionary Heritage. The PhD student will join a vibrant and dynamic team of geneticists and ecologists working on fish and other taxa. Our team also has strong links with the Marine Institute and other government agencies in Ireland and beyond, and we collaborate broadly with top salmonid biologists and geneticists across Europe and North America.

The research will be conducted in the School of BEES which consists of 30+ faculty, ca. 20 postdocs and 50 PhD students across Zoology, Ecology, Plant Sciences and Geology. Cork is situated on the south coast of Ireland, 2.5 hours from Dublin, is served by an international airport, has a population of about 200,000, and is on the doorstep of some of the most beautiful coastline in Europe.

Candidates interested in this position should hold a minimum of a BSc, and ideally also an MSc, with a background in evolutionary biology or populations genetics/genomics, and have a strong interest in studying landscape drivers of intraspecific diversity and global change biology. Previous experience with data analysis, in particular bioinformatics and GIS, are essential. The project will be largely desk/lab based, but there are opportunities for fieldwork too. Prior experience with molecular lab work is a major plus too. We are looking for someone with fluent English, good communication and writing skills, and ability to work in a team.

The position is funded for 4 years and the start date is 1 March 2026. The primary supervisor will be Dr Tom Reed, and the secondary supervisor Prof. Phil McGinnity. A senior postdoc will also play a key mentorship role. Please write to Dr Tom Reed (treed@ucc.ie) if you have further questions about the project or position.

University College Cork is committed to equity and diversity and actively promotes equal opportunities. To apply for this position, please send a letter of motivation and CV, together with contact details of two references and your certificates as a single pdf (<10 MB) to treed@ucc.ie with the subject "Application: Your Name [PhD Salmon Genetics]". The deadline for applications is Feb 2, 2026, or until the position is filled. Interviews to be held shortly thereafter, online.

Associate Prof. Dr Tom Reed University College Cork Evolutionary Ecology of Fish and other taxa GROUP: https://www.ucc.ie/en/fisheye/ [under reconstruction] DEPARTMENT: https://www.ucc.ie/en/bees/ SUPERVISORS: https://research.ucc.ie/en/persons/thomas-reed/ https://research.ucc.ie/en/persons/philip-mcginnity/ Thomas Reed <treed@ucc.ie> Philip McGinnity <P.McGinnity@ucc.ie>

Thomas Reed <treed@ucc.ie>

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

UGeneva PopulationGenomicsBiodiversity

Opening PhD position in population genomics and biodiversity conservation

We are seeking a highly motivated PhD candidate to join an exciting research project exploring the spatiotemporal dynamics of hybridization between the European wildcat (Felis silvestris) and the domestic cat (Felis catus). This project addresses a timely and societally relevant challenge at the intersection of evolutionary biology and conservation.

The PhD position is fully funded for four years and will be based at the Department of Genetics and Evolution, University of Geneva (UNIGE), within the PhD School of Life Sciences (lifesciencesphd.unige.ch/). The Department of Genetics and Evolution offers a stimulating scientific environment, an excellent infrastructure, and is located on the Science Campus in the heart of the city of Geneva. Both English and French are working languages in the laboratory. More details about the research group can be found at: https://genev.unige.ch/research/laboratory/Mathias-Currat. The PhD candidate will work in a dynamic, international research environment and benefit from close collaborations with researchers from the Swiss Federal Research Institute (WSL) and the University of Zurich (UZH).

The project aims to uncover how introgression from domestic cats spreads through wildcat populations across space and time, identify the key ecological and evolutionary processes driving these patterns, and assess the effectiveness of alternative conservation strategies. By combining population genomics, spatially explicit modelling, and applied conservation, this PhD offers a unique opportunity to contribute both to fundamental research and to evidence-based wildlife management. The project is embedded within the COST Action Genetic Nature Observation and Action (www.cost.eu/actions/CA23121/).

Requirements

Master's degree in biology or an equivalent field;Skills in population genetics, genomics, biostatistics, and English;Skills in modelling, bioinformatics, and ecology are an asset;Experience in high precision labwork is an asset;Strong interest in applied conservation biology and interdisciplinary research;Good communication skills and the ability to work both independently and collaboratively;

Terms of employment

Duration: 4 years, subject to successful completion of the first year (trial period);Start date: Position available from 1st May 2026;Salary: According to the SNSF salary scale for doctoral candidates at the University of Geneva;

Other conditions The PhD candidate will participate in teaching and other laboratory activities, as well as in the doctoral program in Ecology and Evolution at the University of Geneva (ecovo.unige.ch).

How to apply Applications should be sent as a single PDF file by email to Dr. Mathias Currat (mathias.currat@unige.ch). Initial review begins on February 20, 2026, but applications will be accepted until the position is filled. The application should include: a CV including publication list if existing, a cover letter explaining the motivation for the project, a brief summary of the master project and optionally two letters of reference, including one from the Master's thesis supervisor.

Dr. Mathias Currat, PhD Department of Genetics and Evolution

University of Geneva Sciences II - Quai Ernest-Ansermet 30 1205 Geneva - Switzerland https://agp.unige.ch/en/person/mathias-currat https://lifesciencesphd.unige.ch/program/ecology-and-evolution Mathias Currat <Mathias.Currat@unige.ch>

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

UHalle Germany EvolVenomPeptidesInAnts

PhD position

within the project

"FormiDablE - Function, Diversity and Evolution of formicine ant venom peptides"

The position is fixed term (65% according to TV-L 13, for 36 months) and starting on the 01.06.2026 (or as soon as possible).

Project description:

Venomous animals and the venoms they wield are a remarkable example of repeated evolution. In preliminary work, we have discovered so far unknown venom peptides in the highly acidic, formic acid containing venoms of non-stinging ants of the subfamily Formicidae (genus Camponotus). Aim of this project is to as-sess the diversity of these peptides in additional Formica and Lasius ant species, to manually annotate these peptides in genomes, to investigate the evolution of these peptides, and to investigate their potential biological function. To achieve this aim, in this interdisciplinary project within the Priority Program "GEvol: Genomic Basis of Evolutionary Innovations", we combine organismic (Simon Tragust,), comparative ge-nomic and transcriptomic (Barbara Feldmeyer) as well as analytical chemistry (Timo Niedermeyer) know-how and methods.

We require: We are seeking a highly motivated candidate with an inquisitive, solution-oriented and frustration-tolerant mind that has excellent organisational skills to independently plan and conduct as well as analyse chemical, genomic and transcriptomic work. The following qualifications are required: - Applicants must hold a Scientific University degree (MSc/Diploma) in biology, biochemistry or related fields - Prior knowledge and/or experience with techniques and analyses involved in either proteomics, tran-scriptomics and/or genomics of insects (DNA/RNA extraction and analysis, next-generation sequencing, bioinformatics, HPLC) - Driver's license and/or experience with insect maintenance and dissection is a plus - Fluency in English (lab working language) with good communication and social skills

We offer: - A friendly and inspiring working atmosphere in a young research group (for more information check out: https://www.zoologie.uni-halle.de/-allgemeine_zoologie/staff/tragust/). The prospective PhD will be hosted in the lab of Simon Tragust (Halle) and will work in close collaboration with Barbara Feldmeyer (Frankfurt, https://www.senckenberg.de/-en/research/institutes-overview/sbikf-institut/sbikf-ag-molecular-ecology/) and Timo Niedermeyer (Berlin, https://www.bcp.fu-berlin.de/pharmazie/-faecher/pharmazeutische_biologie/team/professoren/-niedermeyer/index.html) - The group is embedded in the Department General Zoology sporting excellent, state of the art research facilities in the delightful, historic city of Halle with good and affordable living conditions and good con-nections to e.g. Berlin (~1h by train), Leipzig-Halle airport (~15min by train) or Frankfurt (~3h by train) - A project that will help to develop and foster the applicant's academic profile combining diverse tech-niques in an interdisciplinary project.

Application: Please submit your full application in English with registration number Reg.-Nr. 5-13320/25-D until 30th of January 2026 via e-mail as a single PDF to simon.tragust@zoologie.uni-halle.de. Applications should include a cover letter detailing their motivation to join the project against the background of their research interests and experience, a CV, certificates (MSc/Diploma) and the names and email addresses of two potential referees. Interviews of applicants will take place in February/March.

Looking forward to your applications.

Simon Tragust

Simon Tragust <simon.tragust@zoologie.uni-halle.de>

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

ULodz VertebrateEvolution

OPEN PHD POSITION IN AMPHIBIAN THERMAL PHYSIOLOGY

The STELLAR Research Group (https://-www.philippekok.com/stellar-research-group/), based in the Department of Ecology and Vertebrate Zoology, University of Lodz (central Poland), is seeking an outstanding, curiosity-driven PhD candidate with a strong interest in evolutionary biology.

The successful applicant will join an NCN-funded project entitled: “When the chill hits: respective role and importance of low molecular weight cryoprotectants, ice-binding proteins and skin microbiota in supercooling amphibians (SUPERCOOL)”

Supervisor: dr hab. Philippe J. R. Kok, prof. UL

Project description Starting in October 2026 (position funded for 48 months), the PhD student will investigate how amphibians cope with extreme cold, with a particular focus on antifreeze proteins in tropical species. The project combines challenging fieldwork with laboratory and computational approaches. Fieldwork will involve collecting biological samples from cold-exposed and control animals, often under demanding environmental and logistical conditions. Laboratory work (both in the field and in Poland) will include assessing antifreeze activity, contributing to the identification of proteins and genes involved in cold tolerance, and analysing gene expression patterns. Parts of the molecular work will be conducted in collaboration with specialised research facilities. Overall, the PhD project offers interdisciplinary training spanning field biology, molecular techniques, and data analysis, addressing fundamental questions in cold adaptation.

Minimum requirements

* MSc degree in Biology or a related discipline * Proficiency in spoken and written English * Ability and willingness to conduct fieldwork in remote areas under physically demanding conditions(good physical condition is required; access to the field laboratory involves up to three days of hiking in rugged terrain)

Highly desirable qualifications

* Strong interest in amphibian biology and thermal physiology * Experience with molecular biology techniques * Strong writing and communication skills

Additional skills considered an asset

* Experience in bioinformatics * Experience in statistical data analysis * Evidence of scientific outreach or dissemination

Place of work

ódÂ, Poland

How to apply

Please send an email to philippe.kok@biol.uni.lodz.pl containing:

* A CV * A cover letter including a statement of research interest and relevant experience * Contact details for 1-2 referees

For informal enquiries, prospective applicants are welcome to contact Philippe Kok at philippe.kok@biol.uni.lodz.pl and/or pjrkok@gmail.com. Review of applications will begin immediately and continue until the position is filled. Shortlisted candidates will be invited for an online interview and guided through the formal application process.

“Philippe Kok Jacques R.” <philippe.kok@biol.uni.lodz.pl>

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

UMainz InsectPhysiology

PhD position: insect ecophysiology and land-use intensity

Application deadline: February 4th, 2026 Intense land-use and climate change are considered to be the main drivers of insect decline. This PhD project addresses a potential interaction between the two factors. Intense land-use changes the temperature of available micro-habitats, e.g. by reducing shade and decreasing the availability of humid micro-refugia. Increasing temperatures are not only challenging by themselves, but especially because they increase drought stress. This is why drought resistance may be a key ecological trait that confers tolerance to intense land-use in insects. Cuticular hydrocarbons (CHCs) cover the body of all insects like a waxy layer and are the most important protection against desiccation in insects. Their composition varies strongly between insect species and determines the drought resistance of insect species.

In this project, the PhD candidate will study how land-use of grassland and forest habitats is linked to physiological traits of the present insects, namely their drought resistance and their cuticular hydrocarbon (CHC) profile. The project is embedded within the Biodiversity Exploratories consortium (https://www.biodiversity-exploratories.de/en). The successful applicant will do extensive field work in three sites across Germany (Schwï¿½bische Alb, Hainich, Schorfheide), monitor insects, measure their drought resistance, analyze their cuticular hydrocarbon profile, and perform statistical analyses on the relation of these traits. The study will include ants, hoverflies, solitary bees, beetles, true bugs and grasshoppers. Publication of the results in international, peer-reviewed, English-speaking journals is expected.

We offer a 3-year PhD position (65% TV-L E13), based in Mainz and potentially in Wï¿½rzburg. The project is a collaboration of PD Dr. Florian Menzel (Johannes-Gutenberg-Universitï¿½t Mainz) and Prof. Dr. Thomas Schmitt (Julius-Maximilians-Universitï¿½t Wï¿½rzburg).

The project links chemical ecology, community ecology, insect physiology and climate change research. The PhD candidate will gain experience in a wide range of methods, including field studies, species identification, GC-MS analysis, and biostatistics.

We are looking for a highly motivated candidate with an MSc degree (or equivalent) in Biology or a related field. The successful applicant should have a strong background in entomology, ecology and/or evolutionary biology. Experience with insect identification, chemical analysis, statistics (in R), a driving licence valid in Germany, as well as German-speaking skills are advantageous but not required. The working language of both groups is English. The Universities of Mainz and Wï¿½rzburg aims to increase the number of women and diverse people in science, and applications by women and diverse people are strongly encouraged. Similarly, qualified candidates with disabilities will be preferred.

The successful applicant will join an international and dynamic scientific environment. Our groups investigate ecology, evolution and behaviour of ants and other insects (see https://www.blogs.uni-mainz.de/fb10-evolutionary-biology/research-groups/group-menzel/ and https://www.biozentrum.uni-wuerzburg.de/zoo3/team/schmitt).

Please send your application as a single pdf file containing your CV, a motivation letter (including your motivation why to apply for this particular project and your previous research activities; max. 2 pages), certificates (including grades) of your MSc, BSc and A-level exam, publications (if applicable), and the names and email addresses of two potential referees. In addition, please send a pdf copy of your Master thesis. Applications should be sent to PD Dr. Florian Menzel (menzelf@uni-mainz.de) and Prof.

Dr. Thomas Schmitt (thomas.schmitt@uni-wuerzburg.de) until February 1st, 2026. The position can be started from April or May 2026. Please do not hesitate to contact us if you have further questions.

Priv.-Doz. Dr. Florian Menzel Institute for Organismic and Molecular Evolution (iomE) Johannes Gutenberg University Biocentre I Hanns-Dieter-Hï¿½sch-Weg 15 55128 Mainz, Germany phone: 0049-6131-3927848

https://www.blogs.uni-mainz.de/fb10-evolutionary-biology/research-groups/group-menzel/ https://www.blogs.uni-mainz.de/fb10-evolutionary-biology/menzel-florian-pd-dr/

— / —

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

---

Uppsala RhodesU DoublePhD CapeGladiolusSpeciation

Double PhD degree in Plant Evolutionary Ecology, Uppsala University and Rhodes University: Adaptive divergence and incipient speciation in Cape Gladiolus https://uu.varbi.com/en/what:job/jobID:886908/ We are hiring a PhD student in plant evolutionary ecology for a double degree between The Department of Ecology and Genetics (IEG), Uppsala University, and the Department of Botany, Rhodes University under the supervision of Prof. Nina Sletvold and Dr. Ethan Newman. A key research area in evolutionary biology is bridging the gap between microevolutionary processes and the resulting macroevolutionary patterns. In this project, we use the Gladiolus carneus (Iridaceae) species complex to study ecological speciation of Cape Gladiolus. The G. carneus complex is endemic to the Cape Floristic Region (CFR), one of the most species-rich floristic regions in the world, and includes multiple morphologically distinct varieties associated with variation in pollination and the abiotic environment. To disentangle various drivers of diversification, the project combines phylogenomic comparative methods, population genetics, and extensive field and common garden experiments. This project represents an ambitious and unprecedented evaluation of ecological speciation in the CFR, and the successful PhD candidate will contribute to advancing our understanding of drivers of phenotypic and genomic divergence across different time scales. The PhD student will be responsible for designing and maintaining various field and common garden experiments, including reciprocal translocations along elevational gradients and plant collections in the growth facilities. The PhD project will involve intense periods of field work, including driving and hiking in rough terrain and mountains. A component involving molecular lab work is also included. The PhD student is further expected to actively participate in the academic activities of our research group, develop analytical frameworks, prepare manuscripts for publication, and present their work at national and international meetings.

To meet the entry requirements for doctoral studies, you must

- Hold a Master's (second-cycle) degree in biology, evolutionary biology, plant biology, or equivalent - 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 - Have a drivers licence, and be willing to spend considerable time away from the lab, doing field work

We attach great importance to personal qualities such as motivation, independence, and problem-solving analytical skills. Candidates must be able to express themselves fully in spoken as well as written English.

Qualifications desired

- Publication of at least one first author paper (may also be under review or in press) - Experience presenting research at an international or local conference - Experience with statistical analyses and associated software (e.g., R) - Demonstrated capacity to design and troubleshoot experiments - Previous experience with field and common garden work - Previous experience with molecular lab work - Capacity to work as part of a team - Ability to drive a 4x4 vehicle for field work

The PhD candidate will obtain two degree certificates, one from each university, in which the prerequisites from each institution needs to be fulfilled. The research project will ensure satisfaction of the requirements for a PhD degree at both universities, individually. The PhD candidate will be funded by a combination of salary in Sweden and scholarships in South Africa. Scope of position: full-time, 4 years. Starting date 2026-02-01 or as agreed. For further information about the PhD opportunity, please contact Professor Nina Sletvold (Uppsala University): nina.sletvold@ebc.uu.se or Dr Ethan Newman (Rhodes University): e.newman@ru.ac.za

The application should include 1) your research interests, and a motivation of why you want to pursue a PhD, your interest in this specific project, and your suitability for the position, 2) your CV including your education, research experience, and references to publications, 3) names and contact details of two referees (email address, institution, and phone number). The application should be written in English. Shortlisted candidates will be interviewed. Please send your application directly to botany@ru.ac.za, using the subject heading "Application double PhD degree". You are welcome to submit your application no later than 15 January 2026.

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:

— / —

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

---

UTartu Estonia InsectThermalTraits

PhD positions: evolution of thermal traits in insects

We are seeking PhD students to join our team working on the project entitled "Evolution of Thermal Traits in Insects: A Comparative-Ecological Approach," funded by the Estonian Research Council and carried out at Estoniaï¿½s leading research centre, the University of Tartu (https://www.ut.ee/en). The lab-wide project focuses on a macroevolutionary analysis of the evolution of thermal traits (such as the minimum suitable temperature) in insects. The ultimate aim is to evaluate the potential of insect populations to respond to ongoing climate change. Our research relies on a diverse set of methods, including analyses of geographical distribution patterns, meta-analyses of published data, and empirical work to collect comparable data on various insect species across Europe. Specific PhD projects will be tailored based on the research interests of the students.

The work will be supervised by Prof. Toomas Tammaru (http://www.ut.ee/~tammarut) and other members of his team (https://zooloogia.ut.ee/en/content/chair-of-entomology-members-of-the-chair). Our group has a unique combination of interests and expertise, covering evolutionary ecology, advanced statistical methods, phylogenetic comparative analyses, and the taxonomy of insects, Lepidoptera in particular. You will experience a work atmosphere that combines the spirit of an old university town with a highly modern and international research environment. On the other hand, Estonia is rich in nature providing ample opportunities for outdoor activities.

PhD studies in Estonia last four years, and publishing research papers is a requirement. PhD students receive competitive salaries, allowing them to work on their theses full-time while also taking some relevant classes.

A successful candidate will have an excellent academic record, experience with statistical analyses, and an interest in evolutionary biology. Some experience and/or a genuine interest in the ecology, evolution, or taxonomy of insects would be an advantage. The candidate must have obtained their Masterï¿½s degree by August 1, 2026. Enrolment as a PhD student will be on September 1, 2026.

To apply, please send your CV and a motivation letter (200 to 300 words) outlining your experience and interests related to the subject to Toomas Tammaru (toomas.tammaru@ut.ee) before the end of February 10 (any time zone).

Toomas Tammaru <toomas.tammaru@ut.ee>

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

UTuebingen PlantGeneticDiversity

PHD POSITION: GENETIC DIVERSITY OF SOUTH AFRICAN PROTEAS

The Plant Evolutionary Ecology group at the University of Tuebingen in Germany is offering a PhD position to work on genetic diversity of Protea (sugarbush) species, and its biological and environmental drivers, in the South African fynbos biome. Proteas are key species in one of the world's richest biodiversity hotspots, and they are exceptionally beautiful. We plan to use a combination of molecular tools, quantitative genetics, and population genetic modelling, to understand genetic diversity in DNA sequence and phenotype.

The project will be embedded in the new Cluster of Excellence TERRA "Terrestrial Geo-Biosphere Interactions in a Changing World" (www.terra-cluster.org), a large interdisciplinary research initiative linking the Universities of Tuebingen and Hohenheim with the Senckenberg Society in Frankfurt. Specifically, the project will be part of a team of four complementary PhD students working on biosphere-geosphere interactions and ecoevolutionary processes in proteas. There will be a close collaboration with the Leigh lab (https://deborahmleigh.weebly.com/) at Senckenberg, where the student will have a longer research stay. The PhD project will include field work in South Africa, and it will be supported by the TERRA Molecular Biodiversity Lab, and the TERRA Graduate School of Terrestrial Geo-Biosphere Interactions.

Candidates interested in this position should hold an MSc with a background in evolutionary biology or populations genetics/genomics, and have a strong interest in studying genetic biodiversity. Previous experience with molecular lab work is a must, additional skills in bioinformatics and/or statistics are a plus. We are looking for a team player with good communication skills in English. Additional German language skills are welcome.

The position is funded for 3.5 years and will be paid at E13 TV-L 65% (usual level for PhD contracts in Germany). The place of work will be Tuebingen. If you have more questions about the project or position, please write to Oliver Bossdorf (oliver.bossdorf@uni-tuebingen.de).

The University of Tuebingen is committed to equity and diversity and actively promotes equal opportunities. Equally qualified candidates with disabilities will be given preference in the hiring process. To apply for this position, please send a letter of motivation and CV, together with contact details of two references and your certificates as a single pdf (<10 MB) to bewerbung@geo.uni-tuebingen.de with the subject "Application: Your Name [FUN01_1]". The deadline for applications is January 26, 2026, or until the position is filled.

