EvolDir

March 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.

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Conferences

Belgium EcoEvoAnthropocene Apr29-30

Two-day symposium on “ECOLOGY AND EVOLUTION IN THE ANTHROPOCENE”

DATE: 29-30 April 2026 # LOCATION: UCLouvain, Louvain-la-Neuve, Belgium # FEE: 80 EUR # WEBSITE: https://lnkd.in/e8yshCeD ## ABOUT THE SYMPOSIUM The symposium focuses on ecological and evolutionary responses to rapid human-induced environmental change. The symposium is open to researchers at all career stages.

CALL FOR CONTRIBUTIONS We invite submissions for: - short talks (12min) - poster presentations

REGISTRATION AND ABSTRACT SUBMISSION –> https://lnkd.in/e4C6ra9W ## DEADLINES for abstract: 27 February for registration: 31 March

CONTACT Nicola Mauro, UCLouvain (BEL) nicola.mauro@uclouvain.be

Simon Baeckens <simon.baeckens@uclouvain.be>

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Bialowieza Poland Mustelid CallForAbstracts Oct6-9

Dear Sirs,

We are pleased to announce that the call for abstracts is now open for the second edition of the BiaÂ³owieÂ¿a Ecology Conference (BEC). This edition will host the 36^th European Mustelid Colloquium and is organised in collaboration with the Vincent Wildlife Trust (VWT), an organisationspecialising in scientific research and the active conservation of threatened mammal species. The European Mustelid Colloquium is an international conference with a long-standing tradition, held regularly for nearly 70 years.

The conference will take place from *6 to 9 October 2026* in *BiaÂ³owieÂ¿a, Poland*, set within the pristine natural environment of Europe’s last primeval lowland forest.

Key dates

- Abstract submissions open: February 9th, 2026

- Submission deadline: March 31st, 2026

- Notification to authors: July 2026

- Early-bird registration deadline: March 31st, 2026

Conference Theme and Scope

The BiaÂ³owieÂ¿a Ecology Conference is an international scientific conference series held in the heart of Europe's last primeval lowland forest. In 2026, during its second edition, BEC will host the *36th European Mustelid Colloquium* an international conference that has been held regularly for 70 years in various locations across Europe and has successfully brought together researchers studying mustelids, one of the largest and most diverse groups of carnivores.

We warmly invite submissions of abstracts covering broadly understood mustelid ecology, biology, evolution, conservation, monitoring methods, and population dynamics, as well as studies examining both the impact of these predators on the environment and the effects of environmental and climate change on mustelid populations.

For a more detailed description, please visit BEC website < https://bialowiezaecologyconference.org/ >, and VWT website < https://www.vwt.org.uk/36th-european-mustelid-colloquium >.

Submission guidelines

- Abstracts should be prepared in English (up to 300 words for the main text).

- Please indicate your preferred presentation format: full-length talk, rapid-fire talk, poster, or no preference.

- Submissions should clearly outline the aims, methods, and conclusions.

To submit your abstract, please download 36EMC-Abstract-template.docx < https://vwt-production.ams3.digitaloceanspaces.com/uploads/Vincent-Wildlife-Trust/European-Mustelid-Colloquium/36EMC-Abstract-template.docx > and send the completed form to enquiries@vwt.org.uk.

*Registration is now open!*Purchase tickets here:

https://app.evenea.pl/event/36th-european-mustelid-colloquium/?lang=en

For any inquiries regarding the call for abstracts or the conference in general, please do not hesitate to contact us at info@bialowiezaecologyconference.org or bec_conference@ibs.bialowieza.pl.

We would be grateful if you could share this information with colleagues from other institutions (call file attached).

Any updates can be followed on our accounts on Facebook: https://www.facebook.com/BEConference and Bluesky: https://bsky.app/profile/mripas.bsky.social

We are looking forward to your submissions and welcoming you to BEC 2026/36^th EMC.

Best regards,

Anna Wereszczuk, PhD, on behalf of the 36^th European Mustelid Colloquium Organizing Committee

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Cincinnati AnimalBehavior Jul14-18

The Animal Behavior Society (ABS) is offering multiple Charles H. Turner Awards to attend its annual conference in Cincinnati, Ohio, US. from July 14 - 18, 2026. Turner Awardees will receive financial support to travel to the annual conference, including conference registration, airfare, ground transportation, hotel/lodging, and some meals.

Position Overview: The Turner Award is a travel grant that supports the goals of increasing the participation of undergraduates at the ABS annual conference and the diversity of our membership within the society. Awardees will work one-on-one with mentors and facilitators, in cohorts of their peers, and in individual reflection to understand how graduate education and membership in the Animal Behavior Society may become part of their professional trajectory.

Responsibilities: Turner Fellows will participate in a one-day workshop (July 13) structured to integrate students into both the meeting experience and the broader community of the Animal Behavior Society. Throughout the conference (July 14-18) they will engage in professional development activities, cohort building, and identity tasks that will celebrate the uniqueness of "Being a Turner."

Qualifications / Requirements: Students who are members of groups traditionally under-represented in the sciences are particularly encouraged to apply (including but not limited to students from diverse racial and ethnic backgrounds, ability/disability status, gender diversity, etc.).

Applicants for the Turner award may be at any stage of their undergraduate career (not secondary school) or recently graduated, but may not have started a graduate program prior to the annual meeting covered by the award.

As part of the application process you will be asked to have one individual familiar with your academic or research work submit responses to a recommendation form within one week of the application deadline. The link to submit the recommendation will be sent directly from the ABS to the person you list in your application once the completed application is submitted.

Note: students are responsible for acquiring all required documentation (visas, passport) to enter the US.

How to Apply: https://www.animalbehaviorsociety.org/web/awards-turner.php Application Deadline: March 23, 2026

Flavia Barbosa (she/her) Associate Professor of Biology Lake Forest College 555 N. Sheridan Rd. Lake Forest, IL 60045 Office: LIL 262 https://sites.google.com/view/barbosalab/ barbosa@lakeforest.edu (847) 735-6046 Book office hours: https://calendly.com/flaviabarbosa/flavia-s-office-hours "Barbosa, Flavia (She/Her/Hers)" <barbosa@lakeforest.edu>

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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>

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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>

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Cornwall UK EvolutionxEcology Jun29-Jul3

*** Evolution x Ecology 2026 Conference in Cornwall, UK ***

Registration is now open for ExE 2026, a conference aimed at evolutionary ecologists from around the world, hosted by the University of Exeter's Centre for Ecology and Conservation in beautiful Cornwall.?

Register now at evoxeco.uk!

In addition to cutting-edge research at the interface of evolution and ecology, we have excursions to some of best places in Cornwall and a fantastic set of pre- and post-conference workshops. Places are filling fast so make sure you don't miss out!

Any questions, email the organising team at info@evoxeco.uk

We looking forward to welcoming you to Cornwall!

Erik Postma Barbara Tschirren Ben Longdon Alastair Wilson Mark Hanson

evoxeco.uk https://sites.exeter.ac.uk/exe/ E.Postma@exeter.ac.uk

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Ede Netherlands EvolutionaryBiology Apr14

Dear colleagues,

We are excited to welcome you to the 2026 NLSEB meeting that will be held on Tuesday April 14th at the Akoesticum in Ede, the Netherlands.

We have two very exciting plenary talks by Prof. Dr Marta Szulkin (University of Warsaw), by Dr. Daniel Tamarit Chulia (Utrecht University) and a plenary talk by the winner of the 2026 Netherlands Evolutionary Biology Prize (will be announced during the meeting). The program, as always, includes two parallel presentation sessions, a cultural intermezzo, and plenty of time for poster presentations and socializing with your fellow evolutionary biologists, to strengthen your networking connections and to establish new collaborations.

Registration is now open. To join us on April 14th visit our website (https://www.nlseb.nl/nlseb-meeting-2026) and follow the registration link. Via the same registration link you can also submit an abstract (to be considered for a talk or poster presentation). The deadline for registration and abstract submission is February 20.

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

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Firenze Evolution2026 Sep6-10

ITALIAN SOCIETY FOR EVOLUTIONARY BIOLOGY Congress 6-10 September 2026, Firenze, Italy

Dear Colleagues, we are finally ready to share with you most of the details of the SIBE 2026 conference, which will take place in Firenze from 6 to 10 September. The scientific programme will be structured around five themed symposia:

Symposium 1 "Host-microbiome interactions" Symposium 2 "Evolutionary roots of behavioural diversity" Symposium 3 "Phylogeography and Conservation Genomics: understanding evolutionary history to sustain species resilience" Symposium 4 "Human evolution" Symposium 5 "The evolution of ecological diversification: mechanisms, interactions, and outcomes"

Contributions that do not fall within the themes listed above are also welcome and will be included in a dedicated miscellaneous symposium. *_Registration will open on March the 9th._* In addition to the scientific sessions, the conference will offer a rich programme of events, including a dedicated poster session, a crash course on wet-lab techniques in genomics, the meeting of the Italian group for conservation genetics and genomics, an original outreach theatre event entitled "Queer Botany", and a charming social dinner hosted at the Firenze Botanical Garden.

As for the venues, the conference will take place across several locations in the city. All scientific sessions will be held in the Novoli area, home to the University Social Sciences Campus, while social events and the poster session will take place in the historic city centre. Participants may therefore choose to stay either in the city centre or in Novoli, which are conveniently connected by tram. Please note that the last tram service runs at around 00:30; after this time, public transportation becomes more limited. September is peak season in Florence and several other conferences are scheduled in the Novoli area during the same period, so we strongly recommend booking accommodation well in advance.

We invite you to visit the conference website www.sibe-iseb.it/firenze2026 for full details on Evoluzione2026 and to stay tuned for further updates. More exciting information will be released soon, including the opening lecture speaker, the full crash course programme, and a preview of the Evoluzione2026 t-shirt.

The chairs of the congress

Alessio Iannucci Sara Fratini

Alessio Iannucci Tenure Track Researcher (RTT) Department of Biology University of Florence Via Madonna del Piano 6, I-50019 Sesto Fiorentino (FI), Italy email:alessio.iannucci@unifi.it Tel. +390554574741

Alessio Iannucci <alessio.iannucci@unifi.it>

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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>

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Glasgow EuroEvoDevo AbstDeadlineMar5

Dear EvoDevo researchers,

The EuroEvoDevo abstract submission deadline is only one week away, on Thursday 5th March!

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

Check the conference website here: https://www.evodevoconference26.com/ *Please **click here* < https://hg3.co.uk/eed/ >* to submit an abstract. *(Note that registration is required for your abstract to be considered, please *click here* < https://registrations.hg3conferences.co.uk/hg3/335/register > to register)

*Please visit the conference website page for updates and further information, please **click here* < https://www.evodevoconference26.com/ >*.*

Should you have any questions at all about the meeting, please do not hesitate to contact us at events@hg3.co.uk

Best wishes,

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

<eed.soc@gmail.com>

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Glasgow EuroEvoDevo Jun12

Dear Evo Devo researchers,

We are excited to let you know that abstract submission and registration for *10th European Society for Evolutionary Developmental Biology Meeting 2026 *(Euro Evo Devo 2026) is now open.

The meeting will take place at the* University of Glasgow* *from* *8th - 12th June 2026*.

Please note that we extended the early bird registration deadline to *5th of March*.

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.*

- The early bird deadline is Thursday 5th March 2026.

*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.

*Accommodation for the conference can be booked using our allocation. Please **click here* < https://book.passkey.com/gt/220842781?gtid=3D963118a2155a79026780b4d3773f891 > *.*

*Please visit the conference website page for updates and further information, please **click here* < 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<mailto:golding@mcmaster.ca>)

Kelowna BritishColumbia ViralEvolution May19-22

ABSTRACT SUBMISSION DEADLINE EXTENDED! Submit your abstracts here: [https://dynamicsevolution.org/event/7/abstracts/ | https://dynamicsevolution.org/event/7/abstracts/] EXTENDED abstract deadline: February 10 , 2026

If you require a visa to attend, you may request early abstract review.

May 19 -22, 2026 33rd Dynamics & Evolution of Human Viruses UBC Okanagan, Kelowna, Canada

The 33rd International Dynamics & Evolution of Human Viruses conference will be held May 19 -22, 2026 at the University of British Columbia Okanagan Campus, in British Columbia, Canada. This will be a hybrid meeting, which will include a live in-person meeting and a virtual option.

This meeting series is designed to promote discussion between specialists in quantitative and computational approaches in two areas in the field of virology where these are particularly important:

* Modeling of viral and cellular dynamics * Viral evolution and population genetics

Many of these approaches were originally developed for HIV but are now applied to many viruses where extensive data are available. We encourage the submission of abstracts relating to work on HIV, SARS-CoV-2 and other human viruses. We consider topics on statistical, mathematical, computational, and integrative approaches to analyzing the dynamics and evolution of human viruses within the scope of this meeting. Abstracts are being accepted under the following topics from which the final conference schedule will be constructed:

* Vaccines & Immune escape * Zoonoses & Emerging Infections * Genomics & Bioinformatics * Software Tools & Methods * Transmission Dynamics & Clusters * Within-Host Dynamics & Adaptation * Phylodynamics & Phylogeography * Evolutionary Dynamics of HIV

This year, we will once again be using the [https://getindico.io/ | Indico] platform for abstract submission and review. You will be prompted to create a user account to submit an abstract if you do not already have one. We welcome and actively encourage researchers from diverse backgrounds and locations around the world to participate, including early-career scientists and members of underrepresented groups. Program Chairs

Jeffrey Joy, PhD , BC Centre for Excellence in HIV/AIDS, University of British Columbia

Manon Ragonnet-Cronin, PhD , University of Chicago

Jeffrey Joy <jjoy@bccfe.ca>

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KielGermany EvolutionMedicine Jul28-31

ABSTRACTS are due March 1, 2026 for the 11th Annual Meeting of the International Society for Evolution, Medicine, and Public Health in Kiel, Germany, July 28-31. Researchers, clinicians, and students are all welcome at this congenial meeting about the most recent developments in the field.

Full information at https://ISEMPH.org . PLEASE FORWARD this invitation to all who have an interest in how evolutionary biology can improve understanding, prevention, and treatment of disease.

KEYNOTE SPEAKERS -Johannes Krause ?¿‘ Max Planck Institute Jena, Germany -Trevor Graham ??” Institute of Cancer Research London, UK -Lynette Leidy Sievert ?¿‘ UMass Amherst, USA -Brendan Bohannan ??” Univ. of Oregon, USA -Marisa Azad ?¿‘ Univ. of Ottawa, Canada

REGISTER NOW to get the discounted rate, you can get a refund if you later find you can’t make it. Be sure your membership is up to date to get meeting registration discounts. If you are not an ISEMPH member, you may wish to join ISEMPH before registering for the meeting in order to take advantage of the substantial member discount.

DEADLINES March 1, 2026: Abstract submission deadline and travel award decision announcement April 1, 2026: Abstract decision announcement April 15, 2026: Early-bird registration deadline; all presenters must be registered and paid June 15, 2026: Regular registration deadline

PROGRAM COMMITTEE Michelle Blyth, Louisiana State University School of Medicine New Orleans, USA Emily Emmott, University College London, UK Manuel Irimia, Pompeu Fabra University, Spain Monica Kidd, physician in Calgary, Canada Susie Lee, Max Planck Institute for Demographic Research, Germany Michael Muehlenbein, Baylor University, USA Dipongkor Saha, North Carolina Agricultural and Technical State University, USA Lisa Stabryla, University of Illinois Chicago, USA Misty Thomas, North Carolina Agricultural and Technical State University, USA

LOCAL EXECUTIVE COMMITTEE John Baines, Christian Albrecht University of Kiel, Germany Barbara Cania, Christian Albrecht University of Kiel, Germany Hinrich Schulenburg, Christian Albrecht University of Kiel, Germany

LOCAL GENERAL COMMITTEE Philipp Altrock, Christian Albrecht University of Kiel, Germany John Baines, Christian Albrecht University of Kiel, Germany Barbara Cania, Christian Albrecht University of Kiel, Germany Tal Dagan, Christian Albrecht University of Kiel, Germany Mathieu Groussin, Christian Albrecht University of Kiel, Germany Ben Krause-Kyora, Christian Albrecht University of Kiel, Germany Almut Nebel, Christian Albrecht University of Kiel, Germany Olivia Roth, Christian Albrecht University of Kiel, Germany Hinrich Schulenburg, Christian Albrecht University of Kiel, Germany

We are looking forward to seeing you all in Kiel!

nesse@umich.edu

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Kiel Germany EvolutionMedicineSociety Jul28-31

ABSTRACTS are due March 1, 2026 for the 11th Annual Meeting of the International Society for Evolution, Medicine, and Public Health in Kiel, Germany, July 28-31. Researchers, clinicians, and students are all welcome at this congenial meeting about the most recent developments in the field.