Prof. Dr. Oliver Bossdorf University of Tuebingen Plant Evolutionary Ecology oliver.bossdorf@uni-tuebingen.de

GROUP: www.uni-tuebingen.de/plantevoeco
HERBARIUM: www.uni-tuebingen.de/herbarium
PUBLICATIONS: https://scholar.google.com/citations?user=hAPepaEAAAAJ "Bossdorf, Oliver" <oliver.bossdorf@uni-tuebingen.de>

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

Jobs

Colombia UndergradRes Biodiversity

IRES: UNDERSTANDING POLLINATOR-MEDIATED DIVERSIFICATION IN NEOTROPICAL PLANTS

PAID research opportunity for Summer 2026 for U.S. undergraduate students

Application Deadline (extended) - January 22, 2026

This IRES program is funded by the National Science Foundation's International Research Experiences for Students and implemented by the Missouri Botanical Garden. It provides U.S. undergraduate students with a paid opportunity to engage in high-quality international collaborative research for eight-weeks in Cali, Colombia.

IRES students will conduct individual research projects that address key questions in pollination biology and evolutionary ecology while receiving in-depth mentorship and training from US-based and Colombian researchers.

Program Highlights:

Hands-on field research in Colombian forests

Study the pollination biology and floral scent chemistry

Learn floral scent analysis techniques and pollinator observation methods

Explore biodiversity hotspots while gaining international research experience

Eligibility:

Undergraduate students enrolled full-time at a U.S. institution and returning to their program in the fall following their international experience.

Per NSF rules, applicants must be U.S. citizens or U.S. permanent residents(i.e. green card holders).

No prior international experience or knowledge of Spanish language required Students must be available to participate for the entire duration of IRES program activities, including:

Three-month Virtual Pre-Departure Program focused on preparations for international travel, Colombian culture, and research (weekly, one-hour Zoom sessions, March-May)

Eight-week International Research Experience in Colombia where students will take part in training bootcamps, perform field research and data collection, and engage in cultural activities (in person, with flexibility in travel timelines, June-August).

Three-month Virtual Post-Travel Program focused on data analysis, research dissemination, and career development (weekly, one-hour Zoom sessions, September-November)

IRES students will receive a $650 weekly stipend for the duration of the 8-week international research experience in Colombia. In addition, IRES students will have all travel to and within Colombia, lodging, and research expenses covered.

Please visit our website for more information: https://www.missouribotanicalgarden.org/plant-science/plant-science/about-science-conservation/-resources-databases/study-opportunities/ires Monica Carlsen-Krause <monica.carlsen@mobot.org>

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

CSU MontereyBay CommunityEvolution

The Department of Biology, Agriculture and Chemistry at California State University, Monterey Bay invites applications for a tenure-track faculty position at the assistant professor level to begin in Fall 2026. We seek a teacher-scholar whose work examines the structure, dynamics, evolution and/or function of ecological communities. Successful candidates will demonstrate a commitment to excellence in undergraduate teaching, inclusive mentoring, and a sustainable research program that actively engages undergraduates. California State University, Monterey Bay is a mid-sized university in California's Central Coast that grants undergraduate and graduate degrees. Many appreciate living and working close to the shores of beautiful Monterey Bay, with easy access to recreational areas from Big Sur to Santa Cruz. Nearby opportunities for collaborative research include working in the Monterey Bay National Marine Sanctuary and Silicon Valley, and with colleagues at local research universities, including UC Santa Cruz and Stanford University.

RESPONSIBILITIES: - Teach lower and upper division courses in Biology and Ecology (like BIO 211 - introductory biology, BIO 340 - Ecology, BIO 449 - community ecology, and a potential new upper division elective course for the Ecology, Evolution, and Organismal Biology concentration

- Employ innovative teaching and learning techniques that engage students through the use of technology, hands on experience and problem solving

- Mentor undergraduate and graduate students in research

- Advise and mentor undergraduate and graduate students in academics, capstone projects, internships, and post-degree career options

- Sustain innovative and extramurally-funded research in Ecology, leading to publications and professional visibility

- Contribute to Department, College, and University-wide shared governance through participation in faculty meetings and committee work

- Help implement the goals of the College of Science and the CSUMB Vision

MINIMUM QUALIFICATIONS:

- Ph.D. in Ecology, Biology, Evolutionary Biology, or related field by the time of appointment from an APA accredited doctoral program

- Experience working effectively in an ethnically and culturally diverse campus community

- Commitment to and experience in teaching undergraduates

- Excellent written and oral communication skills

PREFERRED QUALIFICATIONS:

- Expertise in community ecology (including theoretical and/or field based community ecology)

- Demonstrated leadership skills in professional or academic areas are desirable

- Research and teaching interests and expertise that complement and strengthen those of existing faculty in the department.

- Strong interest in contributing to teaching of an introductory course in ecology as well as upper division courses in community ecology and other relevant areas of expertise

- Interest in mentoring undergraduate student research and/or internships

- Demonstrated experience with course and curriculum development

- Proven ability and desire to mentor and teach students from diverse cultural, ethnic, educational, and economic backgrounds

- Record of external funding and writing grant proposals

Those interested should look here - https://careers.csumb.edu/en-us/job/552990/assistant-professor-of-community-ecology The deadline for the priority screening data is 01/13/2026.

Nate Jue Associate Professor Cal State Monterey Bay njue(at)csumb.edu

Nathaniel Jue <njue@csumb.edu>

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

FloridaIntlU EvolutionaryBiology

Hi,

we are searching broadly and would welcome applications from evolutionary biologists addressing creative questions at the interface of methods and systems and those using or developing innovative methods for biological discovery.

Florida International Universityis a Top 50, preeminent public research university with 55,000 students from all 50 states and more than 140 countries, as well as an alumni network of more than 340,000. Located in the global city of Miami, the university offers more than 200 degree programs at the undergraduate, graduate and professional levels, including medicine and law. FIU faculty are leaders in their fields and include National Academy members, Fulbright Scholars and MacArthur Genius Fellows. A Carnegie R1 institution, FIU drives impactful research in environmental resilience, health and technology and innovation. Home to the Wall of Wind and Institute of Environment, FIU stands at the forefront of discovery and innovation. With a focus on student success, economic mobility and community engagement, FIU is redefining what it means to be a public research university.

Open Rank Tenure-Track Faculty Position in Big Data/AI/Bioinformatics

The Department of Biological Sciences at Florida International University (https://biology.fiu.edu) invites qualified candidates to apply for an Open Rank (Assistant, Associate, or Full Professor) position. Scientists addressing groundbreaking questions at the interface of Big Data/AI/Bioinformatics and biological systems and those using or developing innovative Big Data/AI/Bioinformatics methods for biological discovery are encouraged to apply. Research that aligns with FIUs long-term goals in innovation, environment and health is desirable. Successful candidates could become affiliated with several preeminent research institutes and centers including the Biomolecular Sciences Institute (https://bsi.fiu.edu/), the Institute of Environment (https://environment.fiu.edu/), the Extreme Events Institute (https://eei.fiu.edu/), and the Biscayne Bay Campus Robotics and Autonomous Systems Laboratory for Coastal Conservation and Restoration. The minimum requirements are a doctoral degree in a related field from an accredited institution and evidence of active research. Applicants with postdoctoral experience are preferred. The successful candidate will be expected to build an internationally prominent research program by bringing and maintaining an active, externally funded research program, publishing in peer-reviewed journals, mentoring graduate students in our Ph.D. program, and contributing to undergraduate and graduate teaching.

Application Details Qualified candidates are encouraged to apply to Job Opening ID 536602 at careers.fiu.eduand attach one combined pdf including (1) cover letter, (2) curriculum vitae, and (3) statements of teaching, and research. Candidates will be requested to provide names and contact information for at least three (3) references who will be contacted as determined by the search committee. Applications will be accepted until the position is filled. Please direct inquiries about this search to the chair of the search committee, Dr. Janna Fierst (jfierst@fiu.edu).

Review Date Review of candidates will start February 12, 2026, and continue until the position is filled. The expected start date is August 13, 2026.

FIU is a State University System of Florida member, Equal Opportunity, Equal Access, and Affirmative Action Employer for individuals with disabilities and veterans. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, age, national origin, disability,or protected veteran status. For inquiries regarding nondiscrimination,contact FIU's Office of Civil Rights Compliance and Accessibility at 305.348.2785 or email ocrca@fiu.edu.

Janna L. Fierst

Associate Professor Biomolecular Sciences Institute Florida International University Miami, FL 33199

Janna Fierst <jfierst@fiu.edu>

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

Fribourg Switzerland ConservationBiol Mar31

Job opening: Professorship in Animal Ecology at the University of Fribourg, Switzerland.

The Faculty of Science and Medicine of the University of Fribourg (Switzerland) and the Department of Biology (https://www.unifr.ch/bio/en/) invite applications for an open-rank Professorship in Animal Ecology.

Qualified applicants must have an outstanding track record of fundamental research in animal ecology, using quantitative, state-of-the-art approaches with a strong field component.

Topics of interest include, but are not limited to, biotic interactions, community ecology, conservation biology, ecological modelling, and eco-evolutionary feedback loops. The successful candidate will develop an internationally recognized, competitive research program sustained by external funding.

Teaching experience at the university level is expected. The candidate will teach at the Bachelor level and contribute to the Master program "Environmental Biology".

The University of Fribourg (https://www.unifr.ch/home/en/) is bilingual (French and German). Knowledge of the second language (oral level B1) is expected. If this requirement is not met, the candidate must acquire it within two years of taking up the position.

The University of Fribourg is a signatory to the DORA declaration and attaches great importance to a qualitative assessment of academic performance.

The University of Fribourg is an equal opportunity employer and strives towards gender balance and diversity at all levels.

Further information on the position is available here: https://www.unifr.ch/scimed/de/faculty/positions Application deadline: 31 March 2026.

Informal inquiries can be addressed to Christian Parisod (christian.parisod@unifr.ch) and/or Rudolf Rohr (rudolf.rohr@unifr.ch).

Prof. Thomas Flatt Department of Biology University of Fribourg Chemin du Musée 10 CH-1700 Fribourg Switzerland

e-mail: thomas.flatt@unifr.ch phone: +41 26 300 8833 <tel:+41263008833> phone: +41 26 300 8850 <tel:+41263008850> (secretary)

https://www.unifr.ch/bio/en/groups/flatt/ European Drosophila Population Genomics Consortium: http://droseu.net/ FLATT Thomas <thomas.flatt@unifr.ch>

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

IowaStateU EnvironmentalChangeAdaptation

This open position should be of interest to evolutionary biologists working on any aspect of adaptation to environmental change at any scale of biological organization, including (and not limited to) molecular biology, evolutionary genomics, epigenetics, adaptability and resilience, evolutionary medicine, etc.

###

Tenure-Track Faculty Position in Integrative Environmental and Organismal Health

The Department of Ecology, Evolution, and Organismal Biology (EEOB) in the College of Liberal Arts and Sciences at Iowa State University (ISU) seeks an integrative biologist working on the effects of environmental change on ecological or organismal health. The ideal candidate will have an integrative research program at any biological scale, from molecules to ecosystems, using any mixture of advanced experimental, computational, and/or analytical approaches and technological tools (e.g., artificial intelligence, remote sensing, environmental informatics, predictive modeling, and/or environmental genomics). Research should address pressing societal questions about organism responses to environmental change, disease risk, environmental resilience, adaptability, evolutionary medicine, ecological health and well-being, epigenetics, or other related topics. The successful candidate is expected to establish an externally funded research program and contribute to undergraduate and graduate education, including an introductory course in environmental health and an advanced course in an area of expertise. This is a tenure-track 9-month position at the rank of assistant professor, with a tenure-home appointment in EEOB (100%). Candidates must hold a Ph.D. by the time of appointment.

All applications must be submitted electronically at https://isu.wd1.myworkdayjobs.com/IowaStateJobs (job # R18375, full link below*). Please be prepared to attach a letter of application, a research statement, a teaching and mentoring statement, a curriculum vitae, and the names and contact information of three referees. The position will remain open until filled. Full consideration will be given to applications received by February 15, 2026. For additional information please email physiol@iastate.edu.

EEOB is a vibrant and collegial department of 16 faculty. EEOB has a strong mentoring system for junior faculty and is committed to ISU's principles of community. Faculty contribute to undergraduate and graduate education through departmental and interdepartmental programs, and conduct innovative research in ecology, evolution, and organismal biology, using integrative approaches that bridge traditional scientific disciplines and levels of biological organization.

Iowa State University is an equal opportunity/affirmative action employer. All qualified applicants will receive consideration for employment without regard to race, color, age, religion, sex, sexual orientation, genetic information, national origin, marital status, disability, or protected veteran status, and will not be discriminated against.

Iowa State University is a comprehensive, land grant, Carnegie Doctoral/Research Extensive University with an enrollment of over 30,000 students. The university is located in Ames, IA, one of the nation's most highly rated metropolitan areas of its size (https://www.iastate.edu/life-at-iowa-state/-campus-and-ames) and is only 35 miles north of Des Moines.

*Position URL: https://isu.wd1.myworkdayjobs.com/-IowaStateJobs/job/Ames-IA/Assistant-Professor-in-Integrative-Environmental-and-Organismal-Health_R18375 Dr. Nicole Valenzuela (she/her) Professor Dept. of Ecology, Evolution, and Organismal Biology Iowa State University Ames, IA 50011-4009 URL https://faculty.sites.iastate.edu/nvalenzu/ "Valenzuela, Nicole [EEOB]" <nvalenzu@iastate.edu>

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

LundU Biodiversity

The Biology Department at Lund University, Sweden, is recruiting a senior lecturer in Biodiversity (equivalent to associate professor).

The successful candidate is expected to be placed within the Division of Biodiversity and Evolution, which consists of fifteen lecturers and professors, together with their associated research groups, as well as a number of independent researchers. The research conducted within the division is situated at the intersection of biodiversity, ecology, and evolution, with strong connections to conservation biology, ecosystem ecology, biological environmental monitoring, and the Biological Museum.

The position involves research, teaching, and outreach. The appointee is expected to contribute to strengthening research and teaching within the subject area. Over time, the appointee is also expected to contribute to the department's activities by undertaking various types of leadership assignments. The content and distribution of duties may change over time, but at least 50% of the position should include research.

Application deadline is February 11th. For more details and information about how to apply, see: https://lu.varbi.com/en/what:job/jobID:848749/-type:job/where:4/apply:1 Dr. Jessica K. Abbott Professor of Evolutionary Genetics Department of Biology Division of Biodiversity and Evolution Lund University Kontaktvï¿½gen 10 223 62 Lund, Sweden Phone: 046 222 9304 Website: https://tinyurl.com/jessicakabbott "It is those who know little, and not those who know much, who so positively assert that this or that problem will never be solved by science." - Charles Darwin, Descent of Man

Jessica Abbott <jessica.abbott@biol.lu.se>

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

MaxPlanckInst Ploen Directorship

The Max Planck Institute for Evolutionary Biology in Plï¿½n/Germany (http://www.evolbio.mpg.de/) has open positions at the level of a Max Planck Director. Accordingly, the Institute invites expressions of interest from outstanding scientists in all areas of evolutionary biology.

Supported by generous long-term funding, Max Planck Directors are free to pursue their scientific dreams (see https://www.mpg.de/directors). Directors also play pivotal roles in creating and sustaining vibrant and inclusive research environments. More information can be found at https://www.evolbio.mpg.de/3856225/-Directors. Please submit your expression of interest to managingdirector@evolbio.mpg.de.

Arne Traulsen <managingdirector@evolbio.mpg.de>

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

PennsylvaniaStateU ResTech GeneticsSymbiosis

JOB DESCRIPTION:

The Bordenstein Laboratory at Penn State University's Departments of Biology and Entomology and the One Health Microbiome Center seeks a full-time Research Technologist in the Life Sciences (Advanced Professional) field. This role involves advancing research on the molecular biology and evolutionary ecology of a widespread symbiosis between a lysogenic phage, Wolbachia bacteria (found in the reproductive tissues), and Drosophila melanogaster. The ideal candidate will design, implement, support, analyze, and report using gene-to-organismal approaches to dissect a male lethality trait. This position will focus on various techniques such as fly rearing, transgenic expression, genetic editing, fitness assays, reproductive tissue dissections, molecular biology, fluorescent and electron microscopy, and collaborative discovery. The position is funded for 12 months from the date of hire.

APPLICATION INSTRUCTIONS:

Applicants must submit a single PDF file containing the following: 1. A cover letter summarizing relevant experience and reasons for interest in the job. 2. A CV that includes contact information for at least three references (name, position, telephone number, and email address). 3. Full-length (all pages) and first-authored works of research spanning papers, reports, posters, and presentations.

Application website: https://psu.wd1.myworkdayjobs.com/PSU_Staff/job/Penn-State-University-Park/Research-Technologist—Life-Sciences-Advance-Professional—Bordenstein-Lab_REQ_0000074535-1 Lab website: https://bordensteinlab.com/ POSITION INFO:

The successful candidate will have priority responsibilities in the following areas:

- Experimental design, implementation, analysis, time management, and reporting - Preparation and adherence to new scientific protocols, specimen evaluation, and biostatistics - Coauthorship on scientific papers, grants, presentations, and summary reports - Contribution to research methods, solutions, and technical approaches for problem-solving - Data collection, data analysis, statistics, and visualizations - Management of trainees for molecular biology skills, biosafety measures, lab policies, equipment, proper record-keeping, organismal maintenance, and performance reviews -Conduct various experimental tasks, including insect handling, tissue dissections, biological marker staining, fluorescent microscopy, microinjections, and genotyping and quantifying insect and symbiont cells using PCR and qPCR -Daily manage and maintain laboratory insect colonies, handling hundreds to thousands of insects daily -Troubleshoot emergencies, answer day-to-day questions from lab members, and manage laboratory schedules -Assist lab management and participate in ongoing entomology, microbiology, and molecular biology experiments as assigned -Maintain a welcoming, safe, and professional environment that aligns with lab expectations.

EDUCATION AND COMMUNITY:

-Requires a Bachelor's degree or higher, plus three or more years of relevant work experience, or an equivalent combination of education and experience -Essential skills include problem-solving, interpersonal, organizational, communication, and documentation -Successful candidates should be able to work effectively in a team, demonstrating genuine appreciation for working, leading, and managing diverse audiences.

Pennsylvania State University, a premier Land-Grant university, is situated in the picturesque Appalachian mountains of central Pennsylvania. State College and its surrounding communities are home to approximately 100,000 people, including over 45,000 students. The area is renowned for its high quality of life, access to stunning natural landscapes, including majestic mountains, serene streams, and beautiful parks, and a wide range of recreational activities and sports. State College boasts an excellent school system and offers numerous cultural events.

s.bordenstein@psu.edu

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

UCalgary Canada ResearchChair OpenCall

The University of Calgary has launched an internal competition for the new Canadian Impact+ program of hiring for international scholars. These prestigious professorships will come with 500k or 1M CAD annual research budget. Please see this link for more details.

https://careers.ucalgary.ca/jobs/17170542-canada-impact-plus-research-chairs-university-of-calgary . The program is oriented towards several areas of focus, but these are fairly broadly written and could readily include an evolutionary biology research program. Calgary is a wonderful place to live, the winters are relatively warm (for Canada), and the natural beauty of the area is incredible (Banff is a little over 1h drive).

Samuel Yeaman <samuel.yeaman@ucalgary.ca>

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

UGothenburg Two PlantSystematics

We are hiring two Senior Lecturers (Associate Professors) at the Department of Biological and Environmental Sciences at the University of Gothenburg, Sweden in plant systematics 1. Vascular plant systematics https://web103.reachmee.com/ext/I005/1035/job?site=7&lang=UK&validator=9b89bead79bb7258ad55c8d75228e5b7&job_id=39395 2. Non-vascular plant and other cryptogram systematics https://web103.reachmee.com/ext/I005/1035/job?site=7&lang=UK&validator=9b89bead79bb7258ad55c8d75228e5b7&job_id=39401 Join us!

Christine D. Bacon

Senior Lecturer in Biodiversity University of Gothenburg Gothenburg, Sweden

Gothenburg Global Biodiversity Centre Box 461, SE 405-30 Gï¿½teborg, Sweden

I work flexibly and so you may receive an email from me outside of traditional working hours. While flexibility works for me, please do not feel obliged to respond outside of your own working hours.

Christine Bacon <christinedbacon@gmail.com>

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

UppsalaU Biology

Assistant Professor in Biology

Uppsala University is hiring an Assistant Professor in Biology, placed at either of the following departments: Ecology and Genetics, Organismal Biolog, Cell and Molecular Biology.

Preference will be given to applicants who have completed their PhD or attained equivalent expertise no more than seven years before the deadline for applications.

Read more about the position and the application procedure: https://www.uu.se/en/about-uu/join-us/jobs-and-vacancies/job-details?query=893394 Last application date: 11 March 2026

Nï¿½r du har kontakt med oss pï¿½ Uppsala universitet med e-post sï¿½ innebï¿½r det att vi behandlar dina personuppgifter. Fï¿½r att lï¿½sa mer om hur vi gï¿½r det kan du lï¿½sa hï¿½r: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: http://www.uu.se/en/about-uu/data-protection-policy Nina Sletvold <nina.sletvold@ebc.uu.se>

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

UTexas ElPaso Tech UTEP GlobalChange

Are you a recent graduate or about to graduate with your bachelor's degree in Biological Science, Environmental Science, or related fields?

Not sure what your next step is?

The UTEP ROADS Postbaccalaureate program could be for you!

UTEP ROADS is an NSF funded RaMP (Research and Mentoring for Postbaccalaureates) program that aims to provide the next generation of global change scientists with transformative research training and professional development - all while engaging them within a supportive academic network at the University of Texas at El Paso and beyond.

The ROADS program is seeking applicants who:

Have received a Bachelor's degree in Biological Sciences, Environmental Science (or related field) within the last 4 years (May 2022 - May 2026)

Have a minimum GPA of 3.0 (preferred)

Have US Citizenship or Permanent Residency

Why should you apply?

ROADS students will:

Be awarded one-year of full support ($32.5K stipend, funds for research, travel, and subsistence)

Develop and conduct a year-long research project at UTEP within a faculty members lab

Experience innovative science that focuses on identifying the effects global change has on ecological, evolutionary, and environmental processes in the extreme dryland environments of the Arctic and Desert

Participate in expert led workshops, seminars, and networking events that aim to enhance the professional skills needed to thrive in graduate school or STEM careers

Have an opportunity to publish their findings in scientific journals

Be part of a supportive and collaborative team of mentors and peers!

How can you apply? Applicants must submit:

Online Application and Registration https://etap.nsf.gov/ Emails of 2 professional references for letters of recommendation

A personal essay on interest in the ROADS program and research background

Unofficial Academic Transcript

Applications for the ROADS Postbaccalaureate program are due March 1st , 2026

Please see the full Application Details on our UTEP ROADS Website!

https://www.utep.edu/science/ramp/ Have additional questions? Please contact ramp@utep.edu

“Schaeffer, Kathleen E” <keschaeffer2@utep.edu>

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

UVetMedBudapest GlobalChangeParentalCare

Post-doctoral Researcher Position 2026

The impact of global change on parental care systems and population resilience Department of Zoology, University of Veterinary Medicine Budapest (UVMB), Budapest, Hungary

Rapid global change, including human disturbance and climate warming, poses mounting risks to wild animal populations. Successful parental care strategies may buffer against the negative consequences of global change. However, both human disturbance and climate warming may disrupt parental behaviour, accentuate the costs of care and sexual conflict, interfere in parental cooperation and ultimately cause lethal and non-lethal damage to offspring. Yet we currently lack information on how global change may influence sex roles in care and parental cooperation, the physiological impacts on parents and offspring, and its consequences for the viability of populations.

Our project will examine how climate change and human disturbance shape parental strategies and its consequences for population productivity by utilising (1) large scale studies across multiple species exhibiting diverse patterns of parental care in varied climatic regions, (2) field experiments of climate and disturbance in natural populations, and (3) detailed studies within populations to determine how climate change and human disturbance may interact to shape parental care strategies and the consequences for population resilience and productivity.

We will achieve this by combining fieldwork, behavioural research, experimentation, population monitoring, movement tracking and molecular lab research across multiple populations of a diverse avian group (shorebirds). Shorebirds are an ideal group to investigate the impact of global change on parental care as they provide a wide variety of parental care systems, are globally distributed, reproduce in varying climatic environments and are facing threats globally due to climate variability and human encroachment.

We seek to recruit a post-doctoral researcher to contribute to this project.

>Who are we Our international team led by Dr Grant C. McDonald (UVMB, Hungary) in collaboration with Dr Mike Weston (Deakin University, Australia), Prof. Andrew McKechnie (University of Pretoria, South Africa), Prof. TamÃÂs Székely (University of Bath, UK) and Dr AndrÃÂs KosztolÃÂnyi (UVMB, Hungary) comprises diverse experience in reproductive strategies research, investigating the detailed evolutionary and social underpinnings of parental care strategies, the impacts of climate on behaviour and physiology, and the impact of human disturbance on avian populations both on local population and global scale.

>Main responsibilities of the post-doctoral researcher - Organising and conducting avian fieldwork at selected study locations (e.g. Africa, Asia and Europe) in association with collaborators for several months per year - Conduct experiments and behavioural observations in the field - Blood sample collection and close cooperation with molecular laboratory collaborators - Coordinate data collection by collaborating international research teams - Conduct statistical analyses of datasets to address within- and between-population questions - Writ-

ing manuscripts targeted towards top-ranked journals in the field - Support the supervision of students and research assistants - Work in partnership with locally based conservation NGOs and participating institutions - Communicate results at international conferences, to stakeholders and to the broader public - Support additional scientific activities that are important for the success of the project

>What we are seeking - PhD in life sciences (evolutionary biology, zoology or comparable field) - Foundational knowledge in behavioural ecology, animal behaviour or evolutionary ecology - Hands-on experience conducting international fieldwork with wild populations, preferably in birds - Firm skills in data management and statistical analysis using R - Track record of converting scientific research into peer review publications - Excellent written and oral communication skills in English - Ability to work independently and collaborate as part of international team - Openness to live in different cultures during extensive fieldwork periods - Strong project management and leadership skills - Valid driving licence

>What we offer - A 2.5 year position (with the possibility of extension) based at the University of Veterinary Medicine Budapest - Fieldwork in multiple locations across the globe (incl. Cabo Verde, and sites in Europe and Asia) - Extensive opportunities for networking and mentoring with international research teams - Competitive local salary (including paid holiday, fieldwork per diem) - English speaking research team - Opportunity to contribute to conservation and collaborations with NGOs at the different field sites - Opportunities to present research at national and international meetings

— / —

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

Other

ESEB OutreachInitiativeFunds DueMar15

ESEB Outreach Initiative Fund

The European Society for Evolutionary Biology (ESEB) welcomes applications to the ESEB Outreach Initiative Fund for projects that promote evolution-related activities. The goal of this initiative is to improve public knowledge about evolution globally.

Applications for funding will be accepted for educational initiatives that promote evolution, public outreach seminars, public exhibitions,workshops,etc.

There will be a single call per year with a total budget of 12,000 Euro. A single project can be funded with up to 4,000 Euro, but smaller projects are welcome. We are requesting a report after one year, at which time the project should be completed.

Descriptions of previously funded projects are available at https://eseb.org/prizes-funding/outreach-fund/

Please use the ESEB application form to submit your proposal and note the word limits given herein. The form can be downloaded at the ESEB website:https://eseb.org/prizes-funding/outreach-fund/ We request that at least one of the applicants be an ESEB member, and submissions are limited to one per member per call. You can become a member by registering here:

https://eseb.org/society/eseb-membership/

Proposals will be accepted until *15th March 2026***and should be submitted by email to the ESEB office (Email: office@eseb.org; Subject: Outreach 2026). We will acknowledge receipt of all applications within a week. If you have not received our confirmation by then, please contact the ESEB office again!

Please note that scientific meetings are not supported by ESEB Outreach Initiative funds. These fund also do not work as a mechanism for continual funding. Once the potential of a project has been demonstrated, this should be used as a basis to convince other funding sources on continuation funds. Hence, submissions by a group that has been successful in past calls may be penalised if the proposals are mere follow-ups of previous projects.

The applications will be evaluated by the Outreach Initiative Committee:

Florence Debarre, Chair (FR) Trine Bilde (DK) Hannah Dugdale (NL) Andy Gardner (UK) Efe Sezgin (TR)

European Society for Evolutionary Biology Email: office@eseb.org Website: eseb.org

ESEB Office <office@eseb.org>

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

Houston STEGGinteract

We are accepting applications for the STEGG-INTERACT Research and Mentoring for Postbaccalaureates (RaMP) program. This NSF-funded program provides recent college graduates with a year-long mentored research experience on the evolutionary genetics of biological interactions, in addition to training in technical and professional skills. The program is hosted by the University of Houston, Texas A&M University, and Rice University.

More information about the program, including eligibility requirements and a link to apply, can be found here: https://uh.edu/nsm/stegg-interact/ The deadline to apply is February 15, 2026. Apply here: https://etap.nsf.gov/award/3961/opportunity/11435 Interested applicants can contact the program (stegg@central.uh.edu) with any questions.

“Meisel, Richard P” <rpmeisel@Central.UH.EDU>

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

HumanEvolGenetics

We are happy to say that the third edition of our textbook Human Evolutionary Genetics will be published in February.

If you are interested in using this textbook and would like to see some of the chapters pre-publication please contact us. Inspection copies of the book can also be requested from the publisher: https://www.routledge.com/Human-Evolutionary-Genetics/Jobling-Henn-Hollox-Kivisild-Pagani-Tyler-Smith/p/book/9780815345633 Best wishes,

Mark Jobling, Brenna Henn, Ed Hollox, Toomas Kivisild, Luca Pagani, Chris Tyler-Smith

<maj4@le.ac.leicester.ac.uk>; <bmhenn@ucdavis.edu>; <ejh33@leicester.ac.uk>; <toomas.kivisild@kuleuven.be>; <luca.pagani@unipd.it>; <ylxcts@googlemail.com>

“Jobling, Mark A. (Prof.)” <maj4@leicester.ac.uk>

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

JoVE Non-model OrganismsCollection

From: Sophie Tandonnet <sophie.tandonnet@gmail.com> Subject: Other: Invitation to contribute - Non-model Organisms Collection

Dear Evolutionary Community,

As a Guest Editor for < https://www.jove.com/ >JoVE, I am organizing a Topical Collection on Emerging Model Organisms (https://app.jove.com/methods-collections/4483/emerging-approaches-for-non-model-organisms-challenges-and-innovations). We’re aiming to cover experimental approaches currently used to study non-model organisms including data collection, functional experiments (CRISPR, RNAi), nucleic acid extraction protocols, sampling strategies, bioinformatics pipelines and imaging techniques.

JoVE is the leading peer-reviewed scientific methods video journal, aimed at increasing the visibility and reproducibility of research. JoVE's team takes care of the entire process of filming and producing your video (https://www.jove.com/authors/publication).

This Collection will hold a record of techniques used to study non-model organisms, for which standard protocols often require adaptation, and help establish reproducible best practices for the community. We envision it as the go-to methods resource for researchers working in evolutionary and comparative biology for years to come.

Would you be interested in contributing to this collection? If so, I would be happy to discuss a potential abstract submission with you (email me at sophie.tandonnet@ub <dot> edu). Please also feel free to forward this invitation to colleagues or labs who may be interested.

I look forward to hearing from you!

Best Wishes,

Sophie Tandonnet

MSCA post-doctoral fellow

University of Barcelona

Sophie Tandonnet <sophie.tandonnet@gmail.com> Sophie Tandonnet <sophie.tandonnet@gmail.com>

KelloggBiologicalStation Michigan REUOpportunity

Hello,

I hope this finds everyone well. I'm happy to share a fun Research Experience for Undergraduates at the Kellogg Biological Station in Hickory Corners, MI! Please find more information here: https://www.kbs.msu.edu/education/undergraduate-program/research-experiences-for-undergraduates-reu/ Applications are due February 1st! Any questions please email KBSsummer@msu.edu

Cheers,

Angelia

Angelia Lane

(she/her/hers)

Interim Academic Programs Coordinator

Administrative Support

Kellogg Biological Station

Michigan State University

laneang1@msu.edu

“Lane, Angelia” <laneang1@msu.edu>

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

PlantThermalAdaptation InvitationToCollaborate

Dear Prof. Golding,

I'd like to share a brief announcement on EvolDir to invite collaborators for a new Thermal Ecology Alliance project: “Thermal Strategies in a Cosmopolitan Plant”, using Bidens pilosa as a model to test how temperature (cold and heat) shapes life-history, functional traits, and thermal performance across globally distributed populations.

The project is designed to be simple and accessible (short life cycle; small plants; basic controlled chambers/BODs; flexible participation). I'm especially hoping to reach collaborators across a wide range of climates, latitudes, elevations, and anthropogenic contexts.

Project link: https://www.thermalecologyalliance.org/projects, clicking on the referred project

Best regards, Cleber Chaves

Cleber J. N. Chaves Postdoc fellow Department of Plant Biology University of Campinas (UNICAMP) - Brazil https://cleberchaves.wixsite.com/website Cleber Chaves <cleberchaves@gmail.com>

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

QuestForOrthologs SpecialIssue

Dear EvolDir colleagues,

We would like to briefly share the publication of a new Quest for Orthologs special issue in the Journal of Molecular Evolution: https://link.springer.com/collections/-hcifbfjbhe The issue comprises 12 articles covering recent methodological, conceptual, and applied developments in orthology, including topics such as functional divergence, hierarchical orthologous groups, protein domains and synteny, AI-based approaches, and community tools and resources.

The collection was inspired by discussions in the broader orthology community and may be of interest to researchers working in evolutionary biology, comparative genomics, and functional annotation. We hope you will take a look and that you will enjoy the content.

With best wishes, Natasha Glover and David Liberles

Natasha Glover <Natasha.Glover@sib.swiss>

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

SMBE Call-For2026FacultyAwardNominations

Society for Molecular Biology and Evolution

Call for 2026 Faculty Award Nominations Deadline: February 20, 2026

Dear SMBE Members:

SMBE is now calling for nominations for recipients of theFaculty AwardsforEarly-Career Excellence,Mid-Career Excellence,Lifetime Contribution, andCommunity Service. Please consider nominating those of your colleagues you believe deserve to be rewarded for their extraordinary achievements and dedication to the field.

Nominations require:

a nomination letter, which should clearly indicate the award under consideration and also serve as a recommendation lettera one-page summary of the nominee's qualifications for the awarda CV of the nomineean additional letter of recommendation. Self-nomination is not allowed.The nominator need not be an SMBE member, but the nominee must be a member of SMBE to be considered for the award.

Please compile the required documents aboveas a single PDF and upload via the online award application portal before February 20, 2026.

Submit Nomination

Updated descriptions of the awards follow; please read them carefully.

SMBE Early-Career Excellence Award This award is intended for outstanding members of the SMBE community who are in the early stages of an independent research career (3-7 years post-Ph.D.). The primary signal of research excellence is a trajectory of innovative, creative research that is moving the field of Molecular Biology and Evolution forward. The ideal candidate will be one whose career embodies the values of the society, for example in mentoring, outreach, and teaching. The prize includes recognition at the annual SMBE banquet, a cash prize of $1000 and a travel award ($2000 for intracontinental travel/$3000 for intercontinental travel) to attend the annual meeting. This award will be given annually.

SMBE Mid-Career Excellence Award This award is intended for outstanding members of the SMBE community who are in the midst of their research careers (8-15 years post-Ph.D.). The primary criterion is a record of outstanding research that has contributed broadly to the field of Molecular Biology and Evolution. The ideal candidate will be one whose career embodies the values of the society, for example in mentoring, outreach, and teaching. The prize includes recognition at the annual SMBE banquet, a cash prize of $1000 and a travel award ($2000 for intracontinental travel/$3000 for intercontinental travel) to attend the annual meeting. This award will be given annually.

SMBE Lifetime Contribution Award This award is intended for outstanding senior members of the SMBE community (25 years post-Ph.D.). The primary criterion is a record of truly outstanding research that has contributed broadly to the field of Molecular Biology and Evolution. The ideal candidate will be one whose career embodies the values of the society, for example in mentoring, outreach, and teaching. The prize includes recognition at the annual SMBE banquet, a cash prize of $1000 and a travel award ($2000 for intracontinental travel/$3000 for intercontinental travel) to attend the annual meeting. This award will be given periodically and initiated by the SMBE council.

SMBE Community Service Award This award will be awarded to members of SMBE who have provided exceptional service to SMBE and the broader scientific community. The term “service” applies broadly to include specific service to the community (such as to the SMBE journals, the Council or annual meetings) and also service that includes scientific outreach and education. The prize includes an award of $2000 as well as reimbursement to attend the annual meeting. This award will be given periodically and initiated by the SMBE council.

Questions? Please contactsmbe@am.kwglobal.com

Best Regards, Ziheng Yang SMBE Past President

Society for Molecular Biology and Evolution +1.785.289.2056 smbe@am.kwglobal.com https://www.smbe.org/ https://bsky.app/profile/official-smbe.bsky.social This email was sent on behalf of Society for Molecular Biology and Evolution located at301 Concourse Boulevard, Suite 210,Glen Allen,VA23059.To unsubscribe click here.If you have questions or comments concerning this email contact Society for Molecular Biology and Evolutionat smbe@am.kwglobal.com.

Society for Molecular Biology and Evolution <smbe@am.kwglobal.com>

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

SMBE Call-For2028RegionalMeetingProposals

Society for Molecular Biology & Evolution

SMBE Call for 2028 Regional Meeting Proposals Deadline for submissions: March 15, 2026

Dear SMBE Members,

Starting in 2027, the SMBE Annual Meeting will alternate between the Global Meeting (on odd years) and the SMBE Extended Regional meetings (on even years). The first extended regional meetings are scheduled to take place in 2028.

The SMBE will financially support up to five meetings, ideally one per major region of the world (North America, Central/South America, Europe, Africa, Asia/Oceania). This format will reduce the environmental impact of its meetings while simultaneously increasing accessibility by lowering travel costs for its members worldwide.

SMBE is now calling for proposals for meetings and actions to be held between January 1, 2028, and December 31, 2028. Funds will be awarded on a competitive basis to members of the molecular evolution research community to host meetings that provide opportunities for participation to members with a wide range of interests, as covered by our society. The meetings could also include focused symposia to be determined by the organizers. The number of awards will depend on the quality of the proposals, the total cost, and the available budget.

SUBMIT PROPOSAL

The deadline for submission of proposals is March 15, 2026. Decisions will be communicated to the applicants in mid-June 2026.

Submission opens:November 12, 2025Deadline for submission: March 15, 2026Decisions announced: Mid-June 2026 Questions? Please contact smbe@am.kwglobal.com.

Warm regards, Society for Molecular Biology & Evolution

Society for Molecular Biology and Evolution +1.785.289.2056 smbe@am.kwglobal.com https://www.smbe.org/smbe/ https://bsky.app/profile/official-smbe.bsky.social This email was sent on behalf of Society for Molecular Biology and Evolution located at 301 Concourse Boulevard, Suite 210,Glen Allen,VA 23059.To unsubscribe click here.If you have questions or comments concerning this email contact Society for Molecular Biology and Evolution at smbe@am.kwglobal.com.

Society for Molecular Biology and Evolution <smbe@am.kwglobal.com>

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

SSE AIBS CongressionalVisitsDayGrants

The SSE Public Policy Committee invites applications for funds to attend the American Institute of Biological Sciences (AIBS) 2026 Congressional Visits Day. The event will take place in Washington, DC and includes a free half-day training session on April 21 and meetings with lawmakers on April 22. There is also the option to also attend the Communications Boot Camp for Scientists on April 20-21.

SSE members at all career stages who are interested in communicating the importance of federal investments in scientific research and education to lawmakers are encouraged to apply. Funding can be used to cover the cost of the Communications Boot Camp and contribute toward travel and lodging.

SSE members interested in using these funds for other advocacy opportunities are also welcome to apply. Email policy@evolutionsociety.org for more information.

Learn more about the AIBS Congressional Visits Day: https://www.aibs.org/news/2025/251215-congressional-visits-day Join or Renew your SSE membership:

https://payments.evolutionsociety.org/joinsse/ Apply for the AIBS Congressional Visits Day Grants: https://www.evolutionsociety.org/society-awards-and-prizes/aibs-congressional-visits-day-grants.html Deadline: February 15th, 2026, 11:59 PM Eastern

*Kati Moore*she/her *Communications Manager* *Society for the Study of Evolution* communications@evolutionsociety.org www.evolutionsociety.org SSE Communications <communications@evolutionsociety.org>

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

ZuckerkandlPrizeWinner WuetalJME93 322

The Journal of Molecular Evolution is pleased to announce that the following paper has won the Zuckerkandl Prize for the top paper published in the journal in an issue released in the 2025 calendar year:

Wu C, Paradis NJ, Jain K (2025) Substitution-mutation rate ratio (c/μ) as molecular adaptation test beyond Ka/Ks: a SARS-COV-2 case study. J Mol Evol 93:322349.

https://doi.org/10.1007/s00239-025-10248-6 Congratulations to Chun Wu from Rowan University for winning this award!

We are also pleased to congratulate the runners up for their work on viral origins and evolution:

Karki S, Barth ZK, Aylward FO (2025) Ancient host-virus gene transfer hints at a diverse pre-LECA virosphere. J Mol Evol 93:295305.

https://doi.org/10.1007/s00239-025-10246-8 More details about the 2025 award can be found here: https://link.springer.com/article/10.1007/s00239-026-10302-x . Thank you for your interest.

David Liberles

Editor-in-Chief

Journal fo Molecular Evolution

David A Liberles <daliberles@temple.edu>

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

PostDocs

ClemsonU VertebratePhenotypicDiversity

Postdoctoral Researcher in Patterns of Vertebrate Biodiversity Across Phylogenetic Scales.

Clemson University: College of Science: Biological Sciences

The position is to work on an NSF funded project that seeks to build an empirical understanding of how phylogenetic scale influences the patterns and processes of quantitative trait evolution, using teleost fishes as a model. We are working to determine whether evolutionary patterns are identical, random or vary systematically with phylogenetic scale and how they are influenced by grain size and the method of delimiting scale (e.g. clade age vs taxonomic rank). Establishing whether phylogenetic scale dependency is the exception or the rule, is crucial for understanding if, and how, we can synthesize results across studies and scales. The research involves the generation and analysis of vast morphometric datasets, as well as environmental and ecological data collated from existing sources. These data on thousands of species are analyzed using phylogenetic comparative methods in a high performance-computing framework.

The postdoc is expected to consistently write and publish scientific papers. They will help lead hypothesis development, data management and analysis, as well as assist with data collection and student mentoring. Data collection includes 'field work' which involves travelling with a team of researchers to work in museum collections for 1-2 months during the summer. The postdoc will receive active mentoring and career development tailored to support to their scientific and professional goals.

It is a one-year appointment with potential to extend to a second year. Applicants should have completed a Ph.D. or expect to do so prior to starting in the position. I encourage you to reach out to me with questions about the research and position prior to applying: Dr. Samantha Price sprice6@clemson.edu

Ideal starting date is March 15th 2026, but the precise date is negotiable, depending on individual circumstances.

Qualifications

- A doctoral degree in Biological Sciences or related field.

- A solid track record of scientific publications and international conference presentations commensurate with career stage and experience.

- Experience with one or more of the following: evolution over deep- time, functional morphology or ecomorphology, vertebrate diversity and natural history.

- One or more of the following skill sets: phylogenetic comparative methods, phylogenetics, data management, R programming, high- performance computing (Bash, Slurm etc.) and machine learning.

- Ideally some experience mentoring undergraduate and/or graduate researchers.

Application Instructions

For full consideration, applications should be submitted by January 30th 2026. Review will continue until the position is filled.

Applicants should submit the following items via Interfolio at:

https://apply.interfolio.com/179070 (1) An application letter summarizing your fit to the position, including your research background, interests and goals, as well as your qualifications.

(2) C.V.

(3) Contact information for at least two references.