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We are looking forward to seeing you all in Kiel!

Randolph Nesse <nesse@umich.edu>

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LundU HermaphroditicOrganisms Apr22-23

SHOW (Simultaneously Hermaphrodite Organisms Workshop) is a forum for researchers studying hermaphroditic species to share their findings and plan long-term collaborations. Running since 2011, the workshop initially focused on simultaneous hermaphrodites (organisms producing male and female gametes simultaneously) but now covers hermaphrodite evolution more broadly. The event spans two days and emphasizes diverse presentations from different research groups, fostering a wide range of ideas across various systems and disciplines. Its relaxed environment encourages early-career researchers to present in topics included population genetics, gene expression, sexual conflict, mating systems, gamete evolution, and experimental evolution.

Our website is now open for registration! https://colin-olito.github.io/SHOW2026.github.io/ SHOW 2026 will be held in Lund, Sweden, on April 22nd-23rd. We can offer free registration for up to 50 participants.

Keynote speakers: Beatriz Vicoso (https://ist.ac.at/-en/research/vicoso-group/) Sophie Karrenberg (https://www.uu.se/en/department/ecology-and-genetics/-research/plant-ecology-and-evolution/karrenberg-lab)

Welcome to Lund in April!

On behalf of the SHOW organizing committee.

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>

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Mertola NaturalSelection Apr17-19

MERTOLA EVOLUTION CONFERENCES- 2026 EDITION: NATURAL SELECTION IN THE WILD

!!!! 17 - 19th of April 2026, Mertola, Portugal !!!!!

Registration is now open!

Dear Colleagues,

It is a pleasure to announce that the registration for the second edition of Mertola Evolution Conferences (MECs), which will occur in the Spring at the beautiful historical town of Mertola, Southern Portugal, is now open.

The MECs are annual meetings on Evolutionary Biology (each year a specific topic) for researchers and students to present cutting-edge studies on the field, as well as a forum for informal discussion, fostering new ideas and collaborations among researchers all over the world. Mertola Conferences are promoted by EBM - Biological Station of Mertola in collaboration with other national and international institutions.

Mertola is located in Southeast Alentejo region of Portugal, near the Spanish border, crossed by the Guadiana River and in the center of the Natural Park of Guadiana Valley. The antiquity of Mertola is attested by the many archaeological remains that prove the continuous human occupation of this territory. Despite being and biodiversity hotspot of Mediterranean ecosystems, the first traces of human presence dating back to the Neolithic period, five thousand years ago, with different civilizations, like Iberians, Phoenicians, Greeks and Carthaginians. More information at https://www.visitmertola.pt/mertola-vila-museu/ The MEC 2026 edition, entitled "Natural Selection in the Wild". It counts with prominent speakers in the field: Rosemary Gillespie (University of California, Berkeley, USA), Jeremy Searle (Cornell University, USA), Matthew P. Hare (Cornell University, USA), Silvia Matesanz Garc?a (Universidad Rey Juan Carlos, Spain) Jose Melo-Ferreira (University of Porto)

Important information Venue and date: Cineteatro de Mertola, April 17th to 19th 2026 Abstract submission deadline: 6th of March 2026 Registration deadline: 13 of March 2026

Registration and abstract submission: Among the submitted abstracts, only 8 will be selected for a short oral presentation. For registration and abstract submission, please fill this form: https://forms.gle/gGWuWpgWs4Ak2fDj7 Participation is free of charge for BIODIV Students (M BGE & PhD) & CIBIO's TwinLabs (If applicable, payment will be made to Associacao BIOPOLIS - VAT No. 516033727). Fees: 60 euros (other students and Biopolis non-students) | 120 euros (other participants).

The organizing committee, Jeremy Searle Miguel Carneiro Rui Faria Paulo Celio Alves

Rui Faria, PhD

1. Researcher and SEAGEN Group Leader CIBIO, Centro de Investiga??o em Biodiversidade e Recursos Gen?ticos, InBIO Laborat?rio Associado BIOPOLIS Program in Genomics, Biodiversity and Land Planning Campus de Vair?o Rua Padre Armando Quintas, n? 7 4485-661, Vair?o, Portugal

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

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

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Online ESEB InternalConflictsSTN Feb19

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 February 19, 17:00 UTC. Our speakers for this seminar are:

Joe Alcock (University of New Mexico): Humans and the microbial organ - a conflicted relationship.

Asher Leeks (University of British Columbia): The social lives of viruses.

We expect the meeting to take approximately 1.5 hours.

Meeting details: Date: February 19, 2026. Time: 17:00 UTC < https://www.timeanddate.com/worldclock/fixedtime.html?msg=STN+seminar&iso=20260219T17&p1=1440&ah=1&am=30 > . Meeting link: https://georgetown.zoom.us/j/92854430107?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, Manus Patten, Arvid Ãgren, Nina Wedell, and Thomas Hitchcock

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

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Online ESEB STN Speciation Mar3

Dear colleagues,

The online seminars organised by the ESEB-funded STN network ≪ Integration of Speciation Research ≫ ([https://speciation-network.pages.ist.ac.at/]) is about to restart, with the first session taking place Tuesday 3rd of March at 5pm CET.

This session falls within the theme "Early Career Researchers in Speciation", with a new format featuring two talks (1 hour total):

1. José Cerca (Group Leader @ Swedish Museum of Natural History) "The identity Crisis of Speciation Genomics" 2. Andrea Estandia (Postdoc @ U. Oxford, UK): "Evolutionary Consequences of Island Colonisation in the Silvereye."

followed by a 30 min Q&A with Mark Ravinet (U. Oslo, Norway) about his career path.

We are grateful to José Cerca for stepping in at short notice as our previously announced speaker Nare Ngoepe sadly had to cancel.

To attend, please use the following link: https://gu-se.zoom.us/j/68669501529 Talks (but not the Q&A) will be recorded and made available here: https://www.youtube.com/channel/UClEkDdE_5sDw70SQq78DIAA, where you can also find previous seminar recordings.

The IOS network aims to promote both scientific and community integration across speciation research. A main objective is to foster diversity and inclusion across the field. We alternate time slots every month to maximise the geographic diversity of attendees. The seminar series and subsequent discussions are open to everyone, from students to established researchers and non-scientists. Please share this email with anyone who may be interested, especially those in countries that are typically underrepresented in scientific discourse. However, please do not post the zoom link on social media.

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

We look forward to seeing you there!

The STN IOS organising committee:

Jonna Kulmuni (chair), Sean Stankowski, Carole Smadja, Sonal Singhal (co-chairs), Chris Cooney, Liz Scordato, Joana Meier, Richard Merrill, Konrad Lohse, Nick Barton, Roger Butlin, Jonah Walker, Parvathy Suendranadh, Hilde Schneemann and Rowan Schley

Hilde Schneemann <Hilde.Schneemann@ist.ac.at>

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Oslo SparrowEvolution May6-8

Dear all,

It is our great pleasure to invite you to the Oslo Sparrow Meeting 2026! The meeting will be held on the 6th-8th May at the Department of Biosciences at the University of Oslo Norway. Information on the meeting is here < https://www.mn.uio.no/cees/english/research/news/events/research/other/2026/sparrow.html > and you can register online for using this < https://nettskjema.no/a/sparrow > online form. Please note that the deadline for registering is 11pm CET on 22nd February. The meeting is free to attend but requires registration.

Our confirmed invited speakers are:

- Dr Susan Johnston (University of Edinburgh, UK) - Professor David Westneat (University of Kentucky, USA) - Professor Yanhua Qu (Beijing Academy of Sciences, China) - Professor Henrik Jensen (NTNU, Norway) - Associate Professor Julia Schroeder (Imperial College, London UK) - Professor Simon Griffith (MacQuarie University, Australia) - Professor Glenn-Peter Sï¿½tre (UiO, Norway)

We have places for 50 people and we encourage registration from anyone working on Passer sparrows in any capacity - be it genomics, physiology, behaviour or whatever your field might be. We are currently operating on a first come first serve basis but if we have many more applications, we may select attendees. If this does happen, selection will be balanced to ensure representation across career stages, genders and research areas.

We hope you can join us in Oslo - please feel free to circulate this email to colleagues you think might be interested in joining too - we are keen for attendees from all career stages!

Mark Ravinet, Lynn Martin, Melissah Rowe, Anna Runemark, Britt Heidinger

Mark Ravinet <mark.ravinet@ibv.uio.no>

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Porto Biodiversity Jul8-10

Dear colleagues,

We are delighted to announce the launch of STRiVE (Structural Genomic Variation in Evolution), a new Special Topic Network supported by the European Society for Evolutionary Biology (ESEB).

Our network aims to explore the evolutionary role of structural variants through collaborative research, workshops, and seminars. You can find all the details on our website: https://structuralvariantsstn.github.io/ How to get involved:

- Stay informed: Join our mailing list (link below) and follow us on Bluesky (@strivestn.bsky.social). - Become a member: If you wish to take a more active role in the network's initiatives, we invite you to apply for membership.

Upcoming Activities:

- April 29th, 2026 (6 pm CET / 9 am PST): Online seminar by Loren Rieseberg - July 8th-10th, 2026: Kick-off conference in Porto: "Trends in Biodiversity and Evolution: the evolutionary role of structural genomic variation" (TiBE-STRiVE).

We are also currently co-editing a special issue in JEB < https://academic.oup.com/jeb/pages/call-for-papers-genome-architecture-and-evolution-how-structural-and-genetic-variation-shapes-biodiversity?login=false >, organizing an ongoing online seminar series, and coordinating working groups for joint analyses and methodological workshops over the next two years.

Newsletter Subscription:

To stay updated on our latest news, please sign up here < https://groupes.renater.fr/sympa/subscribe/stnstrive >. (Note: You will need to enter your name and email and click "Confirm". You will then receive a validation email. We apologize as the registration form is currently partially in French.)

We look forward to building this community with you.

Sincerely,

Claire Mérot, on behalf of the STRiVE Committee

Claire Mérot <claire.merot@gmail.com>

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Portugal StructuralVariation Jul8-10

CONFERENCE ON THE EVOLUTIONARY ROLE OF STRUCTURAL VARIATION 8th - 10th of July 2026, Vila do Conde, Portugal

!!!!REGISTRATION and ABSTRACT SUBMISSION is NOW OPEN FOR STRIVE NETWORK MEMBERS!!!

Dear colleagues,

The ESEB Special Topic Network on "Structural variants in evolution-STRiVE" was established in 2025 and brings together researchers from across the globe to study how structural variants, ranging from transposable elements to large chromosomal rearrangements such as inversions or fusions and fissions, shape genome evolution, adaptation, and speciation (https://structuralvariantsstn.github.io/). Through collaborative research, standardised methods, seminars, meetings, and training initiatives, we aim to bridge communities and unlock the diversity of structural variants and their evolutionary implications across the Tree of Life both from an empirical and theoretical perspective.

The Trends in Biodiversity and Evolution (TiBE) conference is an annual meeting organized by BIOPOLIS-CIBIO, Portugal, providing a platform for senior researchers, as well as post-graduate and graduate students, to present and discuss the latest developments in evolutionary biology.

We are organizing a joint conference "Trends in Biodiversity and Evolution: the evolutionary role of structural genomic variation" (TiBE-STRiVE)" that will feature cutting-edge research presentations, foster interdisciplinary discussions, and initiate collaborative projects spanning the breadth of structural variant research. This will be the kick-off conference of the STRiVE network (https://structuralvariantsstn.github.io/).

Registration in the conference (and abstract submission) is now open for members of STRiVE (see link to the form here: https://structuralvariantsstn.github.io/porto_registration/) and will open in March 16th for everyone else. If interested, see the link below on how to become a network member.

IMPORTANT INFORMATION and LINKS: Venue-Location: Quinta do Crasto, Vairao, Vila do Conde, Portugal Dates: 8th to 10th of July, 2026 Registration and abstract submission open on the 25th of February 2026 for STRiVE members, and on the 16th of MARCH for everyone else.

Talks are granted on a first-come, first-served basis. How to register and submit your abstract: https://structuralvariantsstn.github.io/porto_registration/ More information about the conference:https://structuralvariantsstn.github.io/porto_about/ How to become STRiVE member: https://structuralvariantsstn.github.io/committee/ STRiVE network Website: https://structuralvariantsstn.github.io/ Follow us on Bluesky (@strivestn.bsky.social).

INVITED SPEAKERS: Mark Kirkpatrick, Department of Integrative Biology, The University of Texas at Austin, Austin, TX, USA Joana Meier, Cambridge University & Welcome Sanger Institute, UK

Two additional early career speakers will be invited to present a talk based on the quality their abstracts

MAIN ORGANIZERS: Rui Faria, Aurora Ruiz Herrera and Marina Rafajlovic

Other members of the organizing and scientific committee: Marius Roesti, Petr Neguyen, Kay Lucek, Maren Wellenreuther, Jenn Coughlan, Zach Gompert, Claire Merot, Benjamin Dauphin

Local organizing committee; Pierre Barry (CIBIO, U. Porto), Ralph Merrifield (CIBIO, U. Porto), Susana Almeida (U. Algarve), Joï¿½o Carvalho (CIBIO, U. Porto), Leonor Bezerra (CIBIO, U. Lisbon)

On behalf of the organization and STRiVE, Rui Faria

Rui Faria, PhD

1. Researcher and SEAGEN Group Leader CIBIO, Centro de Investigaï¿½ï¿½o em Biodiversidade e Recursos Genï¿½ticos, InBIO Laboratï¿½rio Associado BIOPOLIS Program in Genomics, Biodiversity and Land Planning Campus de Vairï¿½o Rua Padre Armando Quintas, nï¿½ 7 4485-661, Vairï¿½o, Portugal

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

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

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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

Switzerland MicrobialPredation Jul27-31

Microbial Predation Conference 2026 Monte Verità, Switzerland July 27-31, 2026

Join us in lovely Ticino, Switzerland to discuss what microbial predation looks like, how it originates and evolves, and how it shapes microbial communities. Researchers studying diverse aspects of microbial predation with different predator-prey systems will gather to promote conceptual synthesis across systems and questions.

Conference website: https://microbialpredation.ethz.ch Register for conference updates at https://microbialpredation.ethz.ch/registration.html Registration and program structure are expected to be available in early March.

Invited speakers include: Lutz Becks - University of Constance, Germany Yen-Ping Hsueh - Max-Planck Institute for Biology, Tuebingen, Germany Andrew Lovering - University of Birmingham, UK David Queller - Washington University in St. Louis, USA Renske van Raaphorst - University of Groningen, The Netherlands Joan Strassmann - Washington University in St. Louis, USA

With the Conference on Microbial Predation 2026, we seek to bring together microbial-predation researchers who rarely meet under a single scientific umbrella, including molecular microbiologists, ecologists, evolutionary biologists, theoreticians, and biocontrol researchers, promoting integration across microbial systems and connection with concepts largely associated with macroscopic predators. The conference provides a forum where diverse perspectives can converge to build shared conceptual frameworks, new interdisciplinary collaborations can be initiated, and the global community of microbial-predation researchers can more deeply interconnect.

We welcome researchers working with animals who want to think more about microbial predation.

Major themes: Molecular mechanisms Behavior Ecology Evolution Social aspects of predation Applications

Scientific organizers: Marie Vasse, CNRS - University of Bordeaux, France Greg Velicer, ETH Zurich, Switzerland

For administrative questions, please contact us at microbialpredation2026@ethz.ch

gregory.velicer@env.ethz.ch

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GradStudentPositions

CharlesU Prague ConvergentAdaptationGenomics

***PhD position in Ecological genomics of convergent adaptation to whole genome duplication

Group of Ecological Genomics (Filip Kolï¿½r) Department of Botany, Charles University, Prague, Czech Republic https://www.plantecologicalgenomics.cz/ Deadline March 15

When and under which circumstances does evolution repeat itself? Evolution is driven by a combination of deterministic forces and stochasticity, whose relative importance remains a matter of debate. Knowing how predictable is evolution can provide insights into predictive evolution of crops, pathogens or species under climate change.

This project will address genomic basis and phenotypic consequences of repeated genome evolution in response to whole genome duplication (WGD). WGD is a dramatic mutation that may provide evolutionary opportunity but also imposes severe stresses associated with cell division and homeostasis, to which a nascent polyploid has to adapt. By leveraging fascinating natural diversity of Brassicaceae plants which repeatedly underwent change in ploidy level, the project aims at uncovering general mechanisms determining which portion of their genomes evolves in a predictable manner. The successful candidate will conduct detailed analyses of evolutionary history and genomic basis of WGD adaptation in several species using already available short- and long-read genome-wide data. Development of spin-off projects in ecological genomics of selected species, participation in cytogenetic assays and/or additional field sampling campaigns in the Balkans is possible. The project builds on our previous research in wild Arabidopsis (e.g. Konecnï¿½ et al. 2021 Nat. Comms., Bohutï¿½nskï¿½ et al. 2021 PNAS and 2024 Plos Gen, Vlcek et al. 2025 PNAS) but will extend well beyond this system in order to discern generality.

The project will involve close collaboration with other lab members and national and international project partners. The successful applicant will join an established multidisciplinary team of Ecological Genomics at the Department of Botany funded by competitive Junior Star and ERC projects.

We offer ** creative and supporting atmosphere in an international team ** membership to an international, diverse PhD student community at Dept of Botany ** additional interdisciplinary experience through international collaboration in polyploid evolutionary genomics (Levi Yant, SLU Uppsala) and statistical genomics (Sam Yeaman, U Calgary) ** competitive salary covered ** fully covered health insurance and contribution to the social security system ** support for establishment of foreign employees via the Staff Welcome Center of the University ** work in the historical center of a vibrant cultural Prague city

We require ** strong motivation for interdisciplinary research at the border of evolutionary biology and population genomics ** a MSc degree in Biology or related fields (in early fall 2026 at the latest) ** good spoken and written English, communication at the Department is fully in English

Desirable but not required ** experience with evolutionary history reconstruction/biosystematics ** background in population genetics ** experience with processing high-throughput sequence data

Please submit your CV including contact details for two referees and an approximately half-page motivation letter as a single pdf file via the following registration form https://forms.gle/LbDvGuSGWJBHvcJw9. Review of the applications will begin on March 15th 2026 and will continue until the position has been filled. The exact start date is negotiable. For additional questions do not hesitate contacting Filip at filip.kolar@natur.cuni.cz.

Filip Koli¿½r Department of Botany Faculty of Science, Charles University Benatska 2, CZ - 128 01, Prague, Czech Republic & Institute of Botany

Czech Academy of Sciences

252 43 Pruhonice, Czech Republic

https://www.plantecologicalgenomics.cz/ Filip Kolar <filip.kolar@gmail.com>

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

CzechRep EvolutionaryPhysiologyAvianEnergetics

PhD position: Evolutionary Physiology of Avian Energetics

THE RESEARCH PROJECT

We are seeking a motivated PhD candidate to investigate the ecological and evolutionary significance of major energy metabolites (glucose and fatty acids) circulating in avian blood.

Despite the central role of glucose and fatty acids in energy metabolism, we still lack an understanding of how variation in their circulating levels influences individual fitness and shapes life history evolution.

The successful candidate will address these fundamental questions within a project funded by the Czech Science Foundation (GACR). The project provides a unique opportunity to learn and apply diverse methodological approaches: 1. Within-species approach utilising extensive longitudinal physiological data from a long-term study of barn swallows 2. Macroevolutionary comparative analyses across passerine birds, including tropical species 3. Metabolic phenotyping utilising targeted metabolomics and enzyme activity assays 4. Advanced statistical methods, including application of reaction norm analysis, segmented regression, quantitative genetics, Bayesian phylogenetic comparative models, and path analysis

RESEARCH ENVIRONMENT

The successful candidate will join the Avian Evolutionary Ecology Group at the Institute of Vertebrate Biology, Czech Academy of Sciences, Brno (IVB CAS), under the supervision of Dr Oldrich Tomasek. The research group, led by Prof Tomas Albrecht, is a dynamic team of full-time researchers, postdocs, PhD students, and undergraduates focusing on evolutionary ecology and physiology of birds. The candidate will have the opportunity to work with other team members and national and international collaborators.

As IVB is a dedicated research institute, the candidate will enrol in the four-year PhD program at either Masaryk University (Brno) or Charles University (Prague), two of the leading research universities in Central Europe.

FUNDING AND BENEFITS

The position is funded through a combination of research grant salary and tax-free student stipend. The total net income for PhD students is guaranteed by recent legislation of the Czech Republic to ensure a comfortable standard of living. Additionally, IVB provides affordable accommodation in modern, well-equipped student apartments, significantly reducing living costs.

QUALIFICATIONS

Essential: - strong motivation for research at the intersection of evolutionary ecology and physiology - good verbal and written communication in English - MSc degree in Biology or related fields (in early fall 2026 at the latest)

The following experience is an advantage: - capturing and handling birds, lab work, statistical analysis in R, manuscript writing and publication

HOW TO APPLY

Please merge the following documents into a single PDF and start the file name with your surname: - CV with standard details, research interests, previous experience, list of publications (if any) - motivation letter (max. 400 words) - contact information of previous mentors for references (preferable but not required)

Submit your application at https://forms.gle/AFkpt4foeV5i8Zda9 Review of the applications begins on March 16, 2026, and continues until the position is filled. Official PhD enrolment is in June or October 2026, with the opportunity to start earlier in May as a research assistant.

ADDITIONAL INFORMATION AND CONTACT

For more information or if you cannot access the submission form, do not hesitate to contact me at tomasek@ivb.cz.

Oldrich Tomasek Institute of Vertebrate Biology Czech Academy of Sciences Kvetna 8, 603 00 Brno

E-mail: tomasek@ivb.cz https://www.ivb.cz/en/person/oldrich-tomasek/ bit.ly/tomasekscholar

Oldrich Tomasek <tomasek@ivb.cz>

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Europe ancientDNA

The research field concerns “Biological sciences, Zoology, Environmental science, Archaeology ” The description of the offer is as follow:

The Doctoral SchoolPALPROX (Proxies from Small Vertebrates in Prehistoric Archaeology) fosters a unique interdisciplinary and collaborative research frame in which the Doctoral Candidates will work on their Individual Research Projects around a common program: The use of small vertebrates as a proxy in Prehistoric Archaeology.

We aim to focus on the studies of Late Pleistocene small vertebrates to gain insight into the studied taxonomic groups found in archaeological sites, but also to face the new challenges posed by interdisciplinary approaches to archaeological studies, and their contributions to the debate about climate change and biodiversity loss. Small vertebrates, due to their reduced size, small habitat ranges and in most cases low mobility, are known to be more sensitive to regional changes than large mammals and plants, especially in Europe where mountain ranges and sea barriers block their retreat to the south.

In addition, fossil small vertebrates can help to modern conservation biology, providing predictive clues based on long-term biodiversity archives. In general, knowledge of the small vertebrate Quaternary record can help to better understand current extinction dynamics, response to climate changes or ecological turning points.Finally, taking advantage of synergies with other disciplines, fossil small vertebrates studies have incorporated new methodologies such as Geometric Morphometrics, Oxygen Isotope studies or ancient DNA, and introducing Geospatial and MaxEnt tools into the analyses of both fossil and modern specimens. These approaches very much complement, but do not replace, a basal training in the fundamental methods based on osteological and morphometric description. As a result, PALPROX will support nine promising Doctoral worldwide candidates passionate about interdisciplinary research, supporting the increasing diversity of career paths in Europe’s research landscape and providing fellows with the training, mentoring and career development support needed to become leaders in academia and beyond.

The call has been published on the European Portal EURAXESS and the links is the following:

Nine MSCA-Funded PhD positions within the Doctoral Network PALPROX Proxies from Small Vertebrates in Prehistoric Archaeology

JOINT CALL https://euraxess.ec.europa.eu/jobs/395927 IRP 1 https://euraxess.ec.europa.eu/jobs/395964 IRP2 https://euraxess.ec.europa.eu/jobs/395971 IRP 3 https://euraxess.ec.europa.eu/jobs/396315 IRP 4 https://euraxess.ec.europa.eu/jobs/396318 IRP 5 https://euraxess.ec.europa.eu/jobs/395978 IRP 6 https://euraxess.ec.europa.eu/jobs/395975 IRP 7 https://euraxess.ec.europa.eu/jobs/395982 IRP 8 https://euraxess.ec.europa.eu/jobs/404674 IRP 9 https://euraxess.ec.europa.eu/jobs/404678 Sophie Montuire Directrice d’Etudes EPHE EPHE, PSL University Biogéosciences, UMR 6282 uB/CNRS/EPHE Université Bourgogne Europe 6 Bd Gabriel 21000 Dijon - France +33 (0)380396347 http://www.ephe.sorbonne.fr/ http://biogeosciences.u-bourgogne.fr/ Sophie Montuire <Sophie.Montuire@u-bourgogne.fr>

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Europe NinePhD AncientDNA

Dear colleagues,

We would like to advertise several fully funded PhD positions within the Horizon Europe - Marie Sk????odowska-

Curie Actions Doctoral Network *PALPROX* (“Proxies from small vertebrates in Prehistoric Archaeology?? euro ??).

PALPROX is recruiting 9 Doctoral Candidates in total. We would particularly like to highlight three Individual Research Projects (IRP 1, 5 and 7), which may be of interest to the evolutionary biology community.

All positions are fully funded under MSCA-DN regulations and offer competitive salaries, full social security coverage, international secondments and structured interdisciplinary training. The application deadline is *26 February*.

IRP 1 - Geometric morphometrics and evolutionary patterns in bats This project focuses on 3D geometric morphometrics and functional morphology to investigate evolutionary and ecological dynamics in small vertebrates (Chiroptera). Candidates with a background in evolutionary biology, vertebrate morphology, morphometrics or macroevolution are especially encouraged to apply.

Host Institution: IPHES-CERCA (Tarragona, Spain)

Secondment: CNRS (Dijon, France)

https://euraxess.ec.europa.eu/jobs/395964 *IRP 5 - New statistical approaches to estimate Late Pleistocene climate changes* This project aims to develop and implement new statistical and modelling approaches to estimate key climate parameters (e.g. mean annual temperature and precipitation) from Late Pleistocene small vertebrate assemblages. The project integrates radiocarbon datasets, vole aDNA chronological estimations and comparisons with continental and marine climate records (e.g. oxygen isotope and pollen sequences). Candidates with strong quantitative skills (R, Bayesian modelling, palaeoclimate modelling, statistics or related fields) are particularly encouraged to apply.

Hosted Institution: Faculty of Archaeology, Uniwersytet Warszawski (Poland),

A secondment at IPHES-CERCA (Spain) is planned.

https://euraxess.ec.europa.eu/jobs/395978 *IRP 6 - Stable isotope geochemistry and palaeoenvironmental reconstruction* This project applies stable isotope and geochemical analyses to micro-mammals in order to reconstruct past environmental and climatic conditions. It is particularly suitable for candidates with training in isotope geochemistry, biogeochemistry, palaeoclimate reconstruction or Earth Sciences with an interest in evolutionary and ecological questions.

Host Institution: IPHES-CERCA (Tarragona, Spain)

Secondment: CNRS (Dijon, France)

https://euraxess.ec.europa.eu/jobs/395975 *IRP 7 - Ancient DNA and evolutionary responses to climate change* This project explores palaeogenomic data from small vertebrates to investigate evolutionary responses to past climatic shifts. Candidates with experience or strong interest in ancient DNA, population genetics, evolutionary genomics or molecular ecology are encouraged to apply.

Host Institution: Faculty of Archaeology, Uniwersytet Warszawski (Poland)

Secondment: University of Porto (Portugal)

Eligibility is subject to the MSCA mobility rule: applicants must not have resided in or carried out their main activity in the country of the recruiting institution for more than 12 months in the 36 months prior to the application deadline.

Full details, including project descriptions and application templates, are available at: https://palprox.eu/-applicants/ Send applications: pr.palprox@iphes.cat

The positions are also advertised on EURAXESS: https://euraxess.ec.europa.eu/jobs/395927 We would be grateful if you could circulate this information among potentially interested candidates.

Best regards,

_

*Project Assistant PALPROX MSCA - DN *

Funded by European Union (GA: 101226472)

Institut Catal???? de Paleoecologia Humana i Evolucio Social (IPHES-CERCA) Zona Educacional 4 Campus Sescelades URV (Edifici W3) 43007 - Tarragona Tel. (+34) 977 943 003

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GovStateU US InsectReproduction

The Plakke lab is seeking interested students to apply for funded (stipend + tuition) M.S. positions beginning Fall 2026 at Governors State University, as part of a National Science Foundation-supported research project investigating the evolutionary drivers of dichotomous sperm in insects.

Dichotomous spermatogenesis, in which males produce two distinct sperm morphs, with only one fertilizing eggs, is a striking and poorly understood evolutionary phenomenon. This project will examine hypotheses related to sexual selection, sperm competition, life-history tradeoffs, and ecological context to better understand why and how dichotomous sperm evolve and persist across insect lineages.

Governors State University is a public regional university located in the south suburbs of Chicago, offering close proximity to a major metropolitan research and cultural hub while maintaining a supportive, student-centered academic environment. An online informational session for the program will be held on March 26, and attendees will receive an application fee waiver.

Interested students should email a brief statement of research interests and CV to Melissa Plakke at mplakke@govst.edu. Informal inquiries are welcome!

“Plakke, Melissa” <mplakke@govst.edu>

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Helsinki BeetleMacroevolution

We invite applications for a fully funded three-year Doctoral Researcher position at the Finnish Museum of Natural History. The successful candidate will join the research group of Dr. Sergei Tarasov < https://www.tarasovlab.com/ > and an international network of collaborators. The position is part of a broader project on dung beetle evolution funded by the Research Council of Finland.

The PhD project will aim to uncover the macroevolutionary mechanisms driving dung beetle phenotypic diversification. The PhD candidate will investigate how dung beetle phenomes evolved during adaptive radiations by integrating phylogenomic and phenotypic data, high-dimensional phenotypic datasets, and advanced evolutionary models. A central focus will be on testing how major environmental transitions such as the K-Pg extinction and the Late Miocene grassland expansion reshaped dung availability and triggered shifts in phenotypic evolutionary rates.

The position will remain open until March 16th, or until a suitable candidate is found.