For more information, please contact Dr. Samantha Price sprice6@clemson.edu.

About Us:

For more information about the PI lab, please visit the website www.evovert.com For more information about the department of Biological Sciences and its programs, please visit the website https://www.clemson.edu/science/academics/departments/biosci/ . For more information about Clemson, please visit the website http://www.clemson.edu/ . Sam Price <sprice6@clemson.edu>

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

DalhousieU Canada WildlifeCoronvirusComputationalEvol

A funded Postdoctoral Fellow opportunity is available in Dr. Finlay Maguire's group in the Computer Science / Community Health & Epidemiology at Dalhousie University.

This is a full-time one-year position, with the possibility of extension, at the University of Dalhousie. This position is supported by a New Frontiers in Research Fund Explore grant with Dr. Samira Mubareka at Sunnybrook Research Institute/University of Toronto, Dr. Arinjay Banerjee at the Vaccine and Infectious Disease Organisation/University of Saskatchewan, and Dr. Jeff Bowman at Ontario Ministry of Natural Resources/University of Trent.

Responsibilities: The successful applicant will lead computational work in the Maguire lab to characterise the evolution, diversity, and function of accessory genes in Alpha- and Betacoronavirus species (CoVs) associated with wildlife infections. Building on prior work with wildlife- associated SARS-CoV-2 and endemic CoVs, this project seeks to characterise the ecological features of viral activity in specific wildlife hosts, the breadth and distribution of genetic diversity for endemic CoVs, and the principle molecular drivers of their evolution. This will be achieved by mining large-scale sequencing datasets (and our own samples) for the genomes of wildlife-associated CoVs and then characterising the accessory gene mutational and selection landscape using phylogenetic, coupling/autoencoder models, structural prediction, and machine learning approaches. These results will be used to inform concurrent wildlife cell-line/organoid-based experimental work in the Mubareka (Toronto) and Banerjee labs (VIDO).

The successful candidate will also have the opportunity to work with a multi-institutional team of experts in epidemiology, bioinformatics, virology, immunology and human and animal health through the Wildlife-Emerging Pathogen Initiative (https://wildepi.ca < https://wildepi.ca/flock/ >).

Subject to negotiation, there is a possibility of remote employment within Canada.

Qualifications: The ideal candidate will have strong oral and written communication skills, the ability to work independently and as a part of a team, and proven experience with bioinformatics (including genomics and phylogenetics) and predictive statistical or machine-learning modelling. Programming experience in Python or R is essential for this position. Prior experience with viral data is desirable. Selection of the successful candidate will be based on a combination of academic excellence, relevant experience, career goals, and referee assessments.

Application Process: Please submit a letter of interest, a curriculum vitae, and contact information for two references to Dr. Finlay Maguire (finlay.maguire@dal.ca). The ideal starting date is before the end of Q1 2026 and applications will be considered until the position is filled. At the University of Dalhousie, fostering a culture of inclusion is an institutional goal. The University invites and encourages applications from all qualified individuals, including from groups that are traditionally underrepresented in employment, who may contribute to further diversification of our Institution.

Further inquiries related to this position can be directed to Dr. Maguire.

Finlay Maguire <Finlay.Maguire@dal.ca>

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

EMBL-EBI Cambridge Phylodynamics

Postdoctoral position in phylodynamics at EMBL-European Bioinformatics Institute, Cambridge, UK

As previously teased, we now have a postodoc position open at EMBL-EBI on 'pandemic-scale phylodynamics', in collaboration also with the Duchene, Lemoine and Zhukova groups at Institute Pasteur, and the McHardy group at the Helmholtz Centre for Infection Research. We want to hire somebody from as soon as possible until the end of October 2027.

Some details are included below, and please see the official announcement at the application portal at http://tiny.cc/EBIphylodynamics

Best regards, Nicola De Maio and Nick Goldman <demaio | goldman>@ebi.ac.uk

We are looking for somebody with statistical/computational/genomic epidemiology expertise and skills.ï¿½

Interest and/or experience in large-scale genomic data analysis and simulation would be a great plus.

The aims of our side of the project will be: - developing methods for large-scale global genomic epidemiological simulations, and create a general framework for benchmarking phylodynamic inference methods. - extending MAPLE [1,2,3] to allow massive time tree and phylogeographic inference. - benchmarking existing phylodynamic/phylogeographic methods at large scale.

The candidate will be expected to contribute to at least some of these tasks.

We will coordinate work on these topics with our collaborators, who will develop scalable methods for the inference of variant fitness [4] and in phylogeography [5] and phylodynamics [6,7].

Links:

[1] https://www.nature.com/articles/s41588-023-01368-0 [2] https://www.nature.com/articles/s41586-025-09567-x [3] https://doi.org/10.1101/2024.07.12.603240 [4] https://www.nature.com/articles/s41467-025-60231-4 [5] https://doi.org/10.1093/molbev/msz131 [6] https://www.nature.com/articles/s41467-022-31511-0 [7] https://doi.org/10.1093/sysbio/syad059 Nick Goldman <goldman@ebi.ac.uk>

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

InstitutPasteur Paris PandemicScalePhylodynamics

Dear colleagues,

Happy new year 2026!

We are about to open a postdoc position in Institut Pasteur and would be thankful if you could pass the message to interested candidates.

The position will be joint between the Evolutionary Dynamics of Infectious Diseases team (Duchene), the Modelling of Pathogens team (Zhukova) and the National Reference Center for Respiratory Viruses (Lemoine bioinformatics group). The postdoc will work on "pandemic-scale phylogeography and phylodynamics" as part of the SPREAD project in collaboration with the Goldman group at EMBL-EBI, and the McHardy group at the Helmholtz Centre for Infection Research. The contract is to start in spring 2026 for 18-20 months.

We are looking for somebody with statistical and computational skills who recently obtained their PhD and has experience and interest in phylogenetics, phylodynamics and/or phylogeography. A more detailed description is available on request.

Thank you very much!

Best wishes,

Sebastian, Frï¿½dï¿½ric and Anna (sebastian.duchene-garzon|frederic.lemoine|anna.zhukova @ pasteur.fr)

[Posted on their behalf by Nick Goldman, EMBL-EBI]

Anna Zhukova

Group Leader Modelling of Pathogens: Evolution, Adaptation and Spread (MPath)

Institut Pasteur Department of Computational Biology 25-28 rue du Docteur Roux, 75015 Paris anna.zhukova@pasteur.fr 01.45.68.87.78 & Institut de Biologie de l'ENS (IBENS) Ecole Normale Supï¿½rieure - Universitï¿½ PSL - CNRS - INSERM 46 rue d'Ulm, 75005 Paris office 060 anna.zhukova@ens.psl.eu

Nick Goldman <goldman@ebi.ac.uk>

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

LIIGH-UNAM Mexico HumanpPaleogenomics

Postdoctoral Position in Human Paleogenomics at UNAM, Mexico

The Paleogenomics and Evolutionary Biology group at the International Laboratory for Human Genome Research, Universidad Nacional Autï¿½noma de Mï¿½xico (LIIGH-UNAM), is looking for a researcher to work on a project on human pre-hispanic samples from Mexico.

LIIGH-UNAM < https://liigh.unam.mx/research-groups/ > is a internacional renowned research institute in the fields of Human Genomics, Population Genetics, Palogenomics, Rare Disease and Complex diseases. The Paleogenomics and Evolutionary Biology group < https://scholar.google.com/citations?hl=3Des&user=3DeCs-tmMAAAAJ&view_op=list_works&sortby=pubdate > is interested in better understanding the evolutionary history of multiple organisms that inhabited Mexico (particularly human populations) through the integration of data from multiple disciplines (paleogenomics, archeology, anthropology), and an interdisciplinary interpretation.

The postdoctoral researcher will lead a project aimed to better understand the demographic history and social structure of prehispanic populations that inhabited different parts of the current territory of Mexico. The candidate is expected to lead all computation analyses, have an sustancial contribution to generating the data, and work in close contact with anthropologist and archaeologist collaborators. This project is funded through grants assigned to the Paleogenomics and Evolutionary Biology group (i.e. Sï¿½nchez-Quinto lab). The postdoc position will be funded through a UNAM's postdoctoral fellowship (DGAPA) which is assigned based on the competitiveness of the candidate CV and application. This position offers a unique opportunity to join a vibrant and enriching community at LIIGH-UNAM, undertaking a cutting-edge scientific project involving samples from a rich cultural context, with exciting archeological, social and demographic implications both local and worldwide.

Required qualifications are a PhD in paleogenomics, evolutionary biology, genetics, molecular biology, or closely related fields. Candidates must have excellent verbal and written communication skills, as well as an established record of productivity (e.g., at least one first author peer-reviewed publication). Candidates with a past record of publications in population genetics, molecular ecology, or genome biology are strongly preferred. Ideal candidates will have experience in generating and/or analyzing WGS genomic data, performing population genetic and social structure analyses, as well as molecular biology wet lab experience.

Contact: Interested individuals should send an email to Federico Sï¿½nchez-Quinto at fsanchez@liigh.unam.mx, include the following details:

(1) a cover letter addressing your interest in the position and how your expertise meets the position requirements (2) CV (3) Contact information for 3 references, (4) At least one representative publication to the field of study

Candidate materials will be reviewed until the position is filled.

Dr. Federico A. Sï¿½nchez Quinto Investigador Titular "A" Laboratorio de Paleogenï¿½mica y Biologï¿½a Evolutiva Laboratorio Internacional de Investigaciï¿½n sobre el Genoma Humano LIIGH-UNAM Blvd. Juriquilla 3001, Campus UNAM, 76230, Juriquilla, Qro. Mï¿½xico Tel. +52 (442) 238 1000. Ext 34458

federicosq@gmail.com

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

LousiannaStateU MuseumCuratorAssist

Post-doctoral position at the LSU Museum of Natural Science

Job Description:

Candidate will conduct research in coordination with one or more of the Curators at the LSUMNS. The candidate will also be responsible for helping with the laboratory mentoring of graduate and undergraduate research assistants and management of the Museum molecular genetics core facility. Ongoing projects in the lab include systematics and population genetics studies of birds, fish, mammals, reptiles and amphibians.

Job Responsibilities: (75%) Conduct research on a semi-independent basis. Prepare and publish scientific manuscripts under the direction of a curator. Attend, contribute, and where necessary lead relevant meetings. Plan and develop research methods and techniques within the framework of the research program, such as phylogenomics, transcriptomics, comparative and population genomics, target capture, and other high-throughput sequencing methods. Bring new expertise to the research program. Undertake any other duties relevant to the program of research, including field work. Collaborate with research colleagues and support staff internally and develop appropriate external contacts relevant to the project and future funding opportunities. Be an active member of LSUMNS's vibrant academic community by attending seminars, participating in journal clubs, etc.

(25%) Responsible for helping with the laboratory, mentoring, and training of graduate and undergraduate research assistants, and management of the LSUMNS's shared molecular genetics facility. Ongoing projects in the lab include systematics and population genetic studies of birds, mammals, reptiles and amphibians, and fish. Monitor laboratory cleanliness and safety. Order general lab supplies for the department. Establish and enforce lab rules and regulations, and orient new staff/students at beginning of each semester.

Attend regular meetings with the research team and investigators as required.

Required Qualifications:Ph.D. in Biology or related discipline; Expertise in evolutionary biology and computational biology; experience with next-generation molecular methods, such as whole-genome sequencing, target capture, and other genomic tools; strong publication record; ability to manage an active laboratory; and a record of and interest in continuing mentorship and outreach.

Apply at: https://lsu.wd1.myworkdayjobs.com/-LSU/job/0119-MJ-Foster-Hall/Postdoctoral-Researcher_R00111141 We will begin reviewing applications on 15 February.

If you have questions, please contact Jake Esselstyn at esselstyn@lsu.edu

Jake Esselstyn Museum of Natural Science Louisiana State University 119 Foster Hall, Baton Rouge, LA 70803 office 225-578-3083 | fax 225-578-3075 esselstyn@lsu.edu| lsu.edu|

https://esselstyn.github.io Jacob A Esselstyn <esselstyn@lsu.edu>

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

MississippiStateU Phylogenomics

Postdoctoral Research Associate in Phylogenomics

https://explore.msujobs.msstate.edu/cw/en-us/job/-510010 The Brown Lab at Mississippi State University invites applications for a Postdoctoral Research Associate in Phylogenomics. This position will support PhyloFisher v2: Advancing Accuracy and Reproducibility in Deep Phylogenomics, a project funded by the Gordon and Betty Moore Foundation.

The successful candidate will contribute to research at the interface of evolutionary genomics, high-performance computing, and software/database development for large-scale phylogenomic workflows. The position emphasizes reproducible phylogenomic inference across deep evolutionary timescales and diverse lineages.

Qualifications.

Applicants should have experience with next-generation sequencing data analysis and strong written and oral communication skills. Expertise in phylogenomics and proficiency in Python and/or R are strongly preferred. Familiarity with both eukaryotic and prokaryotic phylogenies is desirable.

Research Environment.

The Brown Lab studies the evolution, diversity, and genomic foundations of microbial eukaryotes (protists), with broader interests in deep eukaryotic evolution and comparative genomics. The lab provides a collaborative, interdisciplinary environment with strong support for computational research.

Appointment Details.

- Start date: Available immediately

- Duration: Renewable annually for up to three years, contingent on performance and project funding

Application Process.

Review of applications will begin immediately and will continue until the position is filled. Interested applicants should apply on the application website, but informal inquiries direct to me are encouraged (matthew.brown@msstate.edu):

1. A cover letter describing research interests and qualifications

2. A current curriculum vitae (CV)

3. Contact information for three professional references

Questions and informal inquiries are welcome.

Matthew W. Brown, Ph.D.

Dr. Donald L. Hall Professor of Biology

Department of Biological Sciences

Mississippi State University

matthew.brown@msstate.edu

https://amoeba.msstate.edu "Brown, Matthew" <matthew.brown@msstate.edu>

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

Montpellier EcoEvolutionaryModelling

Postdoctoral position in eco-evolutionary modeling

PHIM, Montpellier, France, Characterizing and modeling epidemics (CAMEPI) group

_Project description _

Climate change is likely to affect how species interact, in turn impacting their ecology and evolution. In particular, the epidemiology of vector-borne diseases depends on the ecology, evolution and reciprocal interactions between the pathogen, the host and the vectors. Understanding how climate change would impact the epidemiology of vector-borne diseases is an active field of research. The position is part of the FORSHARK project funded by the French National Research Agency (ANR, young researcher JCJC grant) to investigate how climate change would affect the epidemiology of the sharka disease, induced by an aphid-transmitted virus infecting cultivated trees of the genus Prunus.Specifically, the project aims at modeling the ecology and evolution of an aphid (vector) life history in relation to the climate-change driven phenological change of its overwintering host tree species. Ultimately, this modeling will be integrated to epidemiological models.

Activities

- Design of eco-evolutionary models of aphid and tree life histories

- Mathematical and theoretical analyses of model dynamics and equilibria

- Numerical analyses

- Writing of scientific articles, participating in international conferences

- Collaborative working with other members of the CAMEPI group and of the local community (Luis-Miguel Chevin, Ophï¿½lie Ronce)

Skills

- Strong motivation and autonomy

- Collaborative mindset

- Written, verbal, and interpersonal skills, a strong work ethic

- Taste for theory, literature survey and data-oriented modeling. Experience in eco-evolutionary modeling using quantitative genetics and/or adaptive dynamics models.

- Programming (R, Mathematica)

- Mathematical analyses

Conditions

- Qualification: PhD degree or equivalent.

- Starting date: June, 2026

- Duration: 24 months, full time

- Working place: PHIM research unit, Baillarguet Campus, Montferrier-sur-Lez (Montpellier area)

- Supervision: Olivier Cotto

- Salary: about 3100 euros (gross); may vary according to the INRAE salary grid (< https://jobs.inrae.fr/-actualites/remuneration-agents-contractuels >)

To apply

Please submit your CV and a motivation letter, detailing your previous research

experience and professional goals, and contact information for 2 referees, to:

olivier.cotto@inrae.fr

Olivier COTTO INRAE, UMR PHIM Researcher +33 4 67 61 75 38

Olivier Cotto <olivier.cotto@inrae.fr>

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

NewYorkU BiologyComparativeBiology

Postdoctoral Associate (Church Evolution Lab) New York University (NYU), New York, NY Department of Biology

Deadline: Rolling consideration beginning on Feb 1, 2026 and continuing through August 31, 2026

Description The Church Evolution Laboratory (CEL) at NYU Biology is looking for a highly motivated and independent individual to work as a Postdoctoral Associate. Projects in the CEL group include comparative phylogenomic analysis of invertebrates, including Hawaiian insects. The objective of this research is to investigate the genomic basis for biodiversity through large-scale sequencing (e.g., genomic, transcriptomic, proximity ligation), genome assembly, and phylogenetic comparison. Planned projects include a combination of field, bench, and computational work; applicants with experience in any of these areas are invited to apply.

This position is for a post-PhD trainee preparing for a research scientist career path. The planned position will provide a transition to career independence through the development of professional skills; supervision by senior scientist incorporating individual development plan in support of training goals and those of faculty mentor; and publication of research findings/scholarship during postdoc appointment period.

In compliance with NYC's Pay Transparency Act, the annual base salary range for this position is $62,500. New York University considers factors such as (but not limited to) the specific grant funding and the terms of the research grant when extending an offer.

Qualifications The ideal candidate will hold a PhD, have prior research experience in any area of field, molecular, and computational biology, and a track record of peer-reviewed publications. Areas of interest include Hi-C sequencing and genome scaffolding; phylogenetic analyses of biogeography; and population genomic analysis.

Application Instructions

Apply here: https://apply.interfolio.com/179354 Please upload your application materials via Interfolio. Include the following items: 1) CV including a list of publications; 2) a short summary (1pg) of your present and future research interests; 3) a list of three references and their contact information.

Samuel Church <samuel.church@nyu.edu>

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

NewYorkU BiologyEvolutionaryGenomics

Postdoctoral Associate (Rocha Lab) New York University (NYU), New York, NY Department of Biology and Genomics

Deadline: Feb 26, 2026 at 11:59 PM Eastern Time

Description: The Rocha lab at NYU Biology is looking for a highly motivated and independent individual to work as a Postdoctoral Associate.

This position is for a post-PhD trainee preparing for a research scientist career path. The planned position will provide a transition to career independence through the development of professional skills; supervision by senior scientist incorporating individual development plan in support of training goals and those of faculty mentor; and publication of research findings/scholarship during postdoc appointment period.

Projects in the Rocha lab address the evolutionary history of populations and species of mammals inhabiting extreme terrestrial biomes. Planned projects combine state-of-the art sequencing methods to generate chromosome-level haplotype-resolved genomes and resequencing methods to address the role of full spectrum genetic variation in speciation and adaptation in natural populations.

In compliance with NYC's Pay Transparency Act, the annual base salary range for this position is $62,500-$65,664. New York University considers factors such as (but not limited to) the specific grant funding and the terms of the research grant when extending an offer.

Qualifications: The ideal candidate will hold a PhD (or equivalent international degree) or be enrolled in a PhD program and about to obtain the degree by the start date, with a track record of peer-reviewed publications.

Required qualifications:

- PhD in the fields of Biology, Evolutionary Genetics, Evolutionary Ecology, Computational Biology, Veterinary Sciences or related field(s), and no more than two years of postgraduate experience. - Experience in bioinformatics, molecular ecology, computational approaches to study genetic diversity and evolution, or related topics. - Willingness to train and mentor students in the lab, develop and share pipelines and workflows for reproducible data analysis, and apply for external research funding.

Candidates with experience in any of these are strongly encouraged to apply:

- Experience analyzing complex structural variation from long-read and short-read sequencing. - Experience analyzing and integrating large-scale genomic with environmental, ecological and historical datasets. - Experience in workflow development and working with high-performance computing systems and code sharing.

Candidates with experience in any of these are also encouraged to apply:

- Wet-lab skills for evolutionary research (DNA/RNA extraction, Library Preparation, Mammalian cell culture). - Field-work skills (monitoring, capture-release, collar tracking, camera trapping).

Application Instructions: Please upload your application materials via Interfolio at the link below. Include the following items: 1) CV including a list of publications; 2) a short summary of your present and future research interests (this can be in the form of a cover letter); 3) a list of three references and their contact information.

Apply here: https://apply.interfolio.com/180051 NYU is an Equal Opportunity Employer and is committed to a policy of equal treatment and opportunity in every aspect of its recruitment and hiring process.

Joana Rocha <jr7362@nyu.edu>

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

Oldenburg CoralPopulationGenomics DeadlineFeb22

Postdoc in coral population genomics and conservation genetics (x/d/f/m)

Background The Marine Conservation group of Dr. Iliana Baums (www.baumslab.org), Helmholtz Institute for Functional Marine Biodiversity (HIFMB), seeks a postdoc to study population genomics and conservation genetics of reef-building corals in the Caribbean. HIFMB < https://hifmb.de/ > is a cooperation between the University of Oldenburg < https://uol.de/ > (UOL) and the Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research (AWI) and has strong ties to regional institutions, including the Max Planck Institute for Marine Microbiology (Bremen), MARUM (University of Bremen), and the Leibniz Centre for Tropical Marine Research (Bremen). HIFMB is located in Oldenburg, Northern Germany, a hub for environmental and marine research. The institute brings together experts from 18 countries and provides state-of-the-art wet-lab and computational facilities.