For more information, please visit: https://jobs.helsinki.fi/job/Helsinki-Doctoral-Researcher-in-Macroevolution-and-Phenotypic-Diversification-of-Dung-Beetles/1352799257/ Sergei Tarasov, Ph.D. Curator of Coleoptera (beetles) Associate Professor Finnish Museum of Natural History (LUOMUS) P.O. Box 17 (Pohjoinen Rautatiekatu 13) FI-00100 University of Helsinki Phone: +358 294128853 Email: sergei.tarasov@helsinki.fi Website: https://www.tarasovlab.com

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HHU Germany GeneticBasisOfDroughtAdaptation

PhD Position (w/m/d, 65 %, EG 13 TV-L, 3 years)

Genetic Basis of Drought Adaptation in Brassica rapa

Institute for Plant Ecology and Evolution, Heinrich Heine University Duesseldorf (HHU)

The Institute for Plant Ecology and Evolution invites applications for a PhD position investigating the ecological and genetic mechanisms of rapid adaptation to climate change. Our group combines ecological studies and resurrection approaches with quantitative genetics and ecological genomics to study evolutionary responses in natural plant populations and the genetic basis of adaptive traits.

PROJECT DESCRIPTION:

The project examines two Californian Brassica rapa populations that show parallel phenotypic shifts under drought but differ genetically. Using common gardens, quantitative genetic approaches, and genomic analyses (SNP data, GWAS, QTL mapping), the PhD student will quantify trait variation and covariation, identify the genetic architecture of drought-adaptive traits, and assess how environmental and genetic factors shape trait correlations.

YOUR TASKS:

- Set up and analyze resurrection-based common garden experiments at HHU

- Process and analyze phenotypic, environmental, and genomic datasets

- Conduct GWAS, QTL mapping and quantitative genetic analyses

- Present results at conferences and publish in peer-reviewed journals

- Supervise students and contribute to teaching activities within the institute

YOUR PROFILE:

Required

- MSc in biology, ecology, evolutionary biology, population/quantitative genetics, or related
- Strong background in evolutionary ecology and quantitative/evolutionary genetics
- Experience with NGS data processing or population genomic analyses
- Strong organizational, solution-focused, and team-working skills
- Excellent English communication skills

Preferred

- Experience with plant experiments (e.g., common gardens/greenhouse)
- Proficiency in statistical data analysis and programming (R, Python, bash)
- Experience with GWAS and QTL mapping workflows
- Demonstrated scientific writing experience
- Good German skills
- Lawful ability to work in the EU

WE OFFER:

- A DFG-funded position in a growing research institute with strengths in plant ecology, evolution, and genomics
- Potential association with TRR 341 and close links to CEPLAS
- Structured doctoral training (iGRAD, JUNO, HeRA)
- An international, supportive, and family-friendly working environment

TO APPLY:

Submit one PDF including: (i) Cover letter (max. 2 pages) summarizing your experience, research interests, as well as motivation and fit for the position; (ii) CV including publication list and contact details of two references; (iii) BSc and MSc certificates and transcripts.

Send applications by 02.03.2026 to elena.hamann@hhu.de, subject line: Application PhD Genetics.

Expected starting date: as early as possible.

For questions contact Prof. Elena Hamann and see https://www.plantecoevo.hhu.de . Jun.-Prof. Dr. Elena Hamann (she/her) Institute of Plant Ecology and Evolution Heinrich Heine University Dï¿½sseldorf Universitï¿½tsstrasse 1 - Building 22.07, Room 01.025 D-40225 Dï¿½sseldorf Germany

Tel: +49-211-8115637

E-mail: Elena.hamann@hhu.de

Lab website: https://www.plantecoevo.hhu.de/ ps. I may work and write at unconventional hours, but do not expect others to do so.

“Hamann, Elena” <Elena.Hamann@hhu.de>

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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>

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RBI Zagreb Croatia AdaptiveEvolutionInCaves

We are inviting applications for a fully funded PhD position at the Division of Molecular Biology, RuÃºer BoÂkoviÃ Institute in Zagreb, Croatia. Our lab focuses on comparative evolutionary biology, with an emphasis on rapid adaptation in extreme environments, using cave-dwelling animals as model systems. Our research combines fieldwork, organismal biology, molecular techniques, and omics approaches to explore both the proximate mechanisms (genetic, developmental, and physiological) and the evolutionary drivers (selection, plasticity, constraint) of adaptation.

The PhD project will investigate how phenotypic plasticity contributes to evolutionary adaptation during cave colonization, using the Mexican cavefish (Astyanax mexicanus) as a model system. It will test whether environmentally induced responses to darkness in ancestral surface fish precede and facilitate the evolution of robust cave-adapted traits. Focusing on eye development and degeneration, the project will examine plastic and evolved changes across developmental and molecular levels to identify mechanisms underlying plasticity, maladaptation, and genetic assimilation. Ultimately, the project aims to bridge the gap between environmental change and the evolution of novel phenotypes. More information about the project can be found on our lab website (https://bilandzija.irb.hr/-Projects-and-Funding) and previous publications: doi: 10.7554/eLife.51830 and doi: 10.24272/j.issn.2095-8137.2022.528.

Position details: Duration: 5 years (funding secured), a 6-month trial period will be required at the start of employment.

Requirements: Master's degree in Biology (or related field) Proficiency in English Strong interest in evolutionary biology

Preferred qualifications: Experience with NGS analysis, statistics/R Wet lab skills (e.g. staining, imaging)

What We Offer A collaborative, English-speaking research environment Access to Institute's facilities, including a dedicated Astyanax mexicanus facility and animal caretaker Professional development opportunities, including in-house workshops No teaching obligations (optional teaching/supervision available) Funding opportunities for conferences, workshops, and research visits abroad

The call will open in March. In the meantime, we warmly encourage interested candidates to contact Dr. BilandÂija (hbilandz@irb.hr) to express their early interest and for preliminary consideration. Please send your CV and a motivation letter. In your motivation letter, tell us about your research interests and career goals, any previous research experience (if applicable), why you would like to join our lab, and how you think you could contribute to the project.

Helena BilandÂija, PhD

Principal Investigator Division of Molecular Biology RuÃºer BoÂkoviÂ Institute Bijenicka cesta 54, P.O.Box 180 10000 Zagreb, Croatia

https://bilandzija.irb.hr/ Helena BilandÂija <Helena.Bilandzija@irb.hr>

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UBern SticklebackEvoBio

PhD position in evolutionary ecology of social interactions in stickleback Socio-Eco-Evo Group, Division of Evolutionary Ecology Institute of Ecology and Evolution (IEE), University of Bern Project Description and Work Environment

A fully funded 4-year PhD position, supervised by Dr. Jordan Martin and Prof. Katie Peichel, is available in the newly formed Socio-Eco-Evo group hosted within the IEE Division of Evolutionary Ecology. This position is part of the SNSF Ambizione project "Socio-eco-evolutionary dynamics in stickleback: The parallel co-evolution of social behavior, morphology, and plasticity in response to predation". We are studying how social plasticity has shaped the pace of stickleback's behavioral and morphological adaptation to predation in novel freshwater environments throughout southern Greenland. The project and position will be completed in close collaboration with Blake Matthew's group at Eawag. Seehttps://besjournals.onlinelibrary.wiley.com/doi/full/10.1111/1365-2435.70132for a theoretical introduction to the topic of social plasticity and socio-eco-evolutionary dynamics, as well ashttps://onlinelibrary.wiley.com/doi/10.1111/ele.14382for an overview of the study population.

The IEE in collaboration withEAWAGprovide a world-leading scientific environment for the career development and intellectual enrichment of the PhD student, along with ample opportunities for networking and collaboration within a large community of graduate students, post-doctoral researchers, and professors. The IEE is full of diverse, international, and interdisciplinary research groups, including our own Division of Evolutionary Ecology. Within our division and the Socio-Eco-Evo research group, we strive to create a lab environment where everyone feels welcome and supported. This includes a zero-tolerance policy for discrimination or harassment.

The University of Bern is situated near the heart of one of Europe's best-preserved medieval cities, which also happens to be a vibrant center for contemporary arts and culture. The quality of life in Bern is very high, and endless outdoor adventures in the alps and elsewhere are in close vicinity. The starting date of the PhD position is ideally September 1, 2026, with some limited flexibility contingent on whether the student has finished their master's program. The starting salary is approximately 50,000 CHF and includes social security contributions.

What You Can Achieve The PhD project will involve collaboration in multiple seasons of fieldwork in Greenland, where we're studying 30 ecologically diverse populations of stickleback, as well as a large common garden experiment in Switzerland. Responsibilities will include intensive, methodical collection of behavioral, morphological, and genomic data, as well as routine animal care in and leadership over the experimental study. Statistical and genomic analyses will be led by the project supervisors, with ample opportunity for learning. Students will be provided flexibility and hands-on mentorship to help develop their own research questions within the broader scope of our two primary project goals:

1. Quantifying phenotypic and genomic diversity across lakes. What is the relative importance of plasticity versus genetic differentiation for explaining variation in social behavior and morphology among populations? How do tradeoffs between or integration among behavior and morphology shape the direction and magnitude of population divergence? How does social plasticity shape the evolvability of behavior and morphology via direct and indirect genetic effects?

2. Inferring the predictability of (co)evolutionary responses to predation. Does predation have consistent effects on genetic variation and plasticity in social behavior and morphology? How predictable is parallel evolution of social plasticity, behavior, and morphology across lakes at the phenotypic and genomic levels? Is behavior a leader or follower of morphological adapta-

tion, and does social plasticity influence the pace of this evolutionary change?

Your Profile Candidates should be highly motivated, independent, and conscientious, while also exhibiting a keen desire to work collaboratively and cooperatively with colleagues. We welcome applications from individuals with a strong background in behavioral ecology and animal behavior, particularly those with training in evolutionary biology. Prior experience successfully carrying out behavioral experiments in the field and/or laboratory is essential, and training with automated coding techniques for such experiments is highly valued. Preference will be given to candidates who have familiarity with R and Bayesian statistics, have worked with fish

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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>

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UCLouvain Belgium LizardEvolutionaryEcology

PHD POSITION IN LIZARD EVOLUTIONARY ECOLOGY

Country: BELGIUM University: UCLOUVAIN Research group: ANIMAL EVOLUTIONARY ECOLOGY LAB PI: PROF SIMON BAECKENS PhD topic: LIZARD ADAPTATIONS TO HUMAN-INDUCED ENVIRONMENTAL CHANGE Anticipated start date: 1 MAY OR ASAP THEREAFTER

The PhD project will investigate (adaptive) phenotypic responses to rapid human-induced environmental change, using lizards as a model system. The research will adopt an organismal and integrative approach, examining (the interplay between) morphological, physiological, and behavioral traits. The overarching aim is to understand how organisms respond to abrupt and novel selective pressures, and to what extent such responses facilitate population persistence under global change.

The precise direction of the project is flexible and will be shaped according to the candidate's profile, interests, and strengths. Possible research themes include anthropogenic drivers of environmental change, such as bioinvasions and urbanization/pollution.Methodological approaches may include field-based experimental work in Belgium or Mediterranean systems and comparative analyses across species or populations.

WHAT WE OFFER: * Fully funded PhD position for up to 4 years * Dedicated funding for fieldwork, research costs, and conferences * Advanced doctoral training and career development at UCLouvain * Supportive and collegial research environment

REQUIRED QUALIFICATIONS AND SKILLS - Profile requirements: * MSc degree in biology, ecology, evolutionary biology, or a related field * Good knowledge of evolutionary and organismal biology and ecology * Ability to work independently while contributing actively to a collaborative research environment * Good command of spoken and written English

- Strongly valued * Strong quantitative skills, including use of R * Interest in field-based research and willingness to conduct extended fieldwork * Ability to communicate scientific results clearly in writing * Previous publications (not required, but an asset)

- Professional conduct and values * Commitment to high ethical standards in research and academic practice * Attention to quality, integrity, creativity, and cooperation in scientific work * Respectful and inclusive attitude toward colleagues, collaborators, and students

- Additional assets * Experience with lizard biology or reptile fieldwork * Knowledge of French (helpful for administrative matters and local integration, but not required)

HOW TO APPLY Applications must be submitted via UCLouvain's online recruitment platform NO LATER THAN 9 March 2026 (23:59, Brussels time). The following documents should be included as attachments: 1. A motivation letter 2. A curriculum vitae (CV) 3. A one-page (A4) description of a potential PhD research idea, outlining your proposed topic and how you would approach data collection and analysis 4. The contact details of 2-3 referees who can provide academic references

All applications will be reviewed by the selection committee as soon as possible after the closing date. Candidates who remain under consideration after the initial screening will be contacted regarding the next steps in the selection process. All applicants will be informed once a final decision has been made.

Contact: Simon Baeckens, Assistant Professor Earth & Life Institute, UCLouvain, Louvain-la-Neuve, Belgium Website: www.simonbaeckens.com Email: simon.baeckens@uclouvain.be

SUBMIT APPLICATION HERE: https://jobs.uclouvain.be/Personnelscientifique/job/PhD-Position-in-Evolutionary-Ecology/1289884901/ Simon Baeckens <simon.baeckens@uclouvain.be>

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UFreiburg TreeShrubGeneticDiversity

The Excellence Cluster Future Forests at the University of Freiburg invites applications for a *PhD position in Functional Tree Genetics & Genome Editing* (75%, TV-L 13), starting 1 May 2026.

The position is limited to 3.5 years. The application deadline is 2 March 2026.

The project aims to establish CRISPR/Cas-based genome editing in poplar to causally dissect the role of epigenetic regulation in stress resilience and stress memory under climate change scenarios. By combining genome editing, epigenome profiling, and quantitative stress phenotyping, we seek to identify predictive molecular markers of tree resilience.

The PhD candidate will:

* Establish CRISPR/Cas genome editing in poplar

* Generate and characterize mutants of epigenetic regulators

* Perform stress priming-challenge-recovery assays (drought Ã heat Ã biotic cues)

* Conduct molecular analyses (DNA methylation, chromatin marks, transcriptomics, hormone responses)

* Contribute to publications, conferences, and cluster activities

The position offers an interdisciplinary training environment bridging molecular plant physiology, forest genetics, and environmental signalling within the Excellence Cluster Future Forests, an internationally visible research center supported by the German Research Foundation.

Applicants should hold an M.Sc. (or equivalent) in plant sciences, molecular biology, biotechnology, forest sciences, or a related field, with strong interest or experience in functional genetics or genome editing. Experience working with poplar is advantageous. Excellent English skills are required.

The position includes structured doctoral training, dedicated project and career development funding, conference participation, and a collaborative, inclusive research environment.

Applications (cover letter outlining motivation and qualifications, CV, transcripts, and two references) must be submitted via the University of Freiburg application portal by 2 March 2026:

https://uni-freiburg.de/en/job/00004838/ For further information, please contact Jürgen Kleine-Vehn (juergen.kleine-vehn@biologie.uni-freiburg.de).

katrin.heer@forgen.uni-freiburg.de

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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>

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UGuelph CaribouMetagenomics

Msc Opportunity - Metagenomics and Metabarcoding for Caribou and Moose diets, at University of Guelph (Ontario, Canada) ?¿' Department of Integrative Biology Co-supervised by: Edeline Gagnon & Quinn Webber

Full ad available here: https://drive.google.com/file/d/1CpCkaSRESdb0zpeHC_96wbpJ5zMqveBJ/view?usp=drive_link We are seeking a highly motivated graduate student (MSc or PhD) to join a collaborative research project focused on developing and applying genomic tools to understand dietary partitioning between caribou and moose. Due to funding constraints, we are only accepting Canadian applicants at the moment to the position.

This project offers an exciting opportunity to help shape the future direction of our research program in collaboration with students from both the Gagnon and Webber labs, as well as academic and non-academic partners.

Application Instructions: Please consult the ad and assemble the requested elements into a single application as a single PDF to:

Dr. Edeline Gagnon (edeline.gagnon@uoguelph.ca) Dr. Quinn Webber (qwebber@uoguelph.ca)

Thank you for your interest. We look forward to hearing from you!

edeline.gagnon@gmail.com

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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>

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UMuenster EvoReproFishMHC

PhD Position

MHC in fish and human reproduction

Group of Prof. J. Kurtz, Institute for Evolution and Biodiversity at the University of Muenster, Germany

Research Assistant (m/f/d) (salary grade E 13 TV-L, 65 %)

This joint project together with Dr. Robert Peuß at the Institute of Integrative Cell Biology and Physiology will address the evolution and role of the Major Histocompatibility Complex (MHC, or HLA in human) for fertilisation and infertility. We combine the strengths of two fish species, stickleback and cavefish, exploiting their natural MHC variability together with analyses of human genomic datasets to identify HLA variants associated with infertility. Your tasks involve the genetic analysis and manipulation of stickleback MHC, using CRISPR-Cas technology, to conduct experiments on the role of MHC for spermatogenesis, sperm function, and gamete interaction. You will further be involved in the analysis of human whole exome sequencing (WES) data of infertility cases and controls.

The position is embedded in the DFG-funded Collaborative Research Centre 1748 'Principles of Reproduction'. The CRC 1748 involves scientists of the University, University Hospital, and Max Planck Institute Muenster as well as of the RWTH Aachen. Our central objective is to elucidate the genetic, molecular, and cellular mechanisms governing the formation and function of the testis, production and function of sperm, fertilisation, as well as early embryonic development - in both health and disease. To this end, we combine interdisciplinary research in molecular, structural, and cell biology as well as in physiology, biophysics, epi /genetics, (bio)informatics, and multimodal data analysis. The Kurtz group focuses on evolutionary ecology, including reproductive biology.

Our expectations: - Applicants must have the equivalent of a master's degree in biology, preferentially with a focus on evolution, molecular biology, reproductive biology or a related field. - A background, and ideally some experience, in any of the following areas will be useful: molecular laboratory skills, functional genomics and/or practical fish work. - Applicants should have excellent communication skills and be able to work both independently and as part of a multidisciplinary team. - The working language of the Institute and the lab is English, therefore good proficiency in spoken and written English is a requirement; a willingness to learn Germany is desirable.

Advantages for you: - Working in the highly collaborative environment of the CRC 'Principles of Reproduction' with access to state-of-the-art technology and datasets. - Benefiting from collaboration with another PhD student carrying out related work in the cavefish and with our external collaborator, Prof. Tobias Lenz (University of Hamburg), who is an expert on both fish and human MHC. - A unique opportunity to combine basic research in evolutionary ecology with applied research on human reproduction. - Appreciation, commitment, openness and respect - values which are important to us. - Our broad range of diverse work-time models offers great flexibility - also when working from home. - If you have family members or young children in your care, our Family Service Office offers concrete support to help you balance your private and professional responsibilities. - As an educational institution, we are deeply committed to offering occupational training and continuing education opportunities tailored to your individual needs. - From A - Z, Aikido to Zumba, our sport and health programmes ensure a healthy work-life balance. - As a university employee, you are entitled to numerous benefits afforded to public servants, e.g. an attractive company pension scheme (VBL), an annual end-of-year bonus and a position that is shielded from economic fluctuations.

The University of Muenster strongly supports equal opportunity and diversity. We welcome all applicants regardless of sex, nationality, ethnic or social background, religion or worldview, disability, age, sexual orientation or gender identity. We are committed to creating family-friendly working conditions. Part-time options are generally available. We actively encourage applications by women. Women with equivalent qualifications and academic achievements will be preferentially considered unless these are outweighed by reasons which necessitate the selection of another candidate.

Are you interested? Then we look forward to receiving your application via our career portal until Feb. 27, 2026

Here is the link: https://stellen.uni-muenster.de/jobposting/cb67e290fde74021cf11e5b7fa1fc1504a15ec080?ref=homepage Please include, in one pdf document: - Cover letter with a statement of research interest and motivation (max 1 page)

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Uppsala Sweden MolecularEvolution

A PhD student position in the Molecular Evolution program is now available, with supervisor Jennifer James. More information about her research can be found here: https://www.scilifelab.se/researchers/jennifer-james/. The position is fully funded for four years. The applicant will become a member of a newly established research group focussing on understanding the patterns and processes that shape genome and proteome evolution. We are excited to welcome you to the group!

Project description Understanding the mutational variation present in populations is a key goal of evolutionary biology. The amount and type of standing variation across the genome determines how well populations can adapt, and how susceptible they are to carrying slightly harmful mutations. However, much of our current analysis focusses on only one type of mutation, known as SNPs, which affect only a single nucleotide. The goal of this PhD project is to consider the effect of other types of mutation on population fitness, in particular, CNVs, which are genomic regions of intermediate size that are present in variable numbers of repeats across individuals in a population. This project will explore patterns of evolution in understudied categories of mutations to assess their effects across species, to understand how they change in copy number within a genome, and to uncover their potential role in adaptation.

Duties This PhD position will be entirely computational, focusing on the large-scale bioinformatic analysis of existing data from a range of species. The successful candidate will be responsible for the creation of bioinformatics pipeline to analyse genomic data, and to apply cutting edge methods to identify and characterise CNVs, and to calculate population genetics summary statistics. The student will then conduct comparative genomics analyses, to assess the likely effects of different types of mutations on fitness. The student will also explore how CNVs may increase of decrease in copy number over evolutionary time within a genome. Finally, the student will consider how to predict the effects that understudied categories of mutation have on fitness. Further specific research projects will be developed collaboratively with the successful candidate, depending on their project findings and research interests.

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

Candidates must be able to express themselves fluently in spoken and written English. We welcome candidates with a training in biology, or related fields (such as mathematics or computer science) as applied to biology. The applicant should also have an interest in learning, or previous experience in, computer programming, particularly using languages such as Python.

The ideal candidate is driven and a creative thinker, with a passion for discovery. We are looking for a person with excellent communication skills who will thrive in a collaborative environment but is also able to work on their own initiative. We're excited to support you in developing your skills and following your scientific interests.

Additional qualifications Prior experience in computational biology, bioinformatics or generally in computer programming is desirable. Experience working in population genetics and evolutionary biology/genomics or proteomics is also desirable. Experience with mathematical modelling and statistics will be considered advantageous.

Rules governing PhD students are set out in the Higher Education Ordinance chapter 5, çç 1-7 and in Uppsala University's rules and guidelines.

About the employment The employment is a temporary position according to the Higher Education Ordinance chapter 5 ç 7. Scope of employment 100 %. Starting date 2026-05-04 or as agreed. Placement: Uppsala

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

To apply, please go to: https://uu.varbi.com/what:job/-jobID:900807/ and apply through varbi. Please submit your application by 2026-03-02.

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: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal

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USussex TransposableElements

PhD Studentship Subject area: Genome biology and transposable elements University of Sussex

Project title: Evolutionary dynamics of transposable elements in the genome ecosystem of eukaryotes

Deadline: 7th March 2026

Link: https://www.findaphd.com/phds/project/-evolutionary-dynamics-of-transposable-elements-in-the-genome-ecosystem-of-eukaryotes/?p194471 Transposable elements (TEs) are small pieces of DNA that move (transpose) and replicate their sequences independently of typical cell division during mitosis and meiosis. As a result of their activity over evolutionary time, TEs comprise the majority of eukaryotic DNA, for example ~50% of the human genome and up to

80-90% of the genome of plants. Initially considered as junk DNA, it is now known that TEs fundamentally shape genome function and evolution by affecting gene expression, rewiring regulatory networks, and driving change in chromosome size and structure.

In recent years, research on TEs has accelerated with long-read sequencing and the exponential release of high-quality genomes, allowing comparisons at genome-wide level across the Tree of Life. In this project and by focusing on plants, the student will explore for the first time the relationship between different TE classes on the 'genome ecosystem' of their plant hosts at scale. TEs, like any other group of organisms, have a complex phylogenetic classification, and we aim to elucidate cases of conflict or cooperation as these arise when different TEs colonise the various niches of the genome, e.g. gene-rich regions, heterochromatic areas, or centromeres, and how this impacts genome function itself. Centromeres drive chromosome segregation during cell division, and are of particular interest because they form hotspots of TE invasion. How TEs invade centromeres is poorly understood, so we will analyse the sequence and folding of key TE genes across a large number of centrophilic and centrophobic TEs, aiming to pinpoint what drives convergent and recurrent centrophilia across TEs and hosts. The insights of this project are fundamental and central to further our understanding of the function and evolution of eukaryotic genomes.

This project will rely heavily on computational analyses, so experience on bioinformatics/informatics is required.

Please contact Dr Bousios directly via email (ab35@sussex.ac.uk) providing a CV and a cover letter explaining their interest and motivation in the project.

Alexandros Bousios, PhD Royal Society University Research Fellow

University of Sussex | UK

alexandros.bousios@gmail.com | email http://www.sussex.ac.uk/lifesci/bousioslab/ | www http://infspire.org/ | www alexandros bousios | Skype

Alexandros Bousios <alexandros.bousios@gmail.com>

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UZurich DolphinGenomics

Two 4-year PhD positions in dolphin genomics and behavioural ecology available at the University of Zurich

Overview: I am seeking two highly motivated PhD students for the Evolutionary Genetics Group of the Department of Evolutionary Anthropology, University of Zurich (www.michaelkruetzenlab.org). My group has broad interests in evolutionary genomics and behavioural ecology of delphinids and great apes. The work will be conducted together with our research collaborators at Shark Bay Dolphin Research (www.sharkbaydolphins.org).

The work will entail a combination of field work in Shark Bay, Australia, and genomic laboratory work at the University of Zurich. The positions are for four years, fixed term and will be remunerated according to UZH PhD salary scales, which include employer social security contributions. Start date for the PhD projects is to be May/June 2026.

Requirements: Successful candidates will have a Diploma/Masters degree in a relevant discipline, a strong interest (with prior experience) in preferably cetacean- or primate-focussed field work, bioinformatic skills, laboratory work, and evolutionary theory. The ideal candidates will have strong oral and written communication skills in English and the ability to work and share ideas in a collaborative environment. Knowledge of German language is not essential, but may help with everyday life whilst in Zurich.

The students will work in a dynamic research environment working on all aspects of evolutionary anthropology (www.iea.uzh.ch). Our department is well connected with numerous close collaborations within the Faculty of Life Sciences and many other international universities. The PhD positions will be embedded in the Zurich Life Science Graduate School's program in Evolutionary Biology (http://www.lifescience-graduateschool.ch/).

Applications: Interested students should send their application package to michael.kruetzen@iea.uzh.ch before 31March 2026. The package must include, in one PDF file: 1) A cover letter expressing research interests and experience relevant to the position

2) A complete CV

3) Contact details of two academic referees

Please also attach copies of your official academic transcripts and degrees, as well as copies of any publications and Diploma/MSc theses.

Informal enquiries can be addressed to:

Prof. Dr. Michael Krï¿½tzen

Department of Evolutionary Anthropology

University of Zurich

Winterthurerstr. 190

CH-8057 Zurich, Switzerland

Email: michael.kruetzen@iea.uzh.ch

Michael Krï¿½tzen <michael.kruetzen@iea.uzh.ch>

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Vienna EvolutionRainforestFrogs

Ph.D. opportunity in evolutionary ecology and ecotoxicology of rainforest frogs Position details: The candidate will be supervised by Assoc. Prof. Bibiana Rojas at the Konrad Lorenz Institute of Ethology, University of Veterinary Medicine Vienna, Austria, and co-supervised by one or more of the following project collaborators: Dr. Jérémy Lemaire (Department of Behavioral & Cognitive Biology, University of Vienna); Asst. Prof. Valeria Marasco (Research Institute of Wildlife Ecology, University of Veterinary Medicine Vienna); Dr. Andrius PaÅukonis (Institute of Biosciences, Vilnius University and Konrad Lorenz Institute of Ethology, University of Veterinary Medicine Vienna), depending on the focus of the PhD project. The position is fully funded by the Austrian Science Fund and includes a gross monthly salary of EUR 3,714.80 for full-time employment, adjusted pro rata to 30 hours per week, and research + travel expenses for 3 years. Position starting in April 2026.

Application requirements and procedures: MSc. degree in biological sciences and related field or an equivalent degree. Full proficiency in written and spoken English, statistical computing skills, strong interest in, and experience with, field research and animal behaviour. Physical and mental preparedness for intensive fieldwork and basic living conditions of tropical field research. Additional qualifications in the following areas will be also highly valued: experience in ecotoxicology and/or ecophysiology, landscape ecology, animal movement and behavioural analyses; scientific publishing and conference presentations, advanced computational skills, good knowledge of experimental design, experience in/with wet-lab work, tropical fieldwork, and/or animal husbandry. Ability to communicate in French is desirable. The application should be sent to bibiana.rojas@vetmeduni.ac.at no later than February 17th and should include a CV (no photo), the contact details of two referees who can provide recommendation letters (no letters needed at the initial stage), and a motivation letter written by the applicant stating their research interests and experiences. Interviews will be held online during the last week of February or first week of March.

Project summary: Artisanal and Small-scale Gold Mining (ASGM) is a tangible threat for Neotropical forests not only because of the associated small-scale deforestation but also because it is one of the main sources of mercury (Hg), an environmental contaminant of global concern due to its toxicity to wildlife. Despite its proven negative effects, studies on Hg contamination in the tropics lag behind those in temperate zones and have mostly focused on birds and fishes, which are associated to large bodies of water. Our recent findings, however, have revealed that high Hg concentrations can be found in phytotelmata, the ephemeral bodies of water contained in vegetation that multiple frog species use as breeding sites. The main aim of the project is to investigate the impact of Hg contamination on the life history, larval health and behaviour of an Amazonian poison frog species endemic of the Guiana Shield, an area with high occurrence of ASGM activities. For this, the candidate will design and carry out field-based behavioural assays as well as experiments under laboratory conditions that fall within the general framework of the project. The project involves, among others, several months of intensive fieldwork in French Guiana, rigorous ecotoxicological experiments in captivity, movement tracking and molecular work.

Main research fields: behavioural and evolutionary ecology, ecotoxicology, movement ecology, ecophysiology.

Contact: Assoc. Prof. Bibiana Rojas, bibiana.rojas@vetmeduni.ac.at https://bibianarojas.co/ Assoc. Prof. Dr. Bibiana Rojas Department of Interdisciplinary Life Sciences Konrad Lorenz Institute of Ethology University of Veterinary Medicine Savoyenstraße 1 1160, Vienna Austria

Virtual Meeting Room: https://vetmeduniwien.webex.com/meet/bibiana.rojas http://bibianarojas.co Bluesky: @biobiiana.bsky.social Tel: +43 (0) 1250777501

Rojas Bibiana <Bibiana.Rojas@vetmeduni.ac.at>

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WesternConnecticutStateU BioDiversity

WHERE: Western Connecticut State University, Danbury, CT, USA

WHAT: M.S. Studentship in Integrative Biological Diversity The M.S. in Integrative Biological Diversity at Western Connecticut State University (WCSU) develops environmentally responsible stewards who apply scientific thinking to conserve biological resources, manage biodiversity, and address concerns of stakeholders. Through coursework and individual projects, students will employ genomic, molecular, computational, and field-based skills to inventory and monitor organisms and to investigate how organisms adapt to changing environmental conditions. Expertise in the Biology Department at WCSU includes:

* environmental effects on fungal communities and pathogen evolution * vector-borne disease and prevention * fish ecophysiology * evolutionary ecology of plant mating systems * arachnid evolution, genomics, venomics, and phylogenomics * evolution and conservation of amphibians and reptiles * neurobiology of animal behavior and brain development * climate change education and outreach

The program requires the completion of a total of 30 credits in one of two options: a course-only or thesis-based degree. All students are required to complete an applied stewardship project in collaboration with a faculty mentor and external partner. The program is designed to complete in as few as 18 months, and summer and intersession courses are available. Students can enroll full-time or part-time.

Qualifications: B.S. or B.A. in Biology, Environmental Science, or a related program. The application should have an undergraduate cumulative average of 3.0 on a GPA scale of 1-4.

Application Deadline: March 15th for Summer or Fall admission.