Your Tasks

* Generate and analyze genomic data for reef-building corals, including eukaryotic genome assembly and annotation, population genomics, quantitative genetics, epigenetics, and gene expression analyses * Use population genomic approaches to estimate population structure, history and introgression * Use quantitative genetic approaches to estimate responses to selection model alternative conservation genetic strategies such as assisted gene flow and selective breeding * Extract and sequence coral DNA and RNA * Plan, execute, interpret, document, and troubleshoot independent research * Collaborate effectively with computational and experimental team members * Mentor junior lab members * Contribute to manuscripts, grant proposals and reports, and communicate results to peers and the public through presentations, writing, and digital media * Engage in professional development and acquire new skills as needed * Conduct work in both laboratory and field settings

Your Profile

* PhD in marine biology, bioinformatics, genetics, molecular ecology, or a related field * Strong background in population genetic theory * Proficiency in at least one programming language (e.g., Python) and in R * Willingness and ability to work in both lab and field environments * Very good English knowledge (approximately equivalent to CEFR < https://europass.europa.eu/en/common-european-framework-reference-language-skills > level C1)

Preferred Qualifications and Skills

* Experience with system administration * Experience making code and data openly available via repositories/databases (e.g., GitHub, NCBI)

Further Information

* Contact in day-to-day work: collaboration mainly with more than 5 people * Communication: almost equal share (internal/external) in the following ways

1. By telephone: occasionally (several times a month) 2. E-mail: frequently (daily or several times a week) 3. Video conferencing (e. g. Webex): frequently (daily or several times a week) 4. Personal contact in presence: frequently (daily or several times a week)

* Movement around the workplace: regularly over longer distances (e.g. other buildings) * Business trips: occasional (several times a year) * Expeditions: occur

Please note that the general conditions listed serve as a guide and may vary depending on the specific area of application.

For further information on the specific position, please reach out to Prof Dr Iliana Baums (iliana.baums@hifmb.de; +49 (471)4831-2536). If you have any general questions about the application process, our Recruiting team will be glad to support you - please contact Sarah Palme (bewerbungsmanagement@awi.de; +49(471)4831-1853) In this overview < https://www.awi.de/en/work-study/-awi-as-an-employer/equal-opportunities/translate-to-english-diversitaet-und-antidiskriminierung/translate-to-english-diversitaet-konkrete-unterstuetzung-des-awi-1.html > you will find further contact persons for various matters.

This is a full-time position, limited to January 31st, 2029. It is also suitable for part-time employment. The salary will be paid in accordance with the Collective Agreement for the Public Service of the Federation (Tarifvertrag des ï¿½ffentlichen Dienstes, TVï¿½D Bund), up to salary level 13. The place of employment will be Oldenburg.

— / —

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

Paris HumanEvolutionaryGenomics

Postdoctoral position in human evolutionary genomics / paleogenomics / statistical genetics (Paris, France)

We invite applications for a *33-month postdoctoral position* in human evolutionary genomics, paleogenomics and statistical genetics, funded by the Foundation for Medical Research until January 2029. The position will start *1 May 2026* (flexible).

The postdoc will investigate the *evolutionary history and selection of genetic variants associated with complex human diseases*, integrating *ancient genomes*, *GWAS summary statistics*, and *genealogical approaches*, including *ancestral recombination graphs (ARGs)*.

Research activities

- Evaluate, apply, and extend methods for reconstructing genealogies and ARGs using modern and ancient genomes - Analyze GWAS data to study disease-associated variants in an evolutionary framework - Develop analytical models and simulations to characterize selective regimes, including polygenic selection - Contribute actively to manuscript preparation and conference presentations

Required profile

- PhD (obtained or near completion) in evolutionary genomics, statistical genetics, bioinformatics, or a related field - Strong background in population/statistical genetics and large-scale genomic data analysis - Experience with computational genomics and scientific programming - Excellent written and spoken English - At least one first-author publication (published or in press) - Ability to work independently and collaboratively in an international research environment

Environment The position is based at the *Jacques Monod Institute (IJM)**, located in the heart of Paris, in a dynamic, international research environment with computing infrastructure adapted for large-scale genomic analyses. The postdoctoral researcher will be supervised by Dr. Stéphane Peyrégne, head of the paleogenomics team at the IJM. This recently created team studies ancient genomes to better understand human evolution and its **relevance** for biology and health.*

Remuneration and benefits Salary starts from approximately * euro **2**,**500 per **month* after taxation, depending on experience, according to French public research scales. Health insurance costs for the candidate and their family are included in the taxation (https://www.cleiss.fr/docs/regimes/regime_france/an_1.html). Foreign nationalities can benefit from government support for housing and children's education depending on their income. French school fees are free or low.

Applications Informal inquiries are welcome and can be addressed to Stéphane Peyrégne (stephanepeyregne@gmail.com). Full applications should be submitted via the CNRS portal: https://emploi.cnrs.fr/Offres/CDD/UMR7592-ZOUZAD-010/Default.aspx?lang=EN Applicants will first register and upload a CV, then submit a brief statement of research interests. Please include contact information for 2-3 referees. Review of applications will begin immediately and continue until the position is filled.

Stéphane Peyrégne <stephane.peyregne@gmail.com>

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

Paris SquirrelGenomics

Postdoc Position in Evolutionary Genomics

The Institut Pasteur and Muséum national d'Histoire naturelle (Paris, France) seek for an evolutionary biologist with strong skills in genome assembly, genome annotation, and comparative analysis of mammal genomes.

Research project: We are looking for a post-doctoral candidate to assemble and annotate high-quality genomes from rope squirrel species identified as the most likely reservoir hosts of the monkeypox virus (Curaudeau et al., 2023; 2025). The selected candidate will assemble PacBio HiFi and Illumina reads to publish the first genome assembly of Funisciurus anerythrus and Funisciurus leucostigma (Mammalia, Sciuridae). Genome completeness will be assessed using BUSCO. The candidate will perform a comparative analysis with other mammalian genomes to detect potential signatures of selection in immune genes. The position is funded by the ANRS MIE (Project ECTZ321229) for two years and will be based at the Institut Pasteur and Muséum national d'Histoire naturelle (Paris, France).

Salary: 40 300 euro brut/year or 44 300 euro brut/year, depending on the year after the PhD.

Closing date: Open until filled. The position is available as soon as possible. Candidates should indicate in their cover letter the date they would be available to start the position.

Required qualifications: - A PhD in evolutionary genomics; - Strong skills in genome assembly and annotation methods, comparative analysis tools and theoretical aspects of molecular evolution; - Good publication record including several first-author publications; - Excellent written and verbal communication skills in English; - Ability to work independently and to lead a research project.

Application: Please send all application files, including a cover letter, CV, copies of relevant published papers and preprints, and two letters of recommendation to Antoine Gessain (antoine.gessain@pasteur.fr) and Alexandre Hassanin (alexandre.hassanin@mnhn.fr).

References: - Curaudeau M., Kerbis Peterhans J., Le Flanchec T., Gilissen E., Granjon L., Barale L., Gessain A., Hassanin A. (2025). Squirrel reservoirs of monkeypox virus are sister species separated by the Sanaga River (Cameroon), as are the two main viral clades. One health 21: 101157. doi: 10.1016/j.onehlt.2025.101157 - Curaudeau M., Besombes C., Nakouné E., Fontanet A., Gessain A., Hassanin A. (2023). Identifying the most probable mammal reservoir hosts for Monkeypox virus based on ecological niche comparisons. Viruses 15: 727. doi: 10.3390/v15030727 - Gessain A., Nakoune E., Yazdanpanah Y. (2022) Monkeypox. N Engl J Med. 387(19): 1783-1793. doi: 10.1056/NEJMra2208860.

Alexandre Hassanin <alexandre.hassanin@mnhn.fr>

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

StockholmU EvoEcoGenomics

Postdoctoral position in Evolutionary Ecology/Genomics

A two year, full time postdoctoral stipend position is available in Prof. Rhonda Snook's research group at the Department of Zoology, Stockholm University.

The Snook lab studies the evolution of reproductive strategies, with emphasis on sexual selection, local adaptation, speciation and the genomics of adaptation, using Drosophila species as model systems. Recent work from the lab has addressed how increasing temperature may impact reproductive strategies, including generating sex-specific effects on fertility, fecundity, mating behaviour and survival and identifying associated genes. There is scope in this project to shape the research, but in the first instance we will take advantage of multiple Drosophila species to experimentally examine how the abiotic environment impacts reproductive physiology, morphology and behaviour and their ecological, evolutionary and genomic consequences. Genetic manipulation can be a focus for more detailed studies, after primary data collection. The role is ideally suited to candidates interested in integrative approaches addressing how environmental variation impacts reproductive strategies. Importantly, this can range from molecular evolution studies (e.g. investment in cells, interactions across tissues) to populations (evolutionary) or to species interactions (evolutionary ecology), and the underlying genetic architecture of these responses. The direction will depend on candidate background and interest.

Thus, the successful candidate will have a PhD in either evolutionary biology, genetics, physiology, or a related discipline, and experience in experimental biological research. Experience with Drosophila is necessary, and familiarity with Drosophila core genetic, molecular or cellular techniques is highly desirable. Demonstrated competence in quantitative data analysis is required. This position offers a supportive environment for early-career development, including opportunities to publish and present at international conferences, and the ability to apply for independent funds. The postdoctoral researcher will work closely with the PI, and contribute to shaping the research, and will interact with other members of the Snook lab (currently, 2 postdoctoral researchers, one PhD student, and two research assistants). The Zoology department provides an excellent, international, and supportive research environment for early career researchers that also focuses on social opportunities, with regular game nights, a Friday pub, etc.

Eligibility: The scholarship is for one year with opportunity for prolongation for an additional year. The take home salary is 30,000 SEK/month (not subject to Swedish income tax), paid out directly to the postdoc. Only PhD candidates that obtained their PhD within 6 years of the application deadline and who have not been employed at Stockholm University previously are eligible to apply.

Application: A single application in pdf form should include: i) a succinct description of research interests and experience. ii) why you are the ideal candidate for this position in the lab, including ideal start date (max 1 page); iii) a CV including a list of publications, briefly detailing your contribution to these publications (max 1 page), and iv) the name and contact information of two professional references. Email this single pdf form to Rhonda Snook: rhonda.snook@zoologi.su.se

Start date: as soon as possible, but there is flexibility in the date for the best candidate.

Deadline to apply: applications will be reviewed on a rolling basis with a final deadline of February 27th 2026.

Contact person: Rhonda Snook – rhonda.snook@zoologi.su.se

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

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

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

StockholmU MalagasyPlantPhylogenomics

Dear colleagues,

Please share this postdoc position I'm offering at Stockholm University with your networks - phylogenomics and evolution of fire adaptations in Malagasy Erica : https://www.su.se/english/divisions/department-of-ecology-environment-and-plant-sciences/news/-articles/2025-12-18-2-year-postdoc-in-phylogenomics-and-evolution-of-fire-adaptations-in-malagasy–erica It's a 2-year postdoc stipend funded by the Swedish Carl Trygger foundation. Candidates should have obtained their PhD no more than 6 years ago (except special circumstances); they also can't currently be employed here at the department and should have a PhD from another institution. I'm looking for someone with skills in phylogenomics and DNA library prep. Interest and experience in doing fieldwork in Madagascar are beneficial but not required!

Deadline 30 January.

Best, Jan

< https://www.su.se/english/profiles/jaha4643 >

–

Jan Hackel

Associate Professor/Universitetslektor

Evolutionary and Systematic Botany

Department of Ecology, Environment and Plant Sciences (DEEP)

Stockholm University

Svante Arrhenius väg 20A - 106 91 Stockholm, Sweden

https://www.su.se/english/profiles/jaha4643 Jan Hackel <jan.hackel@su.se>

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

StockholmU ParasitePopulationGenetics

A postdoctoral position is available with Jessica Stephenson (https://stephensonlab.com/) in the Department of Zoology, Stockholm University, Stockholm, Sweden. We work to understand the interactions between host behaviour and parasitism across scales. In this project, the successful candidate will address how host behaviour may structure parasite population genetics and thus affect parasite evolutionary potential.

The postdoc will use existing data on directly transmitted gyrodactylid parasites, guppies, and localities in northern Trinidad to test how river structure, host community composition, parasite host spectrum, and host social behavior interact to shape the structure and evolutionary potential of parasite populations. Other existing datasets may enable further studies, for example of the fish or environmental microbiome, and how population genomic structure influences the virulence phenotype of the parasite.

The postdoc will work in close collaboration with Mary Janecka at the Carnegie Museum of Natural History and with research groups at the Department of Zoology with strong expertise in population genetics and evolutionary genomics.

**Job duties

Postdoctoral positions are primarily research-oriented. The postdoctoral fellow will work on the analysis of existing SNP (single nucleotide polymorphism) data from two parasite species from multiple locations in Trinidad. Questions that these data can be used to answer include:

- How does the parasite's host spectrum (generalist vs. specialist) affect how parasite populations are structured across different host communities? - How does the complexity of the river network affect the structure of parasite populations? - How does host behavior affect the structure of parasite populations?

In addition to these core questions, there are several additional research directions that the postdoctoral fellow can develop depending on interest and expertise.

**Eligibility requirements

To be eligible for employment as a postdoctoral researcher, a doctoral degree or a foreign degree that is deemed equivalent to the relevant doctoral degree is required. The degree must be completed no later than when the employment decision is made.

**Assessment criteria

It is considered meritorious if the doctoral degree or equivalent has been completed no more than three years before the application deadline. If there are special reasons, a previously completed degree may also be considered meritorious. Special reasons refer to leave due to illness, parental leave, positions of trust in trade unions, service in the total defense, or other similar circumstances, as well as clinical service or service/assignment relevant to the subject area.

In the appointment, special emphasis will be placed on scientific expertise. Ideal candidates have experience working with challenging genomic data, such as data from parasites, other very small organisms or faecal samples. Experience using such data to understand population dynamics, species interactions and/or complex reproductive strategies (e.g. clonal reproduction) is highly desirable. We are also looking for someone with the ability to synthesize ideas and data across different fields, including landscape and riverine genomics, and a strong publication record that demonstrates these skills. Very good written and oral communication skills are required.

**About the employment

The position is full-time and is valid until further notice, however, for a minimum of two years and a maximum of three years, with the possibility of extension if there are special reasons. Entry into force in spring/summer 2026 or by agreement.

**We offer

With us you get the dynamic interaction between higher education and research that makes Stockholm University an exciting and creative environment. You work in an international environment and receive favorable conditions. The university is located in the National City Park with good connections to the city.

Stockholm University strives to be a workplace that is free from discrimination and provides equal rights and opportunities for everyone.

**Contact

Information about the position is provided by Jessica Stephenson, jess.stephenson@zoologi.su.se.

**Application

You apply for the position via Stockholm University's recruitment system. Attach a cover letter and CV as well as the attachments requested in the application form. As the applicant, you are responsible for ensuring that the application is complete and that it reaches the university by the application deadline.

Instructions for applicants can be found on the website: https://www.su.se/om-universitetet/jobba-pasu/att-soka-en-anstallning .Stockholm University contributes to the development of a sustainable democratic society through knowledge, enlightenment and the search

— / —

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

---

UCalifornia Berkeley HawaiianArthropodDiversity

Postdoctoral Position: Hawaiian arthropod diversity and community metabarcoding, UC Berkeley

We are seeking a postdoctoral scholar to conduct research for NSF- and DoD-funded projects that aim to link signatures of arthropod diversity obtained from DNA metabarcoding, across the Hawaiian Islands with broad scale remote sensing. The postdoc will focus on high-throughput arthropod biodiversity sequencing across two orthogonal gradients set within the same native forest type - the first gradient is a geological chronosequence, from 0-5 million years; the second, intersecting, gradient is a landscape matrix from native to heavily invaded forest habitats on each island. Whole arthropod communities are sampled using genetic signatures from the high-throughput sequencing to test models of community assembly over extended ecological-to-evolutionary time; the models will predict trajectories of assembly and disassembly in the face of rapid biotic change. The lab's study the ecology and evolution of Hawaiian arthropods in the context of the assembly of communities through evolutionary time, and the impact of non-native species. Recent work involves collaboration with researchers working with vegetation monitoring, and geospatial and remote sensing data.

The person will be based in the joint laboratory of Professors Rosemary Gillespie and George Roderick (see https://sites.google.com/berkeley.edu/evolab).

Funding is available for two years, beginning as soon as possible. Please send inquiries and applications to Rosemary Gillespie at gillespie@berkeley.edu or George Roderick <roderick@berkeley.edu> Applications (link https://aprecruit.berkeley.edu/JPF05219) should include a cover letter describing your research interests, a CV, and names of three references.

Rosemary G Gillespie <gillespie@berkeley.edu>

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

UCalifornia Davis EvoDevo

Artyom Kopp's lab in the Department of Evolution and Ecology, University of California - Davis, USA is looking for a new —postdoc.Projects will focus on using single-cell sequencing to study the evolution of cell types and developmental pathways, with a particular emphasis on evolutionary innovations.

Our lab studies evolutionary novelties, sexual dimorphism, and the evolution of genetic regulatory circuits in /Drosophila/. We use a wide range of approaches including developmental biology, comparative genomics, phylogenetics, and quantitative/population genetics. Over time, postdocs will be encouraged to develop new research directions reflecting their own interests, within the broad field of developmental and evolutionary genetics.

Candidates should have demonstrated expertise in genomics, developmental biology, or evolutionary genetics.Previous experience in the analysis of single-cell and other complex genomic datasets is especially welcome. The Department of Evolution and Ecology provides a friendly and supportive atmosphere and many opportunities for collaboration. If interested, please contact Artyom Kopp (akopp@ucdavis.edu) with a CV, a statement of research interests and experience, and the names of three references.

akopp@ucdavis.edu

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

UCalifornia LosAngeles PopulationGenetics

UCLA.PopulationGenetics

Postdoctoral research position at UCLA in population genetics

The Garud Lab at UCLA is recruiting a postdoctoral researcher in population genetics to join our group in the Department of Ecology and Evolutionary Biology at the University of California, Los Angeles (https://garud.eeb.ucla.edu). Our group studies evolutionary dynamics in natural populations, with a particular emphasis on the human gut microbiome. A major goal is to understand how evolutionary processes interact with ecological processes across short and long timescales. We also analyze human, ancient human, and Drosophila genomic data to infer the tempo and mode of selection using computational and statistical approaches.

The successful candidate will have substantial input in the specific nature of their research project. However, the project should broadly fit within the lab's goals of learning about evolution in natural populations. There are a wide range of projects to choose from, including developing fundamental population genetic theory, development of novel statistics, as well as application of theory to data.

Candidates should have a Ph.D. in biology, genetics, computer science, bioinformatics, statistics, computational biology, or a related field. A background in population genetics/evolutionary genomics is preferred. As this is a computational position, proficiency in programming in R, Perl, or Python, and shell scripting is essential. Preference will be given to candidates with a strong publication record, evidence of substantial research productivity, and ability to successfully communicate scientific information.

More broadly, UCLA is a vibrant hub for population genomic analyses. Our lab regularly interacts with population genetics research groups lead by Kirk Lohmueller, Amy Goldberg, Nancy Chen, Benjamin Peter, as well as several groups in the EEB, Human Genetics, and Computational Medicine departments, as well as microbiome groups led by Elaine Hsaio and Jonathan Jacobs and the broader Goodman-Luskin Microbiome Center. Your ideas and enthusiasm for collaboration at the intersection of labs are welcome.

Interested candidates should send to Nandita Garud at ngarud@ucla.edu the following:

- A letter describing your background and motivations pursuing a postdoc in the Garud Lab - CV that includes a brief 1-2 sentence description of your contribution to past research projects. - Contact information for two referees who can provide references upon request

The position is available for a guaranteed minimum of two years, with potential for renewal. The University of California is an equal opportunity/affirmative action employer.

Nandita Garud, PhD Associate Professor Department of Ecology and Evolutionary Biology Department ofHuman Genetics, DavidGeffen School of Medicine University of California, Los Angeles 621 Charles E. Young Drive South Los Angeles, CA 90095-1606

Lab website:https://garud.eeb.ucla.edu Nandita Garud <ngarud@g.ucla.edu>

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

UCollege London ComputationalPhylogenetics

Research Fellow in computational phylogenomics in University College London Ref: B02-10021 Hours: Full Time Salary: Grade 7 per annum including London Allowance Closing Date: 9 February 2026

Dear Colleagues,

Application deadline: 9 February 2026

A postdoctoral Research Fellow position in available in the team of Professor Ziheng Yang FRS and Dr Asif Tamuri in UCL to work in the areas of computational phylogenomics and molecular evolution. The successful candidate will become a member of a multidisciplinary research team at the interface of evolutionary genomics, bioinformatics, computer science, and computational statistics.

We are particularly interested in two types of candidates: method developers and/or data analysts. Method developers will implement high-performance computing algorithms to accelerate phylogenetic likelihood calculations in the PAML package and develop new models and methods for genome-scale phylogenetic analysis. Candidates should be proficient in C/C++ and scientific computing, with an interest in applying computational and statistical approaches to evolutionary genetics and genomics; experience in statistical inference or phylogenetics is an advantage. Data analysts candidates will be bioinformaticians or evolutionary biologists with strong computational skills, experience with modern phylogenetic software, and an interest in analyzing genomic-scale phylogenetic data.

The post is funded by the BBSRC with a funding end date of 14 June 2027. Starting date will be on 1 April 2026 or as soon as possible afterwards. Salary will be commensurate with experience on UCL grade 7 (ï¿½45,103 to ï¿½52,586 pa including London allowance).

If you need reasonable adjustments or a more accessible format to apply for this job online or have any queries about the application process, please contact the HR Administrator (fls.hr@ucl.ac.uk) stating the advert reference number in the subject line.

If you have any queries about the role, please contact Professor Ziheng Yang FRS (z.yang@ucl.ac.uk) or Dr Asif Tamuri (a.tamuri@ucl.ac.uk).

Further particulars including a job description and person specification can be accessed at the link below. Please ensure you read these carefully before applying for the post. To apply, please follow the link https://www.ucl.ac.uk/work-at-ucl/-search-ucl-jobs/details?jobId=41139&jobTitle=-Research+Fellow+in+computational+phylogenomics Ziheng Yang <z.yang@ucl.ac.uk>

“Yang, Ziheng” <z.yang@ucl.ac.uk>

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

UGrenobleAlpes ClimateAdaptation

1.5-year Postdoc in ecological genomics:Mediation analysis for investigating gene ˜ environment interactions and climate-driven maladaptation.