Support: Teaching Assistant (TAF) and Graduate Assistant Fellowships are available every semester on a competitive basis. TAF students receive training in pedagogy and assist with instruction of undergraduate students enrolled in biology courses for non-majors. The application for TAF and GA fellowships can be found here and the deadline is March 15th.

How to Apply: Prospective students should submit transcripts, a 500-word essay explaining why they would like to join the program, and a completed application form to https://www.wcsu.edu/graduate/application/ . Contact Program Coordinators: ibdcoordinator@wcsu.edu Relevant Links: https://www.wcsu.edu/biology-msbiodiversity/ https://www.wcsu.edu/graduate/ MS Integrative Biological Diversity Program <ibdcoordinator@wcsu.edu>

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Jobs

AarhusU Denmark Bioinformatics

Tenure-Track Assistant Professor / Associate Professor in Bioinformatics and/or Computational Biology at Aarhus University, Denmark (https://nat.au.dk/en/about-the-faculty/vacant-positions-and-career/job/tenure-track-assistant-professor-associate-professor-in-bioinformatics-and-or-computational-biology-at-aarhus-university-denmark)

A position as Tenure-Track Assistant Professor or Associate Professor in Bioinformatics and/or Computational Biology is available from September 1, 2026, at the Section for Bioinformatics and Computational Biology (BiRC), Department of Molecular Biology and Genetics (MBG), Aarhus University (http://birc.au.dk), Denmark.

The application deadline is 7 April 2026.

The position:

We seek a highly motivated researcher in bioinformatics and/or computational biology to complement and expand our current research portfolio and teaching activities. We welcome applicants within all areas of bioinformatics and computational biology with a strong focus on development of computational and statistical methods, particularly within machine learning and artificial intelligence. The applicant must have earned a PhD degree and have demonstrated excellence in research and scholarship within the field of interest.

As an assistant professor in a tenure track position, you are expected to develop an independent and competitive research program, and you will be offered local mentoring during the tenure track period. Start-up funds to establish a competitive research program are negotiable. In case of more senior applicants, a position as associate professor will be considered.

As a researcher at MBG, you will be part of a vibrant, collaborative and international research environment. Internal communication and teaching are primarily conducted in English and international candidates are therefore not required to learn Danish. BiRC and MBG aim to be an attractive and inspiring workplace for all, and we view equality and diversity as assets. Aarhus University offers a broad variety of services for international researchers and accompanying families, including relocation service and career counselling to expat partners. English is spoken with high proficiency by most Danes, which will ease the arrival and integration of international applicants.

Job description:

The candidate is expected to:

- Establish and lead his/her own research team.

- Define, conduct and deliver a competitive and innovative research programme at the highest international level.

- Engage in collaborations with other researchers at the department.

- Support translational and applied research in future applications, if relevant.

- Manage, develop and undertake teaching in courses for students in Bioinformatics at the Master and PhD levels with a focus on computational and statistical subjects such as programming, algorithms, machine learning, and artificial intelligence.

- Define and supervise projects for Master and PhD students.

- Attract external funding from national and international funding bodies, both independently and in collaboration with local colleagues as well as with external Danish and international collaborators.

- Show leadership by actively engaging in the administration and strategic development of the Department and to establish interdisciplinary collaborations with other relevant departments at Aarhus University.

- Mentor junior researchers with respect to applications for external funding and career development.

- Disseminate research to the outside world and, when relevant, engage in research partnerships with private and public-sector stakeholders

Who we are

BiRC is an interdisciplinary research centre that employs about 40 researchers and PhD students as an independent section of The Department of Molecular Biology and Genetics. The research at BiRC spans major areas of bioinformatics, and BiRC is involved in teaching and supervision of students on all levels from BSc to PhD. In particular, BiRC is responsible for the Master's program in Bioinformatics. Please refer to https://birc.au.dk/ and https://mbg.au.dk/ for further information about BiRC and MBG, and to https://nat.au.dk/ and https://www.au.dk/ for information on Faculty of Natural Sciences and Aarhus University, respectively.

What we offer

The department offers:

- well-developed research infrastructure, including access to computational infrastructure.

- an exciting interdisciplinary environment with many national, international and industrial collaborators.

- a workplace characterized by professionalism, equality and a healthy work-life balance.

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GEOMAR Kiel ProductivityConnectivityAlgae

*** Scientist Position: Productivity and connectivity of Baltic brown algae meadows ***

Location: GEOMAR Kiel, Germany

Funding: 100% full-time (TVöD E13, German public service)

Qualification: MSc or PhD

Required skills: Experience in molecular biology and population genomics

Duration: 2 years

Deadline: 01 March 2026

Start: 01 May 2026 or shortly thereafter

Link to apply: https://www.geomar.de/en/karriere/job-single-en/wissenschaftlerin-m-w-d-produktivitaet-und-genetische-konnektivitaet-von-braunalgenwiesen-in-der-ostsee GEOMAR Helmholtz Centre for Ocean Research Kiel is a foundation under public law jointly financed by the Federal Republic of Germany (90%) and the State of Schleswig-Holstein (10%). It is one of the internationally leading institutions in the field of marine research.

Through our research and our commitment to the transfer of knowledge and technology, we contribute significantly to the preservation of the function and protection of the ocean for future generations.

The research unit 'Experimental Ecology' investigates how coastal ecosystems respond to climate change. Important model organisms in our research unit are brown macroalgae which form productive and biodiverse ecosystems in temperate coastal regions. In the German exclusive economic zone of the Baltic Sea, the serrated wrack /Fucus serratus/ and the sugar kelp /Saccharina latissima/ form dense meadows at up to 15 m depth. However, recent anthropogenic changes such as eutrophication and ocean warming have drastically reduced the extent of brown algae in the Baltic Sea, potentially resulting in fragmented populations vulnerable to change, but harbouring unique genetic diversity. We combine field surveys, experiments in unique outdoor mesocosm systems (Kiel Outdoor Benthocosms, KOBs), and molecular analyses to provide a comprehensive view of ecosystems under change.

The research unit Experimental Ecology of the research division Marine Ecology is offering a position as a

Scientist (m/f/d) "Productivity and genetic connectivity of Baltic brown algae meadows"

starting on May 1^st , 2026 or as soon thereafter.

Project Description

The candidate is going to be part of the collaborative project ROVKA (ca. 10 participants) that aims to (i) understand the blue carbon potential of brown algae meadows in the Baltic Sea, to (ii) identify areas of increased need for protection and to (iii) develop standards of monitoring and restoration. To this end, we aim to conduct a mesocosm experiment with near-natural assemblages of /F. serratus/ and /S. latissima/ to quantify carbon fluxes at modified irradiance and temperature conditions over the course of a year. In addition, we aim to identify vulnerable vs. potential donor populations in the German exclusive economic zone of the Baltic Sea for protection and restoration, respectively. We aim to explore the genetic diversity and connectivity within and between shallow and deep populations to assess their vulnerability. Together, these results will provide a baseline for future monitoring activities and allow informed decisions on the protection and restoration of brown algae habitats.

Position

The successful candidate will (i) design and conduct population genetic surveys and analyses for diversity, structure and connectivity of Baltic brown algae populations, and (ii) supervise regular sampling and maintenance of mesocosm and additional laboratory experiments.

Qualification

Essential

* MSc in evolutionary biology, marine biology, or relevant discipline * Expertise in state-of-the-art molecular biology lab techniques (e.g. nucleic acid isolation, WGS library preparation, RADseq) * Expertise in population genomic analysis of WGS or RADseq data using bioin-

formatic and statistical approaches (e.g. Bash and/or Python, R) * Strong publishing record in peer-reviewed journals and presentations at scientific conferences * Fluency in English both written and spoken

Preferred

* Doctorate (PhD) in evolutionary biology, marine biology, or relevant discipline * Experience working with marine macrophytes * Experience working on biogeochemical cycles * Experience with planning and conducting field work * Driver's license class B or higher

At a workplace, directly on the Kiel Fjord with many leisure and recreational opportunities, we offer you:

* Good conditions for work-life balance: We offer, among other things, the possibility of mobile working and individual working time arrangements, vacation courses for the children of our employees, and good support in finding a place in a daycare center at the Kiel site * Support services for professional and personal life situations

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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>

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NHM Copenhagen CuratorMollusca Deadline30-3-26

Tenure Track Assistant Professor and Curator of Mollusca Natural History Museum Denmark Faculty of Science University of Copenhagen

The Natural History Museum Denmark wishes to appoint a Tenure Track Assistant Professor and Curator of Mollusca (squid, octopus, clams, slugs and snails) with a great vision for natural history museums in a changing world. Duties are divided equally between collection-based research and other museum duties including curation, digitization of the Mollusca collections, research-based teaching and supervision of students, and public engagement work, and to act as the museum's liaison with relevant Danish natural history communities.

The successful applicant will be expected to establish and develop an externally funded collection-based research programme/group Mollusca and publish in influential journals. The successful applicant will be expected to curate the museums historically important Mollusca collections (200,000 specimens) as well as other marine invertebrate collections.

We value collaboration across disciplines and professions. All applicants are expected to demonstrate interdisciplinary thinking and a commitment to working together to create solutions to global challenges. This also goes for collection work. Curators develop the collections that they are responsible for through research, field work, loan activities, digitization, acting as scientific host for visiting researchers, and increasing accessibility for everyone.

All curators at the Natural History Museum Denmark are expected to take a leading role in society as advocates for science and nature, creating impact at all levels while actively promoting the museum's Vision and Values (https://snm.dk/en/about-museum). Further details of qualifications required for appointment at the museum are detailed below.

The position is available starting 1 January 2027, or as soon as possible thereafter.

Qualifications

Applicants at the tenure track assistant professor level are expected to have an academic record demonstrating the potential to deliver high profile internationally competitive research in the area of specialization. They should be a scientific specialist in one of the collection areas of the museum and have experience with collection-based research. Previous curatorial and university teaching experience would be advantageous but is not a requirement at the time of hiring for tenure-track assistant professors. A documented interest in and a vision for public engagement and community-based activities, such as citizen science, is essential.

Assessment of applicants

Assessment of applicants will primarily consider their level of documented, internationally competitive research as well as their curatorial experience and potential to curate one or more of the museum's collections. The ability to attract external funding will be considered together with outreach qualifications. Teaching qualifications are not mandatory, but documented teaching qualifications and teaching experience will be considered. The overall fit for the Natural History Museum will also be considered.

Ideal applicants will have the following qualifications:

An outstanding reputation for high-quality research within Mollusca A proven track record of interdisciplinary research Scientific expertise that ensures ability to curate Mollusca collections held by the museum Curatorial experience of natural history collections Experience from a natural history museum or similar A record of scientific use of museum collections and/or data A vision for how digital, genomic, and other new technologies will drive advances in natural history science A proven ability to work at a strategic level A proven track record of public engagement and creating impact beyond academia Experience working on museum exhibitions, interpretation, and public engagement Experience in fundraising and ability to attract research funding from external sources Supportive and performance-oriented people skills and commitment to an inclusive workplace that celebrates diversity and respect for everyone with equality and opportunity for all A passion for the vision and values of the Natural History Museum Denmark Excellent written and oral communication skills Confidence in ability to provide advocacy for the museum with multiple stakeholders

Six overall criteria apply for assistant professor appointments at the University of Copenhagen. The six criteria (research, teaching, societal impact, organisational contribution, external funding, and leadership) along with the museum-specific criterion, collections curation, are considered a framework for the overall assessment of c applicants. Furthermore, each applicant must be assessed according to the specific requirements stated in the job advertisement. Please read more at

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NHM UCopenhagen CuratorOfBryology

Tenure-track Assistant Professor and Curator in Bryology Natural History Museum Denmark University of Copenhagen

The Natural History Museum Denmark wishes to appoint a Tenure Track Assistant Professor and Curator of Bryology (mosses and allies) with a great vision for natural history museums in a changing world. Duties are divided equally between collection-based research and other museum duties including curation and digitization of the bryophyte collections, research-based teaching and supervision of students, public engagement work, and to act as the museum's liaison with relevant Danish natural history communities.

The successful applicant will be expected to establish and develop an externally funded collection-based research programme/group and publish in influential journals within bryology. The successful applicant will be expected to curate the museum's bryophyte collections (350,000 specimens).

We value collaboration across disciplines and professions. All applicants are expected to demonstrate interdisciplinary thinking and a commitment to working together to create solutions to global challenges. This also goes for collection work. Curators develop the collections that they are responsible for through research, field work, loan activities, digitization, acting as scientific host for visiting researchers, and increasing accessibility for everyone.

All curators at the Natural History Museum Denmark are expected to take a leading role in society as advocates for science and nature, creating impact at all levels while actively promoting the museum's Vision and Values(https://snm.dk/en/about-museum). Further details of qualifications required for appointment at the museum are detailed below.

The position is available starting January 1, 2027, or as soon as possible thereafter.

Qualifications

Applicants at the tenure track assistant professor level are expected to have an academic record demonstrating the potential to deliver high profile internationally competitive research in the area of specialization. They should be a scientific specialist in bryology and have experience with collection-based research. Previous curatorial and university teaching experience would be advantageous but is not a requirement at the time of hiring for tenure-track assistant professors. A documented interest in and a vision for public engagement and community-based activities, such as citizen science, is essential.

Assessment of applicants Assessment of applicants will primarily consider their level of documented,internationally competitive research as well as their curatorial experience and potential to curate one or more of the museum's collections. The ability to attract external funding will be considered together with outreach qualifications. Teaching qualifications are not mandatory, but documented teaching qualifications and teaching experience will be considered. The overall fit for the Natural History Museum will also be considered.

Ideal applicants will have the following qualifications: - An outstanding reputation for high-quality research within bryology - A proven track record of interdisciplinary research - Scientific expertise that ensures ability to curate bryophyte collections held by the museum - Curatorial experience of natural history collections - Experience from a natural history museum, botanical garden, or similar - A record of scientific use of museum collections and/or data - A vision for how digital, genomic, and other new technologies will drive advances in natural history science - A proven ability to work at a strategic level - A proven track record of public engagement and creating impact beyond academia - Experience working on museum exhibitions, interpretation, and public engagement - Experience in fundraising and ability to attract research funding from external sources - Supportive and performance-oriented people skills and commitment to an inclusive workplace that celebrates diversity and respect for everyone with equality and opportunity for all - A passion for the vision and values of the Natural History Museum Denmark - Excellent written and oral communication skills - Confidence in ability to provide advocacy for the Museum with multiple stakeholders

Six overall criteria apply for assistant professor appointments at the University of Copenhagen. The six criteria (research, teaching, societal impact, organisational contribution, external funding, and leadership) along with the museum-specific criterion, collections curation, are considered a framework for the overall assessment of applicants. Furthermore, each applicant must be assessed according to the specific requirements stated in the job advertisement. Please read more at

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

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NHM UCopenhagen CuratorOfLepidoptera

Tenure Track Assistant Professor and Curator of Lepidoptera at Natural History Museum Denmark

The Natural History Museum Denmark wishes to appoint a Tenure Track Assistant Professor and Curator of Lepidoptera (butterflies and moths) with a great vision for natural history museums in a changing world. Duties are divided equally between collection-based research and other museum duties including curation and digitization of the Lepidoptera collections, research-based teaching and supervision of students, public engagement work, and to act as the museum's liaison with relevant Danish natural history communities.

The successful applicant will be expected to establish and develop an externally funded collection-based research programme/group and publish in influential journals. We particularly encourage applications from applicants with a research specialization on Lepidoptera.

The successful applicant will be expected to curate the museum's historically important Lepidoptera collections (2 million specimens).

We value collaboration across disciplines and professions. All applicants are expected to demonstrate interdisciplinary thinking and a commitment to working together to create solutions to global challenges. This also goes for collection work. Curators develop the collections that they are responsible for through research, field work, loan activities, digitization, acting as scientific host for visiting researchers, and increasing accessibility for everyone.

All curators at the Natural History Museum Denmark are expected to take a leading role in society as advocates for science and nature, creating impact at all levels while actively promoting the museum's Vision and Values (https://snm.dk/en/about-museum). Further details of qualifications required for appointment at the museum are detailed below.

The position is available starting January 1, 2027, or as soon as possible thereafter.

Qualifications

Applicants at the tenure track assistant professor level are expected to have an academic record demonstrating the potential to deliver high profile internationally competitive research in the area of specialization. They should be a scientific specialist in one of the collection areas of the museum and have experience with collection-based research. Previous curatorial and university teaching experience would be advantageous but is not a requirement at the time of hiring for tenure-track assistant professors. A documented interest in and a vision for public engagement and community-based activities, such as citizen science, is essential.

Assessment of applicants Assessment of applicants will primarily consider their level of documented, internationally competitive research as well as their curatorial experience and potential to curate one or more of the museum's collections. The ability to attract external funding will be considered together with outreach qualifications. Teaching qualifications are not mandatory, but documented teaching qualifications and teaching experience will be considered. The overall fit for the Natural History Museum will also be considered.

Ideal applicants will have the following qualifications:

- An outstanding reputation for high-quality research within Lepidoptera - A proven track record of interdisciplinary research - Scientific expertise that ensures ability to curate Lepidoptera collections held by the museum - Curatorial experience of natural history collections - Experience from a natural history museum or similar - A record of scientific use of museum collections and/or data - A vision for how digital, genomic, and other new technologies will drive advances in natural history science - A proven ability to work at a strategic level - A proven track record of public engagement and creating impact beyond academia - Experience working on museum exhibitions, interpretation, and public engagement - Experience in fundraising and ability to attract research funding from external sources - Supportive and performance-oriented people skills and commitment to an inclusive workplace that celebrates diversity and respect for everyone with equality and opportunity for all - A passion for the vision and values of the Natural History Museum Denmark - Excellent written and oral communication skills - Confidence in ability to provide advocacy for the museum with multiple stakeholders

Six overall criteria apply for assistant professor appointments at the University of Copenhagen. The six criteria (research, teaching, societal impact, organisational contribution, external funding, and leadership) along with the museum-specific criterion, collections curation, are considered a framework for the overall assessment of applicants. Furthermore, each applicant must be assessed according to the specific requirements stated in the job advertisement. Please read more at

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SimonsFoundation NY ScientificOfficer EcolEvol

Position Summary

The Life Sciences division of the Simons foundation focuses on fundamental research in ecology and evolution, especially at this interface, as well as plant biology. The foundation seeks a temporary Scientific Officer to join the Life Sciences team. The candidate will work closely with the EVP of Life Sciences to refine its strategies, oversee its grant pipeline and review process, work on research and analyses to support the program, contribute to Science Advisory Board communications, manage in-house workshops and annual meetings, participate in grant reviews, and provide general support as needed.

This full-time temporary position is expected to last one year. The position is based in our offices in New York City. For more information, visit www.simonsfoundation.org/careers . Essential Duties and Responsibilities:

- Collaborate with leadership to develop the strategic framework and objectives for grant-making programs in ecology, evolution and plant biology.

- Conduct research and analysis to refine the team's strategy, which may involve desktop research, pulling external datasets, primary data collection, analyzing and visualizing data, and drafting memos and presentations.

- Assist with strategic thinking to increase pathways to science in ecology and evolution, advance scientific collaboration and data sharing, and to identify opportunities to partner with other organizations

- Actively participate in the planning and convening of workshops, meetings and retreats by preparing materials such as agendas, performing background research to identify participants and prepare meeting materials, assisting in running events, and performing other administrative tasks as necessary.

- Support EVP in engaging with its Science Advisory Board (SAB).

- Manage a selection of active grants, including tracking milestones and reviewing reports. Work with grantees to identify and resolve challenges.

- Participate in the evaluation of proposals, as necessary.

- Partner with grants management staff to effectively steward proposals and grants through the grantmaking cycle and provide support, as needed.

- Collaborate with the grant management team to implement no-cost extensions, amendments, and other grants management activities as needed.

- Support or lead in translating grant information to the communications team, board reports, and other purposes.

- Pull and analyze grant and grantee data to inform grants management, portfolio assessment, external presentations, and SAB communications.

- Cultivate prospective grant proposals selected by the Life Sciences team, working with prospective grantees from concept note, proposal and budget draft, external review, revision to SAB recommendation.

- Support administrative and other tasks for multiple RFPs, such as aiding in research and memo drafting.

- Partner with the EVP to design, develop, and manage standard and ad-hoc reports that demonstrate program outcomes.

- Travel to attend on-site meetings of grantees, annual retreats and institutional visits of Simons grantees, and external scientific conferences and meetings to keep current on scientific updates/advances relevant to portfolio

- Perform other duties or tasks as assigned or required

MINIMUM QUALIFICATIONS

Education

- A Ph.D. in ecology, evolution or a related field

Experience

- Minimum of three years of postdoctoral experience integrating ecological and evolutionary dynamics.

- Deep familiarity with contemporary and historical literature in the fields of ecology and evolution, and experience generating conceptual syntheses that bridge ecology and evolution through meta-analysis, data mining and/or theory.

- Comfort evaluating projects and scientific output spanning genes to organisms to ecosystems, using laboratory, field-based and theoretical approaches

- Breadth of experience across approaches (e.g., international field experience, laboratory, experimental evolution) and systems (e.g., plants, animals, microbes) at different biological scales (e.g., genes to communities) with multidisciplinary tools.

Related Skills & Other Requirements

- Expertise in genomic methods, statistical methods and experimental design.

- Excellent interpersonal and communication skills, demonstrating a high level of independent judgment, tact, and diplomacy.

- Ability to prioritize tasks and work independently and as part of a team.

- Flexible, creative, solution-oriented approach to problem-solving.

- Must be detail-oriented

- Excellent written and verbal communication skills, including the ability to convey complex concepts concisely

- Strong analytical and organizational skills to lead or assist in project management and analyses.

- MS Office (Word, Excel, Outlook, Power Point).

- Ability to generate graphics for presentations using any preferred packages.

- Smart Simple grants management platform knowledge helpful but not required.

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StonyBrookU FellowChangeAdaptation

Dear Colleagues,

The Department of Ecology and Evolution (https://www.stonybrook.edu/ecoevo/) at Stony Brook University invites applications for a PRODiG Plus Fellow in "Ecological and Evolutionary Responses to Global Change". The Department of Ecology and Evolution provides an excellent environment for research and creative activities, and we encourage applicants from all subfields whose interests and activities align with the PRODiG Plus Fellows program to apply.

Brief Job Description (link to the full ad provided below): The Department of Ecology & Evolution at Stony Brook University is recruiting a PRODiG + Fellow focused on ecological and/or evolutionary responses to global change. This broad area encompasses major global challenges, including climate change, biodiversity loss, habitat degradation, urbanization, pollution, and landscape fragmentation, and aligns with the Department's strategic priorities to advance research at the interface of ecology, evolution, and anthropogenic change. It includes evolutionary responses to shifting selective pressures, rapid environmental change, urban ecology, and novel ecosystems, as well as ecological dynamics shaped by human disturbance across spatial and temporal scales. A Fellow in this area could work across a range of systems and scales, using theoretical, quantitative, or experimental approaches, any taxa including plants, animals or microbes, with possible emphasis on conservation, evolutionary innovation, macroevolution, organismal biology, genomics, population and community dynamics, ecosystem function, invasion biology, spatial ecology, landscape ecology, or science education. Connections to affiliated programs like the Turkana Basin Institute, Centre ValBio, and the New York Climate Exchange offer additional opportunities for integration and impact.

The State University of New York (SUNY) Promoting Recruitment, Opportunity, Diversity, Inclusion and Growth Plus (PRODIG Plus) Fellows Program (https://www.suny.edu/prodig-plus/) program is designed to achieve two primary goals, (1) increasing the number and share of excellent diverse faculty committed to advancing diversity, equity, and inclusion; and (2) strengthening the pipeline for retention and support of these candidates. The SUNY PRODiG Plus Fellows Program offers full-time, 12-month, non-tenure-track faculty positions at the lecturer level. The fellow will be a part of a mentored research environment and, with successful performance and demonstrated contribution to inclusion, diversity, and equity, will be invited to join the tenure-track faculty at Stony Brook University after two years. The Fellow will receive a reduced teaching load (1 course each year) during the two-year initial appointment. The Fellow will be paired with a faculty mentor or mentoring committee upon appointment. Additional information on the PRODiGPlus Fellowship can be found at https://www.suny.edu/prodig-plus/fellowship/ . The application window ends soon (March 6, 2026). Here is the link for the official announcement, including the mission of the PRODiG Plus Fellows program and application requirements: https://apply.interfolio.com/178040 Best, Tara Smiley, on behalf of the search committee

Tara M. Smiley (she/hers) Assistant Professor Department of Ecology and Evolution < https://www.stonybrook.edu/ecoevo/ > Turkana Basin Institute < https://www.turkanabasin.org/ > Stony Brook University tara.smiley@stonybrook.edu | Smiley Lab Website < https://sites.google.com/stonybrook.edu/smileylab >

tara.smiley@stonybrook.edu

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UBristol Three EvolBiology

The School of Biological Sciences at the University of Bristol is advertising three Lecturer positions (equivalent to Assistant Professor).

We would be delighted to welcome new colleagues to join our collaborative community. For details on the position and the application process see: https://www.bristol.ac.uk/-jobs/find/details/?jobId=385935&jobTitle=-Lecturer%20in%20Biological%20Sciences Deadline: 8 March 2026

Please share this opportunity with anyone seeking a permanent academic position.

Beatriz Gonï¿½alves Senior Lecturer School of Biological Sciences University of Bristol

Beatriz Goncalves <beatriz.goncalves@bristol.ac.uk>

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

UDenver SeasonalFieldTech

Seasonal Field Tech, Velotta Lab:

Position Summary

The Velotta Lab in the Department of Biological Sciences is seeking to hire one seasonal field technician to assist with research on the ecology of deer mice (Peromyscus maniculatus) in Colorado and in collaboration with Nathan Senner's lab at the University of Massachusetts Amherst. The project is focused on understanding how deer mouse physiology and population dynamics are influenced by parasites and environmental variation. The field technician will assist with all aspects of fieldwork, with opportunities for learning research skills throughout the season. The technician will work closely alongside a PhD student at the University of Denver and another seasonal technician.

The position will run from April 15, 2026 - October 15, 2026. Airfare, shared field housing, food, all necessary equipment, and an hourly rate of $19.29/hour will be provided. To apply see: https://jobs.du.edu/en-us/job/-498599/seasonal-field-technician-velotta-lab This is a non-benefited position not to exceed 1,000 hours in a calendar year.

Essential Functions

Maintenance of a small mammal trapping grid.

Capture, handling, and tagging of deer mice.

Field physiology including respirometry (metabolic rate measurement).

Field behavioral trials.

Working in the plains and mountains in sometimes rugged terrain.

Work collaboratively and effectively to promote teamwork, and inclusiveness.

Required Qualifications

Interest in mammalian ecology, field biology, physiology, species interactions, and/or related fields.

Comfortable living and sleeping in close quarters with the team.

Comfortable working at high elevations in sometimes rugged terrain.

Strong work ethic, eagerness to learn fieldwork and research methods, and ability to work well on a team and independently in challenging physical conditions and sometimes stressful scenarios. Applicant must be adaptable, communicative, cooperative, and detail oriented.

Preferred Qualifications

Previous experience with fieldwork and following research protocols

Previous experience with small mammal trapping and handling

Familiarity with respirometry

Evidence of strong teamwork abilities

Physical Demands/Working Conditions

This position requires working in mountain environments in challenging physical conditions - including high elevation, bright sun, rain, snow, fog, and walking long distances.

The position requires lifting heavy objects (~50lbs) at high elevations.

Work Schedule

The position will run from April 15, 2026 - October 15, 2026.

Work hours may vary throughout the season, with efforts requiring both working early in the morning and late into the evening.

Application Deadline

For consideration, please submit your application materials by 4:00 p.m. (MST) February 24, 2026.

Special Instructions

Candidates must apply online through jobs.du.eduto be considered. Only applications submitted online will be accepted.

Salary Information

Airfare, shared field housing, food, all necessary equipment, and a stipend of $19.29 per hour will be provided.

The University of Denver has provided a compensation range that represents its good faith estimate of what the University may pay for the position at the time of posting. The University may ultimately pay more or less than the posted compensation range. The salary offered to the selected candidate will be determined based on factors such as the qualifications of the selected candidate, departmental budget availability, internal salary equity considerations, and available market information, but not based on a candidate's sex or any other protected status.

Benefits:

The University of Denver offers some benefits for non-benefited employees. The University of Denver is a private institution that empowers students who want to make a difference. Learn more about the University of Denver.

Please include the following documents with your application:

1. Resume

2. Cover Letter

The University of Denver is an equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex (including sex stereotypes, sex characteristics, sexual orientation, gender identity, and gender expression), marital, family, or parental status, pregnancy or related conditions, national origin, disability, or status as a protected veteran. The University of Denver does not discriminate and prohibits discrimination on the basis of race, color, national origin, ancestry, age, religion, creed, disability, sex (including sex stereotypes, sex characteristics, sexual orientation, gender identity, and gender expression), marital family, and parental status, pregnancy, genetic information, military enlistment, or veteran status, and any other class of individuals protected from discrimination under federal, state,

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UHawaii EvolutionaryBotany

Description

Title:Professor (Botany)

Position Number:0084189

Hiring Unit: College of Natural Sciences - School of Life Sciences

Location: University of Hawaiâat Manoa

Date Posted: February 5, 2026

Closing Date: Continuous recruitment until position is filled - application review beginsMarch 16, 2026

Salary Information: Commensurate with qualifications and experience

Monthly Type: 9-Month plus one month summer salary

Tenure Track: Tenure

Full Time/Part Time: Full Time

Temporary/Permanent: Permanent

Funding: General Funds

The School of Life Sciences, College of Natural Sciences at the University of Hawaiâat MaÌnoa (UHM), welcomes applications for a Professor (F-5) in Botany. The selectee would be eligible to apply for appointment as the Gerrit Parmile Wilder Chair in Botany which is a 5 year appointment. This is a tenure track, full-time, 9-month faculty appointment to begin approximately August 1, 2026 or as soon thereafter as possible, subject to position clearance, availability of funds, and satisfactory performance. The year 2025 marked the 75th anniversary of the GP Wilder Endowed Chair, made possible by a generous gift from the Wilder family, that has sustained the Botany Graduate Program's commitment to support the research of its faculty in the study of ecology, evolution and conservation of algal and plant communities.

We are searching for a highly creative and interactive scholar whose research will focus on plant or algal biology, including ecology, evolution, or conservation in Hawaiâor the Pacific Island region, with a strong track record of publications, extramurally funded work, professionalism in meetings and conferring with others, and who will contribute to the School of Life Sciences' aspiration to become a Native Hawaiian Place of Learning. The successful candidate will join an integrative life sciences program with broad interests in evolution, ecology, conservation, organismal biology, and molecular biology, offering undergraduate and graduate degree programs in Biology, Botany, Microbiology, Marine Biology, Cell and Molecular Biology, and Zoology.

The University of Hawaiâat MaÌnoa is a Carnegie Research 1 University with a strong emphasis on research as well as undergraduate and graduate education. As the flagship campus of the University of Hawaiâsystem, this vision of UHM is to be locally and globally recognized as a premier student-centered and community-serving university. Our campus welcomes all students but given our responsibilities to the community in which we operate, as part of our strategic mission, we strive to become a Native Hawaiian Place of Learning, a place that is committed to integrating Native Hawaiian language, culture and/or values into its academic and campus environment. For more information on the MÄnoa Strategic Plan, visit https://manoa.hawaii.edu/strategicplan/ .For more information on the School of Life Sciences, please visit https://manoa.hawaii.edu/lifesciences/ . Duties and Responsibilities:

- Building upon a vigorous extramurally funded research program
- Publishing scholarly works in leading academic journals
- Mentoring undergraduates, graduate students and postdoctoral scholars, and participating in graduate committees
- Developing and teaching courses related to their expertise for undergraduate and graduate students in the life sciences
- Serving on university committees
- Collaborating with scientists in the School of Life Sciences and the University of HawaiÊ≫i community
- Building collaborations with State and Federal agencies and making use of local resources (see below).