** Project: Climate change is having a major impact on biodiversity, posing a significant threat to the health and persistence of natural populations. High-resolution climate models, combined with high-throughput DNA sequencing, provide powerful tools to assess the capacity of populations to respond to environmental change. In this context, genotype-environment association (GEA) methods are commonly used to identify loci associated with local adaptation. More recently, data on adaptive genetic variation have been incorporated into predictive statistical models aimed at estimating the mismatch between populations and future climates, a concept known as genomic offset. This project proposes to adapt the mediation analysis framework, a method widely used in fields such as epidemiology and social sciences, to ecological genomics. The postdoctoral researcher will develop and implement a statistical framework to 1) identify the genetic basis of local adaptation to climate and 2) estimate population maladaptation to climate change. Both simulated and empirical data will be used to evaluate the potential of this approach in predictive ecological genomics.

** Activities:

During this project, the postdoc will be expected to: * Develop a mediation analysis model integrating phenotypes, genotypes, and environmental variables to detect signals of local adaptation. * Conduct simulation studies to assess the strengths and limitations of the model. * Apply the model to real-world datasets. * Evaluate the potential of this approach for predicting population maladaptation under future climates.

** Skills: We are looking for a motivated early-career researcher with a strong interest in statistical modeling and ecological or evolutionary genomics. Ideal candidates may come from one of two backgrounds: * A biologist with enthusiasm for method development and quantitative modeling, or * A statistician/data scientist with a strong interest in evolutionary biology and genomics.

** Work Context: The position is funded by the junior professor chair of Thibaut Capblancq at UniversiteÌ Grenoble Alpes. The postdoc will be hosted at the Laboratoire d'EÌcologie Alpine (LECA), a dynamic and interdisciplinary research lab located in the heart of the French Alps. The project will be carried out in co-supervision with Olivier FrancÌ, a leading expert in statistical modeling and genotype-environment association (GEA) methods. This collaboration will offer the postdoc excellent opportunities for mentorship, technical development, and exposure to cutting- edge research in ecological genomics.

** Conditions: * Starting date: March 2026 * Duration: 18 months * Location: Grenoble, France * Qualification: PhD in evolutionary biology or mathematical biology * Salary: ~2900 to 3400 euros/month (gross) depending on experience

** To apply: Please submit your CV and a motivation letter, detailing your previous research experience and professional goals, and contact information for 2 referees, on this platform before February 20th: https://academicpositions.com/ad/universite-grenoble-alpes/2026/postdoctoral-researcher-in-population-biology-and-ecology-m-f/243400#apply For more information contactthibaut.capblancq@univ-grenoble-alpes.fr and/or olivier.francois@univ-grenoble-alpes.fr

THIBAUT CAPBLANCQ <thibaut.capblancq@univ-grenoble-alpes.fr>

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

UHelsinki ModellingLifeHistory

Postdoctoral Researcher in Statistical Ecology and Evolution

Project: Statistical modelling the Evolution of Sex-Specific Differences in Life History and Immunity

Supervisors: Dr. Elina Numminen, Faculty of Science, University of Helsinki, and Dr. Piret Avila Faculty of Biological and Environmental Sciences, University of Helsinki

We are looking for a highly motivated postdoctoral researcher to develop statistical models and analyses to combine theoretical ecology predictions and empirical data on the evolution of sex-specific differences in immunity and life history traits.

As we intend to conduct interviews also during the application period, we appreciate receiving your application as soon as possible. However, it is possible to apply until February 28, 2026 (at 23:59 UTC +2). The ideal starting date is from March 2026 onwards, and preferably by September 2026.

The position involves developing and fitting models on natural selection shaping sex-specific immune strategies to the related empirical datasets of various kinds and from various sources. For this, novel statistical approaches for assessing hypotheses, comparing models and combining different types of data are developed.

This position is part of the interdisciplinary consortium at the University of Helsinki, Sex Differences in Immunity, led by Dr. Avila, which brings together researchers across evolutionary biology, immunology, genomics, demography, and statistics to bridge evolutionary and mechanistic explanations of sex differences in immunity.

WHAT WE OFFER

- A fully-funded 3-year position at the Department of Mathematics and Statistics of the University of Helsinki (Kumpula campus)

- An opportunity to conduct research as part of a vibrant interdisciplinary consortium, using statistical models to bridge evolutionary theory with immunology, genomics, and demography

- Collaboration across disciplines, with research visits to leading groups in the field

- Funding for attending international conferences to build your scientific network

- A starting salary of 3800-4000 euros/month depending on the appointees' qualifications and experience

- Access to excellent resources and professional development opportunities

- Occupational health care, flexible working hours, and an opportunity for 6 weeks of paid annual leave

- Support for internationally recruited employees with their transition to work and live in Finland

- Academic community that promotes diversity, international engagement and equality. We encourage all qualified applicants from diverse backgrounds to apply for our positions.

YOUR PROFILE

- PhD in statistics, mathematics, biology, evolutionary anthropology or a related field

- Strong background in statistical and mathematical modelling and in the analysis of real-world datasets

- Experience in interdisciplinarity and good collaboration skills

- Ability to develop and pursue independent research questions

- Fluent English skills

APPLICATION INSTRUCTIONS

Applications shall be submitted through the University of HelsinkiÂs recruitment system and include the following documents:

- A CV, including a list of publications

- An application letter describing your suitability for the position and motivation to apply for it (max. 2 pages)

- Contact information of two person who are willing to provide a reference letter upon request

The application deadline is February 28, 2026 (at 23:59 UTC +2).

ADDITIONAL INFORMATION

- About the position: Dr. Elina Numminen, elina.numminen@helsinki.fi

- Recruitment system: recruitment@helsinki.fi

- Department of Mathematics and Statistics: https://www.helsinki.fi/en/faculty-science/faculty/-mathematics-and-statistics - Kumpula Campus: https://www.helsinki.fi/en/about-us/visit-us/-campuses/kumpula-campus - Why University of Helsinki: https://www.helsinki.fi/en/about-us/-careers/why-university-helsinki - 10 reasons to work in Helsinki: https://www.helsinki.fi/en/about-us/careers/why-university-helsinki/why-helsinki - Why Finland: https://www.helsinki.fi/en/about-us/-careers/why-university-helsinki "Numminen, S Elina" <elina.numminen@helsinki.fi>

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

UHelsinki StatisticalEcolEvolution

Postdoctoral Researcher in Statistical Ecology and Evolution

Project: Statistical modelling the Evolution of Sex-Specific Differences in Life History and Immunity

Supervisors: Dr. Elina Numminen, Faculty of Science, University of Helsinki, and Dr. Piret Avila Faculty of Biological and Environmental Sciences, University of Helsinki

We are looking for a highly motivated postdoctoral researcher to develop statistical models and analyses to combine theoretical ecology predictions and empirical data on the evolution of sex-specific differences in immunity and life history traits.

As we intend to conduct interviews also during the application period, we appreciate receiving your application as soon as possible. However, it is possible to apply until February 28, 2026 (at 23:59 UTC +2). The ideal starting date is from March 2026 onwards, and preferably by September 2026.

The position involves developing and fitting models on natural selection shaping sex-specific immune strategies to the related empirical datasets of various kinds and from various sources. For this, novel statistical approaches for assessing hypotheses, comparing models and combining different types of data are developed.

This position is part of the interdisciplinary consortium at the University of Helsinki, Sex Differences in Immunity, led by Dr. Avila, which brings together researchers across evolutionary biology, immunology, genomics, demography, and statistics to bridge evolutionary and mechanistic explanations of sex differences in immunity.

WHAT WE OFFER

- A fully-funded 3-year position at the Department of Mathematics and Statistics of the University of Helsinki (Kumpula campus)

- An opportunity to conduct research as part of a vibrant interdisciplinary consortium, using statistical models to bridge evolutionary theory with immunology, genomics, and demography

- Collaboration across disciplines, with research visits to leading groups in the field

- Funding for attending international conferences to build your scientific network

- A starting salary of 3800-4000 euros/month depending on the appointees' qualifications and experience

- Access to excellent resources and professional development opportunities

- Occupational health care, flexible working hours, and an opportunity for 6 weeks of paid annual leave

- Support for internationally recruited employees with their transition to work and live in Finland

- Academic community that promotes diversity, international engagement and equality. We encourage all qualified applicants from diverse backgrounds to apply for our positions.

YOUR PROFILE

- PhD in statistics, mathematics, biology, evolutionary anthropology or a related field

- Strong background in statistical and mathematical modelling and in the analysis of real-world datasets

- Experience in interdisciplinarity and good collaboration skills

- Ability to develop and pursue independent research questions

- Fluent English skills

APPLICATION INSTRUCTIONS

Applications shall be submitted through the University of HelsinkiÂs recruitment system and include the following documents:

- A CV, including a list of publications

- An application letter describing your suitability for the position and motivation to apply for it (max. 2 pages)

- Contact information of two person who are willing to provide a reference letter upon request

The application deadline is February 28, 2026 (at 23:59 UTC +2).

ADDITIONAL INFORMATION

- About the position: Dr. Elina Numminen, elina.numminen@helsinki.fi

- Recruitment system: recruitment@helsinki.fi

- Department of Mathematics and Statistics: https://www.helsinki.fi/en/faculty-science/faculty/-mathematics-and-statistics - Kumpula Campus: https://www.helsinki.fi/en/about-us/visit-us/-campuses/kumpula-campus - Why University of Helsinki: https://www.helsinki.fi/en/about-us/careers/-why-university-helsinki - 10 reasons to work in Helsinki: https://www.helsinki.fi/en/about-us/careers/why-university-helsinki/why-helsinki "Numminen, S Elina" <elina.numminen@helsinki.fi>

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

UHelsinki TheoreticalEvolutionaryBiology

A postdoctoral researcher position is available to join a theoretical evolutionary ecology group at the University of Helsinki to work on the evolution of sex-specific differences in immunity and life-history traits.

Position details:

3-year fully funded position Starting salary ˜ euro 3,625/month Ideal start date: February/March 2026 Methods: optimal control theory, life history modelling, adaptive dynamics, population genetics

The position is part of an interdisciplinary consortium on sex differences in immunity, bridging evolutionary theory with immunology, genomics, and demography.

Requirements:

PhD in biology, mathematics, or related field Strong background in mathematical/computational modelling

Apply here: https://www.helsinki.fi/en/about-us/careers/open-positions/postdoctoral-researcher-theoretical-evolutionary-biology Applications accepted until the position is filled.

For questions, contact me at piret.avila@helsinki.fi

Thank you for sharing!

Best wishes,

Piret Avila

Academy Research Fellow

University of Helsinki

"Avila, Piret" <piret.avila@helsinki.fi>

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

UInnsbruck EvolutionaryEcol

Dear EvolDir Community!

JOB OFFER Postdoc Position: Subject line "UInnsbruck.EvolutionaryEcology" Start date: 13th April 2026 / Duration: 3 years

Position: This position provides an opportunity to conduct independent research in aquatic evolutionary ecology, with a focus on defence strategies against multiple enemies such as parasites and predators. The freshwater snail Lymnaea stagnalis will serve as the primary study organism. The project should investigate how organisms respond to simultaneous threats, for example, by examining the fitness consequences of, and trade–offs among, traits involved in defence against different types of enemies.

You will develop the initial project idea and refine it in collaboration with Prof. Seppälä. Collaboration with other research groups within the department and faculty is encouraged. The project is expected to connect broadly to evolutionary and ecological dynamics, and to incorporate innovative approaches from across the biological sciences.

Qualifications:

PhD in Biology Research expertise in evolutionary ecology and/or aquatic ecology Desirable qualifications: Postdoctoral experience; publications in high-ranking international journals; experience supervising students; success in acquiring third-party funding; international research experience Independence, strong teamwork and communication skills, flexibility

Good knowledge of English

For this position, please submit a CV, a motivation letter, and a brief description of your research idea (maximum two pages), including the study question, proposed approach, and potential collaborators.

Location: The Research Department for Limnology is situated on the edge of the Alps in the small town of Mondsee (Upper Austria). The nearby city of Salzburg offers a rich variety of cultural, historical, and recreational opportunities.

Our offer: The minimum gross salary for this position (full-time) amounts to €5.014,00 per month (14 times).

Further information and the legally binding text can be found at www.uibk.ac.at/karriere, Code BIO-15524.

Application: We are looking forward to receiving your online application by 12.02.2026 stating the code BIO-15524.

Please note that travel costs cannot be reimbursed.

For further information about the research, please contact Prof. Otto Seppälä: otto.seppaelae@uibk.ac.at. The subject line should read: Postdoc 2026

Prof. Otto Seppälä

Universität Innsbruck

Forschungsinstitut für Limnologie, Mondsee Sonja Burggraf Institutssekretariat Mondseestraße 9, A-5310 Mondsee Telefon +43 512 507-50201

E-Mail sonja.burggraf@uibk.ac.at, office-ilim@uibk.ac.at

"Burggraf, Sonja" <Sonja.Burggraf@uibk.ac.at>

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

UKansas EvolutionaryGenomicsMammals

Postdoctoral Position in Evolutionary Genomics, The University of Kansas

The Mack lab (ww.katyamack.com) seeks a postdoctoral researcher to work on an NIH-funded project on gene expression evolution in mice. The Mack lab, within the Department of Ecology and Evolutionary Biology at the University of Kansas, is an evolutionary genomics lab focused on questions related to population genetics, adaptation, and speciation. We work in diverse systems, but focus on mice as a model for understanding mammalian evolution.

The postdoctoral researcher will contribute to work in the lab aimed at understanding the genomic basis of complex traits using a combination of wet-lab and bioinformatic approaches (e.g., transcriptomics, population genomics, phenotyping, and genome-editing). The aims of the position will be tailored to the expertise of the successful applicant to complement the lab's broad interest in the genomics of adaptation, gene expression evolution, and the role of gene-by-environment interactions in phenotypic evolution. This position offers a unique opportunity to utilize diverse phenotypic and genomic datasets to understand the role of gene expression evolution in shaping phenotypic evolution within and between species in a premier mammalian model system.

Required qualifications are a PhD in evolutionary biology, genetics, molecular biology, or closely related fields. Candidates must have excellent verbal and written communication skills, as well as an established record of productivity (e.g., at least one previous peer-reviewed publication). Candidates with a past record of publications in population genetics, molecular ecology, or genome biology are strongly preferred. Ideal candidates will have experience in generating and/or analyzing genomic data, performing comparative or population genomic analyses, and molecular wet lab experience.

Contact: Interested individuals should first contact Katya Mack at katya.mack@ku.edu. Please include the following: (1) a cover letter addressing your interest in the position and how your expertise meets the position requirements, (2) a CV, (3) contact information for 3 references, (4) 1 representative publication. Candidate materials will be reviewed until the position is filled.

Katya Mack <katya.mack@gmail.com>

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

UNBC Canada WolfPopulationGenomicsHealth

Postdoctoral Fellow: Population Genomics, University of Northern British Columbia, Canada

We seek a Postdoctoral Fellow to lead a multidisciplinary and highly collaborative research project that leverages existing samples and data collected over the past 15 years to determine how harvest influences wolf diet, body condition, parasites/pathogens, and genomic diversity across the Northwest Territories and Nunavut. The Postdoc's responsibilities include next-generation sequencing (RADseq) of >600 samples to quantify genomic diversity, characterize population structure, and identify putatively adaptive loci. The Postdoc will also analyze existing stable isotope data (d13C and d15N of wolves and prey) to infer wolf diet as well as integrate necropsy and parasitological/pathogenic data to produce a holistic understanding of wolf ecology and health.

Please follow the link below for more for information or contact Jamie.Gorrell@unbc.ca: https://tinyurl.com/-5t56kwx7 Jamie Gorrell <Jamie.Gorrell@unbc.ca>

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

UNebraska Lincoln PopBiol

Population Biology Postdoctoral Research Fellowship School of Biological Sciences University of Nebraska-Lincoln

The University of Nebraska-Lincoln (UNL) School of Biological Sciences is seeking applications for a two-year postdoctoral position in the Population Biology Program of Excellence.

The goal of the Population Biology-POE Postdoctoral Fellowship is to stimulate synergistic interactions between faculty and postdoctoral scholars broadly interested in the area of Population Biology. POE postdoctoral fellows pursue a research program under the sponsorship of an Ecology, Evolution & Behavior (EEB) section in the School of Biological Sciences (https://biosci.unl.edu/research-areas) faculty member and are expected to enhance graduate education, serve as a model for graduate students in career development, and promote interactions among faculty at UNL. While in residence, the postdoctoral fellow is expected to lead a seminar, symposium or outreach project that will appeal to Population Biologists across campus.

EEB faculty at UNL are highly integrative and collaborative, using a wide array of approaches and study systems to study a diverse set of biological questions, from the molecular determinants of adaptation and speciation to multimodal animal communication to the community ecology of extinct mammals to the ecology and evolution of infectious disease.

The expected salary will be $49,000 per year, with an anticipated starting date of September 1, 2026 or later.

Lincoln, Nebraska, is consistently rated as one of the best places to live in America, with a low cost of living, over 130 miles of bike trails throughout the city, and a vibrant restaurant and music scene.

Minimum Required Qualifications We are seeking applicants who have recently completed, or will complete before the start date, their Ph.D. and who conduct cutting edge research related to faculty research areas in the Ecology, Evolution, and Behavior (EEB) section of the School of Biological Sciences (https://biosci.unl.edu/research-areas).

Application Process Review of applications will begin March 1, 2026 and continue until the position is filled. Interested candidates should submit application materials to https://employment.unl.edu/, requisition F_260006. Required documents include a curriculum vitae, a 1-page description of previous or current research, and a 2-3 page description of proposed research. Combine these statements into a single document for upload. In addition, arrange for two (2) recommendation letters from non-UNL faculty and one (1) recommendation letter from the UNL faculty sponsor - a total of three (3) letters - to be emailed to Dr. Colin Meiklejohn at cmeiklejohn2@unl.edu by the review date. The subject line should read “Population Biology Post-doc application reference.” The research proposal should be developed in collaboration with the proposed faculty sponsor. Priority will be given to applicants who are new to UNL. Research descriptions for past and current POE postdoctoral fellows can be viewed at https://biosci.unl.edu/research/population-biology-poe-postdoctoral-fellowships/ . As an EO/AA employer, the University of Nebraska considers qualified applicants for employment without regard to race, color, ethnicity, national origin, sex, pregnancy, sexual orientation, gender identity, religion, disability, age, genetic information, veteran status, marital status, and/or political affiliation. See https://www.cms.unl.edu/equity/notice-nondiscrimination . Colin Meiklejohn <56362071@nebraska.edu>

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

UNorthCarolina Charlotte CnidarianGenomics

Postdoctoral Position: Cnidarian genomics and immunity, UNC Charlotte

We are seeking a postdoctoral scholar to conduct research for a NSF-funded project that aims to link genomic structural diversity to function of the immune system in cnidarians. The postdoc will focus on high-throughput genomic and transcriptomic sequencing across multiple populations of a coastal sea anemone (Nematostella vectensis) and lab assays to measure immune responses at the molecular and organismal levels. This research is part of a larger focus of the Reitzel lab to characterize local adaptation in marine invertebrates and the roles for the microbiome in mediating ecologically-relevant responses.

Qualifications

- PhD in the fields of Biology, Genomics, Bioinformatics, Computational Biology, or related field(s).

- Demonstrated expertise in large sequence data analysis
- Strong computational and statistical skills for handling high-throughput datasets.

- Excellent communication skills evidenced by peer reviewed publications and conference presentations

- Strong collaborations skills

The person will be based in the laboratory of Dr. Adam Reitzel (see https://pages.charlotte.edu/adam-reitzel/) and the CIPHER Center (see https://cipher.charlotte.edu) at the University of North Carolina at Charlotte.

Funding is available for at least two years, beginning as soon as possible. Please send inquiries to Adam Reitzel at areitze2@charlotte.edu. Submit applications to: https://jobs.charlotte.edu/postings/66089. Applications should include a cover letter describing your research interests, a CV, and names of three references.

Adam Reitzel <areitze2@charlotte.edu>

Adam Reitzel <adam.reitzel@charlotte.edu>

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

UNottingham UK AdaptationToCaptivity

Postdoctoral Research Associate on adaptation to captivity conditions Job reference: MED397426 Application deadline: February 26, 2026

A Postdoctoral Research Associate position is available in Dr. Ylenia Chiari's research team in the School of Life Sciences at the University of Nottingham (UK) to work on a funded research project supported by Montana Fish, Wildlife, and Parks (MFWP).

The project aims to investigate the role of epigenetic signatures in adaptation to captivity, with direct conservation applications for aquaculture and conservation, and the potential to advance fundamental understanding of transgenerational epigenetic inheritance. This project is in collaboration with Mr. Matt Boyer (MFWP) and Dr. Gordon Luikart (University of Montana and Flathead Lake Biological Station).

The post holder will be responsible for the day-to-day running of this programme of work as part of Dr Chiari's research team within the Cells, Organisms and Molecular Genetics (COMGen) group (https://www.nottingham.ac.uk/research/groups/cells-organisms-and-molecular-genetics/people/index.aspx).

The role will primarily involve conducting bioinformatic analyses of existing RNA-sequencing and whole-genome DNA methylation datasets from wild and hatchery fish populations. Depending on securing additional funding, there may also be opportunities to carry out fieldwork in Montana (USA).

We are seeking candidates with demonstrable research experience in the analysis of genomic and methylation data. Experience analyzing transcriptomic data and an interest in evolutionary biology and conservation are highly desirable. Experience working with -omic data from polyploid species is welcomed.

Candidates must hold a PhD (or equivalent) in conservation genomics, evolutionary biology, or a closely related discipline.

This is a full-time, fixed-term position available for a duration of 15 months.

The Chiari Lab (www.yleniachiari.it) investigates the causes and consequences of morphological and physiological variation in vertebrates and conducts research in conservation biology. The lab is committed to promoting diversity and fostering a multicultural research environment, and we strongly encourage applications from researchers from underrepresented groups.

Informal enquiries may be directed to Dr Ylenia Chiari at ylenia.chiari@nottingham.ac.uk. Please note that applications sent directly to this email address will not be accepted.

Further details on this position and how to apply can be found here https://jobs.nottingham.ac.uk/-Vacancy.aspx?ref=MED397426 The closing data for applications is February 26, 2026.

The commitment of the School of Life Sciences to Equality and Diversity has been recognised in the awarding of an Athena Swan Gold Award.

Ylenia Chiari, PhD

Associate Professor

My name is pronounced

EE-len-ee-ah Kee-AH-ree

(hear name) < https://namedrop.io/yleniachiari >

E Ylenia.Chiari@nottingham.ac.uk University of Nottingham, School of Life Sciences Life Sciences Building University Park Nottingham UK www.yleniachiari.it ChiariLab - YouTube < https://www.youtube.com/-channel/UCysYzHxkLOsnn4wa-4a26pQ >

“Ylenia Chiari (staff)” <Ylenia.Chiari@nottingham.ac.uk>

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

UTexasSanAntonio EvoDevoGenomics

Post-doctoral position: University of Texas San Antonio in Evolutionary and Developmental Genomics

Description:

The Evolutionary & Developmental Genomics (EDGe) lab (https://www.anti-sense.org) at the University of Texas San Antonio combines experimental and computational approaches to study the evolution of genetic conflicts in the germ line, molecular mechanisms underlying sex chromosome drive, and the developmental processes that are compromised as a result of the activities of selfish genetic elements. We foster an environment of collaboration and mentorship, offering opportunities to develop new skills and pursue independent ideas that align with the lab's mission.

Project Focus:

The successful candidate will investigate the consequences of meiotic drive on male gametogenesis and fertility in Drosophila. The project leverages multiple non-model Drosophila species to uncover the molecular and developmental mechanisms underlying gametic dysfunction, and the consequences of sex chromosome meiotic drive, which leads to impaired segregation of sex chromosomes and reduced fertility/infertility.

Recent publications relevant to the proposed project:

1. Vedanayagam J. Small-RNA-mediated suppression of sex chromosome meiotic conflicts during Drosophila male gametogenesis. 2025. Biochemical Society Transcations 53(1): 281-291

2. Vedanayagam J., Herbette M., Mudgett H., Lin C., Gunasinghe H., McDonough- Goldstein C., Dorus S., Loppin B., Meiklejohn C., Dubruille R., Lai E.C. 2023. Essential and recurrent roles for hairpin RNAs in silencing de novo sex chromosome conflict in Drosophila simulans PLoS Biology 21(6): e3002136

3. Vedanayagam J., Lin C., Papareddy R., Nodine M., Flynt A., Wen J., Lai E.C. 2023. Regulatory logic of endogenous RNAi in silencing de novo genomic conflicts PLoS Genetics 19(6):e1010787

4. Vedanayagam J., Lin C., Lai E.C. 2021. Rapid evolutionary dynamics of an expanding family of meiotic drive factors and their hpRNA suppressors Nature Eco. & Evol. 5(12):1613-1623

Responsibilities:

A successful candidate will conduct genetic crosses in Drosophila and perform genomic and transcriptomic analyses to characterize drivers and suppressors of meiotic drive. Key responsibilities include conducting research, contributing to manuscript preparation and dissemination of results at conferences, participating in regular lab meetings and journal clubs, and working independently while mentoring junior researchers. Additionally, excellent written and oral communication skills are a plus!

Required qualifications:

Ph.D. in Evolutionary Biology, Genetics, Genomics, Developmental Biology, or related field. Demonstration of research productivity with first-author and contributing author manuscripts is highly valued. Furthermore, bioinformatics skills are highly preferred (especially R, but also Python or other relevant languages).

Please contact Jeffrey with a cover letter describing your research experience and interests, a CV including publications, and contact information for 2-3 references. The position is open till 2/15/2026 or until a suitable candidate is identified on a rolling basis.

Salary:

This is a grant-funded position, and the salary range is based on the NRSA stipend levels stipulated by the National Institutes of Health, commensurate with experience and qualifications. This is a full-time position with an initial appointment of one year, renewable annually based on performance and funding availability.

The University of Texas at San Antonio (UT San Antonio) is a nationally recognized, top-tier public research university that unites the power of higher education, biomedical discovery and healthcare within one visionary institution. As the third-largest research university in Texas and a Carnegie R1-designated institution, UT San Antonio is a model of access and excellence advancing knowledge, social mobility and public health across South Texas and beyond. UT San Antonio serves approximately 42,000 students in 320 academic programs spanning science, engineering, medicine, health, liberal arts, AI, cybersecurity, business, education and more. With 17,000 faculty and staff, UT San Antonio has also been recognized as a Top Employer in Texas by Forbes Magazine.

Contact:

Jeffrey Vedanayagam Assistant Professor Department of Neuroscience, Developmental And Regenerative Biology Faculty affiliate: School of Data Science University of Texas San Antonio https://www.anti-sense.org Email: jeffrey.vedanayagam@utsa.edu

Jeffrey Vedanayagam <jeffrey.vedanayagam@utsa.edu>

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

UWesternAustralia MarineGenomics

Senior Research Fellow/ Research Fellow (OceanOmics Centre)

Job no: 521831 Work type: Full Time Location: Crawley Categories: Science

* World-class genomics hub driving breakthroughs in marine biodiversity research and conservation. * Collaborative research environment with cutting-edge facilities and strategic partnerships for global impact. * Full-time appointment on a fixed term basis for 3 years. * Base salary range: Level C, $144,143 - $165,809 p.a. plus 17% superannuation. * Base salary range: Level B, $118,150 - $139,812 p.a. plus 17% superannuation.

About the area

Minderoo OceanOmics Centre at UWA is a world-class research facility established through a collaboration between The University of Western Australia and Minderoo Foundation. Located in the Bayliss Building on UWA's Crawley Campus, the Centre uses groundbreaking genomics-based research to characterise marine biodiversity. Focusing on Australia's native marine vertebrates and regional marine ecosystems, we integrate advanced genomics infrastructure, specialist expertise, and strong collaborative networks to generate large-scale Environmental DNA (eDNA) and whole-genome sequencing datasets. Our work establishes a genomics-enabled foundation for biodiversity discovery, ecological understanding, informed conservation-management and the development of innovative biomonitoring solutions. OceanOmics Centre is staffed by a team of researchers, scientific officers and research technicians who are also part of the UWA Oceans Institute, a multidisciplinary research institution based in the nearby Indian Ocean Marine Research Centre.

About the opportunity

* Minderoo OceanOmics Centre at UWA is a joint initiative with Minderoo Foundation, advancing ocean conservation using marine genomics and whole genome sequencing of marine vertebrates. * The Centre develops innovative laboratory and computational workflows for genome sequencing, assembly, data analysis, and open- access genomic resources to inform biodiversity conservation. * Equipped with state-of-the-art sequencing technologies and robotics, the Centre collaborates with UWA, Western Australian Museum, DPIRD WA Fisheries and global partners to deliver high- impact research and management insights.

About you

* Tertiary qualifications in marine biology and a PhD in a relevant discipline such as genomics, bioinformatics, computational biology, molecular ecology, molecular biology, or molecular genetics. * Proven experience in designing and leading research projects, with a focus on the development, optimisation, and application of genomic tools and technologies to marine species and ecosystems. * Experience in planning and conducting marine fieldwork, including specimen and tissue collection, sample handling, and data recording in accordance with ethical and biosafety standards. * Advanced understanding of molecular biology and high-throughput, next-generation sequencing (NGS) workflows, enabling effective collaboration with laboratory staff and the development and execution of optimised sequencing and analysis pipelines. * Demonstrated experience in deriving biological insights from large- scale genomic datasets, including whole-genome sequencing, population genomics, or transcriptomics data.

How to apply

Please apply online via the Apply Now button at this link https://external.jobs.uwa.edu.au/cw/en/job/-521831?lApplicationSubSourceID Shannon Corrigan <shannon.corrigan@uwa.edu.au>

Shannon Corrigan (she/her).

Principal Research Fellow, OceanOmics Centre Lead

Minderoo OceanOmics Centre at UWA

M310, Bayliss Building , Perth WA 6009 Australia

T: +61 419-260-353 <tel:+61419260353> E: shannon.corrigan@uwa.edu.au

[The University of Western Australia]

We acknowledge we are situated on Noongar land, and that Noongar people remain the spiritual and cultural custodians of their land, and continue to practise their values, languages, beliefs and knowledge. We pay our respects to the traditional owners of the lands on which we live and work across Western Australia and Australia.

shannon.corrigan@uwa.edu.au

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

VrijeU Belgium SexChromosomeEvolution

FWO-funded postdoctoral position in evolutionary genomics of sex chromosomes and sex-specific recombination in anurans

A postdoctoral position is available in the Ma Lab: Evolutionary Genomics of Sex(https://www.wmalab.com) in Research Group of Ecology, Evolution and Genetics in Biology Department at the Vrije Universiteit Brussel in Brussels, Belgium. Our lab aims to understand how sex chromosomes and sex-determination systems originate and evolve, why they are highly labile in some lineages but extremely stable in others, and how recombination shapes these dynamics across the Tree of Life. The successful candidate will work on research topic on evolution of sex chromosomes and extreme heterochiasmy across anuran lineages, with emphasis on: - assembling and analysing large, repeat-rich frog genomes - performing comparative genomics across lineages with different sex- determining systems(XY, ZW, homomorphic vs. differentiated sex chromosomes) - investigating the drivers of sex chromosome turnover, transposable elements and repeat landscapes - analysing the evolution of sex-specific recombination rates and landscapes

The project will involve field sampling and basic molecular lab work, and will combine long-read genome assembly, comparative and population genomics, and the analysis of recombination patterns and structural variation. Depending on the candidate's interests and expertise, there will also be opportunities to integrate cytogenetics and/or evo-devo approaches. What we expect from you:

PhD in evolutionary biology, genomics, bioinformatics or a closely related field. Solid expertise in evolutionary/population genomics and molecular evolution, with a clear interest in sex chromosomes/sex determination, recombination(heterochiasmy), transposable element evolution, or genome evolution in non-model species. Proven experience analysing high-throughput sequencing data, ideally including genome assembly and/or comparative genomics (large or repeat-rich genomes are a plus). Strong programming and data-analysis skills(e.g. Python and/or R, Unix) and familiarity with reproducible workflows. Highly motivated to work on frog genomes to understand sex chromosome turnover and recombination landscapes, and to link genomic patterns to evolutionary mechanisms. Valid EU (or equivalent) driving licence, prior fieldwork experience is preferred Willingness to contribute to ongoing projects, co-supervise MSc/BSc students and (optionally) take on a small amount of teaching. Compliance with the mobility rule: you have not lived or worked in Belgium for more than 12 months in the 36 months before the start of the fellowship.

Please submit the application via VUB link by 10/03/2026: https://jobs.vub.be/job/Elsene-Postdoctoral-researcher-in-evolutionary-genomics/-1285868901/ CV(including publication list) Cover letter(key qualifications, why you are interested, your research directions/career goals) Copy of PhD diploma

Contact details for three referees(who will be contacted after shortlisting The position is initial for 12 months (renewable up to 3 years upon positive evaluation), with planned starting date 01/06/2026 (with some flexibility). Questions about the position and in general? Contact Prof. Wen-Juan Maat wen-juan.ma@vub.be

Wen-Juan Ma <Wen-Juan.Ma@vub.be>

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

YaleU HumanPopulationGenetics

POSTDOC POSITION: Human Population Genetics (Koch Lab, Yale School of Medicine)

The Koch Lab is seeking a postdoctoral scientist with expertise in population genetics and a motivated interest in human genetics. Our lab develops novel methods, theory, and analysis paradigms. We are interested in linking selective and mutational landscapes to patterns of genetic variation associated with human traits and diseases. We do this by integrating evolutionary models with GWAS, biobank, and functional genomic resources across populations to develop broadly useful frameworks for interpreting genetic findings in human health.

Appropriate candidates will possess foundational knowledge in population genetics as well as strong quantitative and computational skills. The postdoc will lead projects that develop and apply new methods for the analysis of human genomic data. Individuals from diverse backgrounds are encouraged to apply.

The Koch Lab is located in the Yale School of Medicine, which offers an outstanding training environment for postdoctoral scientists, with state-of-the-art research facilities and extensive resources to support professional development.

RESPONSIBILITIES - Develop bioinformatics pipelines for the analysis of large genomic datasets - Derive novel statistical and theoretical models - Prepare manuscripts for publication - Attend and present at lab meetings, departmental seminars, and conferences - Participate in collaborations with other labs and consortia - Contribute to mentoring students and junior scientists in the lab - Apply for independent funding and assist the PI in preparation of grant proposals

MENTORING AND PROFESSIONAL DEVELOPMENT We emphasize mentorship and value the opportunity to train future leaders in human genetics. The PI will work with the successful candidate to develop and implement a mentorship plan tailored to their goals and interests. Mentorship will be provided for fellowship applications, manuscript writing, presentations, and independence.

The successful candidate will have access to a range of career development opportunities at Yale, including seminars from internationally renowned researchers, “Meet the Speaker” lunches, and professional development and networking activities through the Yale Postdoctoral Association and Yale Office for Career Strategy.

QUALIFICATIONS Candidates should have or be close to obtaining a PhD in genetics/genomics, evolutionary biology, computational biology, or a related field. Experience with Python and the command line is required. Experience with one or more of the following is desired: statistical and theoretical population genetics, high performance computing environments, statistical genetics.

The ideal candidate will also demonstrate: - High drive and initiative, with a track record of impactful research outcomes - Experience writing manuscripts published in peer-reviewed journals - Ability to work independently and as part of a team - Eagerness to learn and establish new methods, and strong problem- solving skills - Excellent written and verbal communication - Desire to contribute to mentoring students and junior scientists

APPLICATION INSTRUCTIONS Please apply with: (1) A cover letter summarizing your experiences, research interests, and career goals, and why you are interested in pursuing a postdoc in our lab (2) Your CV, including contact details of three references and a representative manuscript (3) Your earliest available start date

Application link: https://apply.interfolio.com/177328 Contact: Evan Koch, PhD Assistant Professor, Department of Genetics Yale School of Medicine 100 College St. New Haven, CT 06510 Email: evan.koch@yale.edu

“Koch, Evan” <evan.koch@yale.edu>

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

WorkshopsCourses

Campania Italy Two EMBO Genomics June07-22

Registration is now open for the upcoming EMBO Practical Course "Population Genomics: background and tools" to be held in Italy, 15-22 June 2026!

IMPORTANT DATES for this Course:

Deadline for applications: 10/02/2026

Latest notification of acceptance: 25/02/2026

Course dates: 15-22/06/2026

Registration fee waivers, travel and child care grants available!

Full details, including the course programme, invited speakers and the application form: https://meetings.embo.org/event/26-pop-genomics In this EMBO Practical Course, participants will learn fundamental concepts and advanced approaches to reconstruct the demographic history of populations and infer natural selection, using both classic and machine learning-based techniques. Participants will also learn the essential and advanced programming skills required to run the analyses related to the concept presented, with a special focus on machine learning. Keynote lectures focused on major achievements and future perspectives of population genomics will complement the training. Lectures and practicals are delivered by experienced outstanding and inspiring speakers. We expect participants to become fully confident in running analyses on their own after attending this EMBO Practical Course.

This EMBO Practical Course aims at evolutionary biologists who already have basic bioinformatics skills. Good knowledge of R is a pre-requisite and knowledge of Python is a plus. Ph.D. students and Postdoc researchers will benefit the most out of this EMBO Practical Course, but applications from all candidates will be evaluated in their context.

"Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

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

—-

Registration is now open for the upcoming EMBO Practical Course "Pangenomics" to be held in Italy, 07-13 June 2026!

IMPORTANT DATES for this Course:

Deadline for applications: 03/02/2026

Latest notification of acceptance: 17/02/2026

Course dates: 07-13/06/2026

Registration fee waivers, travel and child care grants available!

Full details, including the course programme, invited speakers and the application form: https://meetings.embo.org/event/26-pangenomics Pangenomics has emerged as a transformative paradigm in genomics, moving from single linear reference genomes to pangenomes that capture the full spectrum of genetic variation within species. Recent breakthroughs include the completion of the human pangenome reference by the Human Pangenome Reference Consortium (HPRC), revealing millions of previously hidden variants and structural variations that traditional approaches missed. Advanced graph-based representations now enable comprehensive analysis of complex genomic regions, including highly variable immune loci and centromeres.

Key technological advances include improved algorithms for pangenome construction (PGGB, WFMASH, IMPG), sophisticated visualization tools (ODGI), and novel genotyping methods from graph references (PanGenie, POVU). Course organizers and instructors contributed directly to HPRC, developing these cutting-edge methodologies and software. These advances are transforming genome evolution, population genetics, and disease research across diverse organisms.

This EMBO Practical Course addresses a critical gap in computational biology training. While pangenomics tools are rapidly advancing, researchers lack comprehensive hands-on experience with these specialized methods.

This EMBO Practical Course uniquely combines theoretical foundations with practical implementation across the entire pangenomics workflow-from graph construction through variant analysis. By training the next generation of computational biologists in these cutting-edge approaches, we will accelerate the adoption of pangenomics methods and enable more complete characterization of genetic diversity in research worldwide.

"Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

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

Crete MarineGenomics May25-29

Dear all,

We are pleased to announce the upcoming Marine Genomics course, taking place from 25 to 29 May 2026 at the Hellenic Centre for Marine Research (HCMR) in Heraklion, Crete. This intensive, hands-on course offers a comprehensive introduction to marine and population genomics, designed to equip researchers with the skills needed to analyze genomic datasets in a marine context.

Course website: (https://www.physalia-courses.org/courses-workshops/marine-genomics/)

Over five days, participants will gain practical experience assessing genome assemblies, processing sequencing data, performing population genomics analyses, and integrating genomic with environmental data through seascape genomics. Working with real marine datasets, you will develop the confidence to design and conduct meaningful analyses relevant to marine biodiversity, adaptation, and evolutionary studies.The program balances theoretical foundations with extensive hands-on exercises and expert-led discussions.

Crete's inspiring research environment, combined with expert instruction, makes this an exceptional opportunity to enhance your marine genomics expertise.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/marine-genomics/)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

"info@physalia-courses.org" <info@physalia-courses.org>

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

FUBerlin ProgrammingForEvolBiol Feb17-Mar6

Course on Programming for Evolutionary Biology

When: 2026 February 17th - March 6th 2026

Location: Berlin, Germany

We had two short-notice cancellations by accepted participants, so there is a chance to still participate if you are quick.

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>

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

Glasgow IntroToViralBioinformatics Jun15-19

Course: Introduction to Viral Bioinformatics

Where: Glasgow, UK

When: Monday 15th June - Friday 19th June 2026

Webpage: https://bioinformatics.cvr.ac.uk/training/introduction-to-viral-bioinformatics-training-course-2026/ Applications are now open for our annual training course in Viral Bioinformatics. The Medical Research Council-University of Glasgow Centre for Virus Research (CVR) has been organising an annual training course on Viral Bioinformatics since 2015 and applications are currently open for the 2026 course which will run from Monday 15th June (9am start) to Friday 19th June (12.30 finish).

The course offers a comprehensive introduction to Viral Bioinformatics and comprises a 4.5 day program including lectures and practical exercises tailored towards viral high throughput sequencing data sets. The course is taught by members of the CVR bioinformatics team who have a wealth of experience on a broad range of virological research questions. Topics covered in the course include:

* Linux command line: introduction to working with the command line, navigating the file system and manipulating files * NGS reads and QC: introduction to next generation sequencing, FASTQ reads, read trimming and quality control (trim_galore, FASTQC) * Reference assembly:â€aligning reads to a known reference, SAM/BAM file manipulation and visualisation (bwa, samtools, tablet) * Consensus calling:â€consensus sequence generation and variant calling (samtools, ivar, lofreq) * Phylogenetic analysis: introduction to multiple sequence alignment, phylogenetic reconstruction and visualisation (mafft, clustal, raxml, figtree) * Metagenomics: de-novo assembly and quality assessment, viral contig taxonomic classification and visualisation, and rapid k-mer based metagenomics (spades, idba, quast, diamond, krona, kraken) * Genomics: a dedicated session with the CVR genomics team who do a huge range of viral (and host) high-throughput sequencing on different platforms * Nanopore: introduction to reference alignment and consensus calling for Oxford Nanopore (MinION) data (minimap, samtools, medaka) * nf-core/viralrecon: introduction to using the nextflow nf-core viral bioinformatics pipeline to run common viral bioinformatics analyses * Bash scripting:â€writing simple bash scripts to automate common bioinformatic procedures

For more details including information on how to apply see the webpage: https://bioinformatics.cvr.ac.uk/training/introduction-to-viral-bioinformatics-training-course-2026/ Richard Orton <Richard.Orton@glasgow.ac.uk>

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

Oeiras Portugal EMBO CellularEvolution Jun2-5

Dear colleagues,

We would like to draw your attention to the upcoming EMBO Workshop “The rules of the game: biophysical and molecular principles in cellular evolution”, which will take place in Oeiras (Portugal) on 2-5 June 2026 in a hybrid format.

The workshop aims to bring together researchers working at the interface of biological and statistical physics, molecular biology, and evolutionary cell biology, with a focus on the fundamental principles shaping cellular evolution across scales.

The workshop will be held as a hybrid event, with up to 100 in-person participants and unlimited virtual attendance. A significant number of oral presentation slots will be available, and early abstract submission is strongly encouraged, particularly for those interested in presenting their work.

Thanks to support from EMBO and APS DBIO, a substantial number of travel grants will be available. Early-career researchers and trainees are strongly encouraged to apply for travel support during the application process.

The application deadline is March 1st.

Further details, including the scientific program and application instructions, can be found here: https://meetings.embo.org/event/26-cellular-evolution We would be grateful if you could share this announcement with trainees in your group and with colleagues who may be interested in the topic.

With best regards,

"The Rules of the Game" Organizers: Marco Fumasoni (Gulbenkian Institute for Molecular Medicine) Andrea Giometto (Cornell University) Liedewij Laan (Delft University of Technology)

Confirmed speakers: Alexandre Bisson, Brandeis University Andrea Giometto, Cornell University Andrew Murray, Harvard University Arvind Murugan, University of Chicago Aude Bernheim, Institut Pasteur Ines Anna Drinnenberg, Institut Curie Kabir Husain, University College London Kerry Samerotte, Arizona State University Liedewij Laan, Delft University of Technology Marco Cosentino-Lagomarsino, IFOM ETS - The AIRC Institute of Molecular Oncology Marco Fumasoni, Gulbenkian Institute for Molecular Medicine Monica Bettencourt-Dias, Gulbenkian Institute for Molecular Medicine Mukund Thattai, National Centre for Biological Sciences Sergey Kryazhimskiy, University of California San Diego

Marco Fumasoni <marco.fumasoni@gimm.pt>

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

Online BayesianInference Mar16-20

Dear colleagues,

Transmitting Science is offering the course "Introduction to Bayesian Inference in Practice" (10th edition).

Instructors: Dr. Daniele Silvestro (ETH Zï¿½rich, Switzerland) and Dr. Tobias Andermann (University of Uppsala, Sweden)

Course webpage: https://www.transmittingscience.com/courses/statistics-and-bioinformatics/introduction-bayesian-inference-practice/ Bayesian methods have become standard practice in the fields of phylogenetic inference, evolutionary (paleo)biology and genomics. On this course, we will outline the relevant concepts and basic theory of Bayesian methods and learn how to perform Bayesian inference in practice.

We will demonstrate how to implement the most common algorithms to estimate parameters based on posterior probabilities, such as Markov Chain Monte Carlo samplers, and how to build hierarchical models. We will also touch upon hypothesis testing using Bayes factors and Bayesian variable selection.

After completion of the course, the participants will have gained a better understanding of how the main Bayesian methods implemented in many programs used in biological research work. Participants will also learn how to model at least basic problems using Bayesian statistics and how to implement the necessary algorithms to solve them. The aim is that, by the end of the course, each participant will have written their own MCMC - from scratch!

For any questions, please contact us at courses@transmittingscience.com

Haris

Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com [1]

Links:

[1] http://www.transmittingscience.com
Haris Saslis - Transmitting Science <haris.saslis@transmittingscience.com>

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

Online BiologyStatThinking Mar24-Jun30

Dear evoldir community,

Spots are still available for Modern Statistical Thinking for Biologists, running online from 24 March till 30 June. The course follows the principle that statistics is not merely applied maths: it is a distinct way of thinking about the world. And it is best learned through honing our logical thinking skills and our intuitions about data, rather than through rote memorisation of tests or through excessive mathematical detail. The course therefore has no prerequisites in terms of maths skills.

Importantly, we will approach statistics through the Bayesian framework. Even though Bayesian methods are used throughout biology, they are particularly prevalent in ecology and evolutionary biology. This is because this framework is particularly well adapted to the noisy and complex data sets routinely produced in these fields. It is sometimes also considered to be more intuitive for beginners. The course is therefore open both to those who are beginners to any kind of statistics, as well as those who already have a background in frequentist methods and would like to learn about the Bayesian perspective specifically.

The course is composed of weekly Zoom sessions with lots of interaction and lots of group work in breakout rooms. The concepts learned are immediately applied to real data sets from the biological sciences. There are also weekly assignments, to which the participants receive individual written feedback each time. Towards the end of the course, the students will have the opportunity to put what they have learned to the test in two projects: one on data provided by the instructor and another on each participant's own data.

The course takes on 15 participants on a first-come-first-served basis. For registration and for more information, see here:

https://www.mondegoscience.com/courses/modern-statistical-thinking-for-biologists If you have any questions, don't hesitate to drop me a line on-rosina@mondegoscience.com.

Have a lovely week,

Rosina.

Rosina Savisaar <rosinasavisaar@gmail.com>

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

Online CausalAI Jan19

Hello EVOLDIR members

Last chance to join our 1-day seminar Causal AI for Real-World Data livestreaming January 19 with Meghann Gregg (Statistical Society of Canada). The Causal AI for Real-World Data seminar provides a practical toolkit for designing and defending causal analyses, which is highly relevant for understanding complex evolutionary dynamics. Participants will learn to construct Directed Acyclic Graphs (DAGs) and apply modern estimation strategies in R and Python, skills invaluable for identifying causal genetic variants or environmental drivers of phenotypic evolution. This expertise will enable researchers to strengthen their inferences regarding evolutionary mechanisms, genetic pathways, and the causal factors shaping biodiversity.

Sign up today (https://instats.org/seminar/causal-ai-for-real-world-data) to secure your spot, and please share this opportunity with colleagues and students who might benefit!

Best wishes

Michael Zyphur Professor and Director Instats | instats.org

mzyphur@instats.org

Online ComplexDatasetsWithChatGPT

Hello EVOLDIR members

Instats is offering a new 1-day seminar Exploratory Analysis of Complex Datasets with ChatGPT 2.0 livestreaming February 12, led by Nikolay Oskolkov (Group Leader (PI) at LIOS). This seminar explores advanced techniques for exploratory data analysis, including dimensionality reduction, clustering, and the integration of AI tools like ChatGPT. Researchers in evolutionary biology and genetics can apply these methods to uncover hidden patterns in high-dimensional genomic datasets, such as identifying population structures or classifying genetic variants. Leveraging ChatGPT can further aid in interpreting complex evolutionary models and generating novel hypotheses from large-scale genetic data.

Sign up today (https://instats.org/seminar/exploratory-analysis-of-complex-datasets-2) to secure your spot, and please share this opportunity with colleagues and students who might benefit!

Best wishes

Michael Zyphur Professor and Director Instats | instats.org

mzyphur@instats.org

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

Online DeepLearningInPopGenomics Mar23-26

Dear all,

We are pleased to announce the upcoming Physalia online course "Machine and Deep Learning Methods in Population Genomics and Phylogeography" taking place from 23 to 26 March.

Course website: (https://www.physalia-courses.org/-courses-workshops/deep-learning-in-popgen/)

This 4-day course provides a hands-on introduction to machine learning and deep learning approaches particularly Convolutional Neural Networks (CNNs) for demographic inference, phylogeography, and detection of selective sweeps from genomic data. Participants will learn how to simulate genetic data, apply ABC and machine learning methods, and use deep learning models directly on genetic datasets.

The course combines lectures and practical sessions, with examples from both model and non-model organisms, and is aimed at graduate students, postdocs, and researchers in evolutionary biology, population genomics, and related fields.

Sessions run daily from 14:00 to 19:00 (Berlin time) and include lectures, practical coding exercises, and real-world case studies.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-deep-learning-in-popgen/)

Kind 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 DNAMethylation Apr20-24

Dear all,

We are pleased to announce the Physalia online course "DNA Methylation in Ecology and Evolution", taking place 20-24 April.

Course website: https://www.physalia-courses.org/-courses-workshops/dnamethylation/ This 5-day hands-on course provides a practical introduction to generating and analysing DNA methylation data at genome-wide, nucleotide resolution, with a strong focus on ecological and evolutionary applications, particularly in non-model organisms.

We will cover short-read approaches (Illumina WGBS and EM-seq) as well as long-read methylation analysis with Oxford Nanopore, with discussion of PacBio data as well.

Participants will work through complete analysis workflows, from raw sequencing data to biological interpretation, including differential methylation analyses and integration with genetic and gene expression data.

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>

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

Online eDNANanopore Mar23-25

Dear all, We are pleased to announce a focused 3-day online course on Environmental DNA (eDNA) Metabarcoding using Nanopore Sequencing, running from 23rd to 25th March .

Course website: [https://www.physalia-courses.org/-courses-workshops/nanopore-dnametabarcoding/]

This 3-day program offers a comprehensive overview of the full workflow-from field sampling and molecular lab techniques to real-time sequencing and advanced bioinformatics analysis. Designed for researchers, ecologists, and bioinformaticians, the course combines expert lectures with practical sessions. You will learn to handle Nanopore data, troubleshoot common lab challenges, perform taxonomic assignments, and analyze biodiversity metrics using R.

Sessions run daily from 2 to 6 PM Berlin time and are fully online to enable global participation.

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 [Bluesky](https://bsky.app/profile/physaliacourses.bsky.social) [Linkedin](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 FunctionalTraitDiversity Feb

Dear colleagues,

Transmitting Science is offering a new edition of the online course "Functional trait diversity: calculating and interpreting a key component of biodiversity".

Course webpage: https://www.transmittingscience.com/courses/ecology/functional-trait-diversity-calculating-and-interpreting-a-key-component-of-biodiversity/ This course is suitable for ecologists and evolutionary biologists that are interested in applying and interpreting indices of functional trait diversity and related metrics of community trait structure. We will consider and learn how to compute and interpret different metrics of trait dissimilarity among organisms, learn how to account for intraspecific trait variability and compute functional diversity at different scales (e.g. alpha and beta partitioning of diversity), among others.

For questions, please contact us at courses@transmittingscience.com

Best regards,

Haris

Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com [1]

Links:

[1] http://www.transmittingscience.com Haris Saslis - Transmitting Science <haris.saslis@transmittingscience.com>

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

Online GeometricMorphometrics

Dear colleagues,

There are 2 slots available for the course "Geometric Morphometrics for Beginners".

Geometric morphometrics is useful tool in the study of evolution because it allows researchers to precisely quantify and compare shape variation among organisms.

Course webpage: https://www.transmittingscience.com/courses/geometric-morphometrics/geometric-morphometrics-for-beginners/ The aim of this course is to introduce participants to geometric morphometric methods for quantifying biological shape variation. The course will cover landmark and semi-landmark data acquisition, Procrustes alignment, PCA of shapes, and interpretation of morphometric results.

By the end of the course, students will be able to:

* Understand the foundations of geometric morphometrics. * Interpret morphometric variation in biological datasets.

Instruction will combine lectures, guided examples, and practical exercises.

For any questions, please 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>

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

Online GWAS Jan26-30

Dear all,

only a few seats are still available for our upcoming online course “Introduction to Genome-Wide Association Studies (GWAS)”, taking place 26?¿‘30 January.

Course website: (https://www.physalia-courses.org/-courses-workshops/course49/)

This 5-day hands-on course provides a complete and practical introduction to GWAS, guiding participants through the full workflow??”from study design and data preparation to statistical analysis, pipelines, and post-GWAS interpretation?¿‘using R and Linux command-line tools.

Designed for students, researchers, and professionals in genetics and related fields, the course combines interactive lectures with extensive practical sessions to ensure you gain skills you can immediately apply to your own data.

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

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

Online IntroToMachineLearning Feb16-20

Dear all,

Are you interested in mastering machine learning for biological data? There are a few seats left for our online course “Introduction to Machine Learning with R” (16-20 February).

Course website: (https://www.physalia-courses.org/-courses-workshops/course43/)

Biology today generates complex multivariate data from multi-omics studies (genomics, proteomics, metabolomics, transcriptomics). Machine learning is a powerful tool to help analyze and interpret this data, alongside classical statistics. In this course, you’ll get hands-on experience with multivariate methods and machine learning algorithms applied to biological datasets including practical training using the tidyverse-friendly tidymodels framework.

Course programme (all sessions 2-7 pm Berlin time):

ML basics and tidy ML with tidymodels

Supervised learning: regression, classification, model selection

Overfitting, resampling, model tuning

Tree-based methods: Random Forest, Boosting

Unsupervised learning: PCA, UMAP, Self-Organizing Maps

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-course43/)

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 Metabarcoding Mar16-20

Dear all,

We are excited to announce the upcoming online course "Metabarcoding in Microbial Ecology", taking place from 16 to 20 March 2026.

Course website: (https://www.physalia-courses.org/-courses-workshops/course30/)

This course offers a thorough introduction to metabarcoding techniques and their application in microbial ecology, designed to foster international participation. Throughout five days of combined lectures and hands-on exercises, participants will learn the essential computational steps of a metabarcoding study from processing raw next-generation sequencing data to conducting advanced statistical analyses. By the end of the course, you will understand both the potential and limitations of metabarcoding techniques and be able to process your own datasets to answer relevant ecological questions.

This course is ideal for researchers and students with a strong interest in applying high-throughput DNA sequencing technologies to community ecology and biodiversity studies. While no prior programming experience is required, a basic understanding of command-line tools and R will help you gain the most from the sessions.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-course30/)

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 Pangenomics Apr13-16

Dear all,

we would like to announce the Physalia online course on Computational Pangenomics (2nd edition), which will take place on 13-16 April.

Course website: (https://www.physalia-courses.org/-courses-workshops/computational-pangenomics/)

This practical course introduces participants to the concepts, methods, and software needed to build and analyse pangenome graphs from whole-genome assemblies. The course combines short introductory lectures with extensive hands-on sessions. Participants will learn how to construct and explore pangenome graphs, understand relationships among multiple genomes, and apply pangenome-based analyses to their own research. Practical exercises will use real pangenome datasets, and participants are welcome to bring their own data for discussion.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-computational-pangenomics/)

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 PopulationGenomicsNaturalSelection Apr

Dear colleagues,

Transmitting Science is offering the online course “The Genomic Footprint of Natural Selection: Inference from Population Data”.

Course webpage: https://www.transmittingscience.com/courses/genetics-and-genomics/the-genomic-footprint-of-natural-selection/ This course examines the concepts and analytical methods used to detect genomic signatures of natural selection, with a particular focus on adaptive selection in humans. Through a combination of interactive lectures and hands-on sessions, participants will develop a solid theoretical background in population genetics and measures of genetic diversity relevant to studying selection at the genomic level.

Throughout the course, practical and conceptual challenges, such as demographic confounding, limited statistical power, and difficulties in biological interpretation, will be addressed. By the end of the course, participants will be able to critically assess genomic evidence for natural selection and to understand how such inferences inform research on human evolution and biomedicine.

For questions, please contact us at courses@transmittingscience.com

Best regards,

Haris

Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com [1]

Links:

[1] http://www.transmittingscience.com Haris Saslis - Transmitting Science <haris.saslis@transmittingscience.com>

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

Online RNAseqAnalysis Feb24-26

The Computational Biology Core at the University of Connecticut is hosting virtual bioinformatics workshops this winter! We still have space available in our RNA-seq Analysis Workshop (virtual but live instruction - Feb. 24-26).

This hands-on workshop will guide participants through the complete RNA-seq analysis workflow using a reference genome and annotation. You’ll learn about experimental design, high-throughput sequencing basics, quality control, alignment, differential expression analysis, and gene ontology/gene set enrichment?using real datasets and widely used tools.

A self-guided introduction to Linux, HPC, and R will be provided two weeks before the workshop to ensure participants are ready to dive in.

Learn more & register here: [https://bioinformatics.uconn.edu/cbc-workshops/] WHERE: Virtual (MS Teams) 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

zsc25001@uconn.edu

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

Online RNA-SeqAnalysis FinalCall

RNA-Seq Analysis

RNA-Seq analysis training - live online course covering experiment design, data QC, alignment, gene expression, DESeq2 differential expression, PCA, visualisation, and functional analysis.

ONLY 5 PLACES LEFT! https://prstats.org/course/rna-seq-analysis-rnaa01/ Join our four-day live online workshop:RNA-Seq Analysis (RNAA01). If you’re working with RNA-Seq or planning to generate bulk transcriptome data, and you want to take your analysis from raw reads through to biological insight, this is the course for you.

What you will learn

How to design a robust RNA-Seq experiment and avoid common pitfalls.

How to perform quality control on raw RNA-Seq data, align reads, and assess alignment quality.

How to quantify gene expression and apply the widely-used DESeq2 workflow for differential expression analysis.

How to visualise high-throughput data using principal component analysis (PCA), volcano plots, MA plots and other techniques.

How to perform functional interpretation of differential expression results, turning numbers into biological insight.

Who should attend

Researchers, postgraduate students and industry professionals working with bulk RNA-Seq data.

Anyone who has basic experience with R, RStudio and the fundamentals of molecular biology or transcriptomics.

Those who want to move from raw sequence data to actionable biological conclusions with confidence.

Course format

Four days of live online sessions (approximately 3Â½ hours each day) in a UK / Western European time zone.

Interactive lectures, hands-on practical exercises and dedicated discussion time.

Course materials, code and datasets will be provided, and participants are encouraged to bring their own data for discussion when possible.

Recordings of sessions available after each day for participants across different time zones.

Why this course stands out

It offers an end-to-end workflow from design through QC, alignment, differential expression and functional analysis designed specifically for researchers working in transcriptomics.

It emphasises not just how to run the tools, but how to interpret results, understand the assumptions and recognise where things can go wrong.

Designed by experienced bioinformaticians, the course balances theory, practice and discussion in an accessible live-online format.

How to register / next steps Visit the PR Stats website for full course details, upcoming dates and registration information. Early registration is advisable, as places may be limited. For any questions about suitability, prerequisites or logistics, please contact the course organisers.

https://prstats.org/course/rna-seq-analysis-rnaa01/ –

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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

Online Single-CellRNA-SeqAnalysis

Single-Cell RNA-Seq Analysis

Live online training covering all stages of single-cell transcriptomic data analysis from experimental design to data QC, normalization, clustering, differential expression, and biological interpretation.

https://prstats.org/course/single-cell-rna-seq-analysis-scrn02/ Join our four-day live online workshop: Single-Cell RNA-Seq Analysis (SCRN02). If you're working with single-cell transcriptome data or planning to dive into single-cell workflows, this course will guide you from raw data to interpretable biological insight.

What you will learn

How to design a robust single-cell RNA-Seq experiment, including strategies for cell capture, sequencing depth and batch control. How to perform quality control and filtering of single-cell data to ensure high-quality downstream analysis. How to normalize and process data, cluster cells, and identify cell types or states. How to conduct differential expression analysis, trajectory inference or other advanced single-cell analyses. How to interpret results biologically linking clusters, cell types or trajectories to meaningful insights.

Who should attend

Researchers, postgraduate students and industry professionals working with single-cell RNA-Seq data. Anyone with basic experience in R, data analysis, and transcriptomics who wants to build confidence in single-cell workflows. Those who want to confidently move from raw single-cell data to actionable biological conclusions.

Course format

Four days of live online sessions (approximately 3.5 hours each day) in a UK / Western European time zone. Interactive lectures, hands-on practical sessions and discussion time. Course materials, code and example datasets will be provided - participants are encouraged to bring their own data for discussion when possible. Recordings available after each day to support participants in different time zones.

Why this course stands out

It offers an end-to-end workflow specifically tailored for single-cell data from design through QC, clustering, differential expression and biological interpretation. It emphasises not just how to run analysis pipelines, but how to understand assumptions, interpret results, and avoid common pitfalls in single-cell data analysis. Developed and delivered by experienced bioinformaticians, the course balances theoretical foundations with applied, hands-on training in a live-online format.

How to register / next steps

Visit the PR Stats website for full course details, upcoming dates and registration information. Early registration is recommended, as places are limited.https://prstats.org/course/single-cell-rna-seq-analysis-scrn02/ Oliver Hooker PhD. PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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

Online UnixForBioinformatics Jan12-16

Dear all,

Happy New Year! There are still a few seats for our upcoming online course “Unix and Shell Scripting for Bioinformatics”, taking place on 12-16 January 2026. Course website: (https://www.physalia-courses.org/courses-workshops/unix/)

This hands-on course is designed for biologists with no prior Unix experience who want to gain practical command-line skills for bioinformatics. Participants will learn how to work efficiently in Unix/Linux environments, process large biological datasets (including NGS data), and automate analyses using shell scripting.

Through guided exercises and real-world examples, the course will cover essential Unix commands, file and system management, software installation, text processing, and the construction of reproducible bioinformatics pipelines.

For the full list of our courses and workshops, please have a look at: (https://www.physalia-courses.org/courses-workshops/unix/)

We look forward to welcoming you to this practical introduction to Unix for bioinformatics. 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 VariantDetect Jan27-29

The Computational Biology Core at the University of Connecticut is hosting a virtual bioinformatics workshop this winter! We still have space available in our Variant Detection Workshop (virtual with live instruction - Jan. 27-29, 2026).

This hands-on workshop introduces the core concepts and tools used to identify and analyze genetic variants from high-throughput sequencing data. Participants will learn Linux and high-performance computing (HPC) basics, high-throughput sequencing fundamentals, reference alignment and quality control, and variant calling models and pipelines (GATK, Freebayes, BCFtools). The workshop also covers variant call filtering, comparison, and annotation for downstream analyses.

This workshop is designed for beginnersâprior bioinformatics experience required.

Learn more & register here: https://bioinformatics.uconn.edu/cbc-workshops/ WHERE: Virtual (MS Teams | recordings distributed) WHEN: 10:00 AM - 2:00 PM EST COST: $400 (UConn affiliates) â€â€â€$500 (External participants)

Registration is first come, first served.

Questions? E-mail cbcsupport@helpspotmail.com

“Lambert, Karelyn” <zsc25001@uconn.edu>

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

Ploen Germany WomenInEvolutionaryBiologyII Jun1-3

Dear evoldir community,

We are happy to announce the workshop Women in Evolutionary Biology II that will take place at the Max Planck Institute for Evolutionary Biology in Plï¿½n , Germany from 1st to 3rd of June 2026 . We have invited 6 exceptional women, working in evolutionary biology, as keynote speakers to learn from them and celebrate their journey. Scientists of all genders and different backgrounds in evolutionary biology are welcome to participate in scientific presentations and discussion sessions on topics relevant for women in science.

WOMEN IN EVOLUTIONARY BIOLOGY II WORKSHOP

WHEN: 1st - 3rd June 2026

LOCATION: Plï¿½n, Germany

Detailed information about the workshop and how to apply : https://workshops.evolbio.mpg.de/event/144/-overview REGISTRATION DEADLINE: 20th February 2026

If you have any questions related to the workshop, please do not hesitate to contact us at women@evolbio.mpg.de

Best wishes, Women in Evolutionary Biology II organization team

Manasvi Balachandran Halley Cano Fernandez Amanda de Azevedo-Lopes Linda Kappes Stella Kyomen Rajalekshmi Narayana Sarma

Women in Evolutionary Biology <women@evolbio.mpg.de>

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

WoodsHole MolecularEvolution Jan26

Don't miss the opportunity to attend (or send someone in your lab) to MBL's Workshop on Molecular Evolution, the most prestigious workshop serving the field of evolutionary studies. Founded in 1988, it is the longest-running workshop if its kind, and it has earned worldwide recognition for its rich and intensive learning experience.

Deadline to apply: January 26, 2026

More information: https://www.mbl.edu/education/-advanced-research-training-courses/course-offerings/-workshop-molecular-evolution Thanks, Jeremy M. Brown and Claudia Sol?s-Lemus

solislemus@wisc.edu

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

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.