Minimum Qualifications:

A Ph.D. in an area of algal or plant biology, including ecology, evolution, or conservation biology or related areas, from an accredited institution.Have achieved the rank of Professor or four years of service as Associate Professor.Demonstrated ability in obtaining extramural funding. Evidence of research productivity through publication of scholarly materials. mentoring students. Demonstrated ability to work with and mentor students or varied backgrounds, with a demonstrated commitment to broaden participation as well as commitment to a safe campus environment. Demonstrated successful experience in teaching undergraduate and/or graduate courses in one or more aspects of algal or plant biology, including ecology, evolution, or conservation. Professionalism in meeting and conferring with others. Interest in developing and/or commitment to developing place-based research questions and teaching approaches in the context of UHM being a Native Hawaiian Place of Learning.

Desired Qualifications:

Research interests that complement existing strengths in the Botany Graduate program.Research experience and/or interest in developing

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UNacionalAutonomaDeMexico SystematicMalacology

Faculty Position. Systematic Malacology Institute of Biology. Universidad Nacional Autonoma de Mexico

https://www.ib.unam.mx/ibunam/Convocatoria_Inv_Malacologia_16Feb26.pdf The Universidad Nacional Autonoma de Mexico (UNAM, www.unam.mx) is the preeminent public higher-education center in Mexico and is among the highest-ranking Spanish-speaking and Latin American universities. UNAM's Institute of Biology is a research center on the University's main campus in Mexico City. Its mission is to discover, describe and systematically document biota, conducting scientific research about the evolutionary processes that originate and maintain it, its composition, distribution and interactions, and its sustainable use. The Institute of Biology houses the National Biological Collections of Mexico, including ten zoological collections, and the National Herbarium. Its Faculty include over 160 scientists and academic technicians who conduct research, teach and supervise undergraduate and graduate students, and participate in outreach activities, all to contribute to the understanding and conservation of biological diversity and to improve scientific advancement and the well-being of society.

To fulfill its mission, the Institute of Biology seeks qualified applicants for one tenure-track position as a full-time Research Scientist (Investigador/a Asociado/a C de Tiempo Completo) in the field of Systematic Malacology, in the Department of Zoology.

Candidate's profile: We seek a scientist to conduct research in systematic biology of Class Gastropoda (Mollusca) (e.g., species discovery and description, classification, phylogenetic relationships), applying innovative theoretical concepts and methodological tools for phylogenetic reconstruction with genomic data, or for comparative phylogenetics, to investigate evolutionary processes above the species level (e.g., morphological diversity and evolution, species richness, diversification, distribution), combining field work and use and development of biological collections.

Requirements: - Doctorate or Ph.D. degree in zoology, malacology, systematics or evolution. - Preferably with postdoctoral experience. - Knowledge and professional experience of at least 3 years in research in phylogenetic systematics and evolution of a group of Class Gastropoda (Mollusca). - Experience using or developing biological collections. - Experience in field work. - Ability to teach and supervise undergraduate and graduate students from UNAM's School of Science and Graduate Programs, as well as to participate in outreach and institutional activities. - Develop their own line of independent research, including procurement of funds for research, and interaction and collaboration with other research groups. - Non-native speakers must be fluent in the Spanish language. - Because this position is available through the Subprograma de Incorporacion de Jovenes Academicos de Carrera (SIJA) UNAM, aimed at incorporating early-career faculty, female applicants should be 39 years old or younger, and male applicants should be 37 years old or younger on the day of hire approved by the Consejo Tecnico de la Investigacion Cientifica (CTIC, Technical Council for Scientific Research).

Application and supporting documents: To apply, please send the following documents to sacademica@ib.unam.mx, with copy (Cc:) to secacad_vl@ib.unam.mx 1. Curriculum vitae (CV), including academic degrees, publication history and experience in systematics of Class Gastropoda. 2. Description of research conducted during at least the past 3 years (maximum 2 pages). 3. Research plan to be developed in one year, in the context of a longer research proposal, on the systematics and evolution a group of Class Gastropoda, preferably with a focus on groups distributed in Mexico (maximum 10 pages). 4. Cover letter addressed to the Director, Prof. Susana Magallon, stating the motives and interest in developing an academic career at the Institute of Biology, UNAM (maximum 2 pages). 5. Proof of age (birth certificate or passport). 6. Shortlisted candidates should provide 3 letters of academic recommendation.

Applications, accompanied by supporting documents, will be received from February 16th, 2026 until the close of this call, on April 13th, 2026 at 18:00 h (Mexico City time). Shortlisted candidates will be contacted to request recommendation letters, a seminar and a personal interview.

Contact: For any questions regarding this announcement, please contact the Office of Academic Affairs of the Institute of Biology at sacademica@ib.unam.mx and/or secacad_vl@ib.unam.mx.

"s.magallon@ib.unam.mx" <s.magallon@ib.unam.mx>

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

UNacionalAutonomaDeMexico SystematicOrnithology

Faculty Position. Systematic Ornithology Institute of Biology. Universidad Nacional Autonoma de Mexico

https://www.ib.unam.mx/ibunam/-Convocatoria_Inv_Ornitologia_21Feb26.pdf The Universidad Nacional Autonoma de Mexico (UNAM, www.unam.mx) is the preeminent public higher-education center in Mexico and is among the highest-ranking Spanish-speaking and Latin American universities. UNAM's Institute of Biology is a research center on the University's main campus in Mexico City. Its mission is to discover, describe and systematically document biota, conducting scientific research about the evolutionary processes that originate and maintain it, its composition, distribution and interactions, and its sustainable use. The Institute of Biology houses the National Biological Collections of Mexico, including ten zoological collections, and the National Herbarium. Its Faculty include over 160 scientists and academic technicians who conduct research, teach and supervise undergraduate and graduate students, and participate in outreach activities, all to contribute to the understanding and conservation of biological diversity and to improve scientific advancement and the well-being of society.

To fulfill its mission, the Institute of Biology seeks qualified applicants for one tenure-track position as full-time Research Scientist (Investigador/a Asociado/a C de Tiempo Completo) in the field of Systematic Ornithology, in the Department of Zoology.

Candidate's profile: We seek a scientist to conduct research in systematic biology of Class Aves (e.g., species discovery and description, classification, phylogenetic relationships), applying innovative theoretical concepts and methodological tools for phylogenetic reconstruction with genomic data, or for comparative phylogenetics, to investigate evolutionary processes above the species level (e.g., morphological diversity and evolution, species richness, diversification, distribution), combining field work and development of biological collections, including museomics.

Requirements: - Doctorate or Ph.D. degree in zoology, ornithology, systematics or evolution. - Preferably with postdoctoral experience. - Knowledge and professional experience of at least three years in research in phylogenetic systematics and evolution of a group of Class Aves. - Experience in field work. - Experience using biological collections, as well as interest and ability to continue the development of Mexico's National Bird Collection (Coleccion Nacional de Aves, CNAN). - Ability to teach and supervise undergraduate and graduate students from UNAM's School of Science and Graduate Programs, as well as to participate in outreach and institutional activities. - Develop their own line of independent research, including procurement of funds for research, and interaction and collaboration with other research groups. - Non-native speakers must be fluent in the Spanish language. - Because this position is available through the Subprograma de Incorporacion de Jovenes Academicos de Carrera (SIJA) UNAM, aimed at incorporating early-career faculty, female applicants should be 39 years old or younger, and male applicants should be 37 years old or younger on the day of hire approved by the Consejo Tecnico de la Investigacion Cientifica (CTIC, Technical Council for Scientific Research).

Application and supporting documents: To apply, please send the following documents to sacademica@ib.unam.mx, with copy (Cc:) to secacad_vl@ib.unam.mx 1. Curriculum vitae (CV), including academic degrees, publication history and experience in systematics of Class Aves. 2. Description of research conducted during at least the past 3 years (maximum 2 pages). 3. Research plan to be developed in one year, in the context of a longer research proposal, on the systematics and evolution a group of Class Aves, preferably with a focus on groups distributed in Mexico (maximum 10 pages). 4. Cover letter addressed to the Director, Prof. Susana Magallon, stating the motives and interest in developing an academic career at the Institute of Biology, UNAM (maximum 2 pages). 6. Shortlisted candidates should provide 3 letters of academic recommendation.

Applications, accompanied by supporting documents, will be received from February 23rd, 2026 until the close of this call, on April 20th, 2026 at 18:00 h (Mexico City time). Shortlisted candidates will be contacted to request recommendation letters, a seminar and a personal interview.

Contact: For any questions regarding this announcement, please contact the Office of Academic Affairs of the Institute of Biology at sacademica@ib.unam.mx and/or secacad_vl@ib.unam.mx.

s.magallon@ib.unam.mx

(to subscribe/unsubscribe the EvolDir send mail to 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>

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Other

Austria UGlasgow VolFieldwork May-Sep

Field assistant volunteer interns needed Field study of the Eurasian common lizard- Zootoca vivipara

Research interns are needed to assist in an ongoing study of reproductive modes of the Eurasian common lizard- Zootoca vivipara.

Z. vivipara is a small insectivorous lizard with a broad palearctic distribution- with both oviparous and viviparous lineages extant in its European heartland. We study the ecology- behaviour and evolution of this fascinating species using a unique natural experiment site based in southern Austria. The project is organised by an international team of researchers based at the University of Glasgow (UK) and the University of Ljubljana (SI) led by Professor Kathryn Elmer at the School of Biodiversity- One Health and Veterinary Medicine in Glasgow.

Internships will run between May and September 2025. We are looking for interns who can commit for an extended period- usually 2-3 months. In your application- note what dates you will be available.

We are seeking interns with an interest in herpetology- ecology and/or evolution and who are very keen for gaining experience in the field. Duties will include assisting in all aspects of fieldwork at the site- including but not limited to collection of wild lizards by hand or lasso- recording and measurement, care and husbandry, assisting with experiments- driving to and from field sites and other locations, and contributing to communal camping and household tasks. Full training will be provided. There may also be opportunity for leading or contributing to your own project within the team.

Fieldwork is physically demanding and will take place outdoors in a remote rural location- with fieldworkers based at a commercial campsite for the duration. Interns must be comfortable with living and working collaboratively with others in a small group and long-term camping; maintaining good relations with the team and local community is essential.

All main expenses (food- camping/accommodation fees, and other) and travel costs up to intra-European value will be covered. Travel insurance will be provided including urgent medical care. We can welcome team members from anywhere in the world- but interns are responsible for securing their own Schengen visa in advance- if that is needed. Please contact us to discuss specifics. Interns should provide their own tent- bedding, and outdoor clothing and personal equipment suitable for an extended field season in all weathers.

Essential skills & experience:

- Some background knowledge of topics in herpetology- ecology and/or evolutionary biology - Physically able and willing to work outdoors in challenging conditions (including inclement weather and traversing steep or boggy terrain) - Meticulous attention to detail and organisational skills- including data entry and sample organisation - Good interpersonal and team working skills - Scientific literacy and numeracy and familiarity with experimental design - Fluency in English

Additional desirable skills & experience:

- Academic qualification in a relevant biological discipline (BSc or equivalent) - Experience of animal care and husbandry- particularly in reptiles - Knowledge of/fluency in German (Italian and Slovenian also an advantage) - Drivers licence with significant driving experience

Applicants should send a cover letter (including aspects noted above) and CV along with the names and email addresses of two or more professional or academic references to: John.Smout@glasgow.ac.uk. Please mention on your application- if applicable, any prior experience working with lizards or other fieldwork experience.

Informal inquiries in advance of application are welcome.

Review of applications will begin 1 March 2026 and continue until a team is assembled; we plan on completing the decision by the end of March.

John.Smout@glasgow.ac.uk

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Callosobruchus samples

Looking for individuals of Callosobruchus maculatus. If anyone is working with them and is willing to send a few in order to start a lab culture, it would be greatly appreciated. Contact me at giuliasoff@bio.au.dk

Giulia Soffiantini Section of Genetics, Ecology and Evolution Aarhus University (DK)

Giulia <giulia.soffiantini97@gmail.com>

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Canada DipteranEntomologists

Hello everyone,

I am sending you some very worrying news concerning our Canadian entomologist colleagues. As part of a government plan to “reduce bureaucracy,” Agriculture and Agri-Food Canada has decided to eliminate the entire “Diptera” unit from the Canadian National Collection of Insects (CNC). The CNC is one of the largest and most important insect collections in the world. The disappearance of the unit specializing in Diptera would represent a major loss of scientific capacity, which is difficult to justify at a time when biodiversity and public health require greater expertise.

An open letter written by Art Borkent and David Grimaldi is currently circulating, calling for this decision to be reversed (I copied it below). It will sent to the Canadian Parliament and the press. To sign it, simply send an email to Art Borkent (artborkent@telus.net) by tomorrow (Friday, February 13) with your name and professional address.

Please feel free to share this information within your networks.

Best regards, Antoine Guiguet MaÃtre de Conférences Muséum National d'Histoire NaturelleUMR ISYEB 7205

Antoine Guiguet <antoine.guiguet@protonmail.com>

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GraduateExcellence ResearchGrants

The Society for the Study of Evolution (SSE) is pleased to announce the call for proposals for the 2026 Graduate Research Excellence Grants (GREGs), which consist of the R. C. Lewontin Early Award and the Rosemary Grant Advanced Award.

These grants provide funding for evolutionary biology research for Master's and PhD students. Applicants must be members of SSE. Grants of up to $2,500 USD will be awarded to R. C. Lewontin Early Award recipients, and up to $3,500 USD will be awarded to Rosemary Grant Advanced Award recipients.

Visit the website for further instructions, eligibility requirements, and guidance for writing your research proposal, including samples of previously funded proposals: https://www.evolutionsociety.org/content/society-awards-and-prizes/graduate-research-excellence-grants.html Deadline: May 18, 2026

SSE Communications <communications@evolutionsociety.org>

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InsectsJournal EvolPlantDefenseAgainstInsects

Dear Evoldir community,

I hope this email finds you well. Prof. Juan NÃÂºÃÂ±ez-FarfÃÂn and I have the pleasure of serving as Guest Editors for the Special Issue “Evolutionary and Ecological Mechanisms of Plant Defense Against Insects” in the open-access journal Insects. For those working on research about insects and their interactions with plants, we would like to extend a cordial invitation for you to contribute either an original research article or a comprehensive review to this Special Issue.

Further details about the Special Issue can be found below in this link: https://www.mdpi.com/journal/insects/special_issues/OF7LQRA5K9 The submission deadline is 31 October 2026, but accepted papers will be published online on an ongoing basis as soon as they are accepted. Please ensure that your submission is not under consideration elsewhere.

The article processing charge (APC) is CHF 2,600. If you are interested, please email zena.yu@mdpi.com (Zena Yu). Zena will address any inquiries you may have regarding submission and can also assist with any potential discount arrangements.

We sincerely hope you will consider this invitation, and we look forward to the possibility of your contribution.

Best regards,

Dr. Xosé LÃÂ³pez-Goldar and Prof. Juan NÃÂºÃÂ±ez-FarfÃÂn.

Dr. Xosé LÃÂ³pez Goldar (@XGoldar < https://urldefense.com/v3/__https://twitter.com/XGoldar__;!!HXCxUKc!0XDjtF8Abz_PZ2QQJRlxTMDEQT8PjOqN59UxA7fADKs3sbWczuFv9eDxavQwqgu.JhPDvLki70htQDa >) Assistant Professor in Evolutionary Ecology 125 S. Fell Avenue, Science Laboratory Building (SLB < https://maps.illinoisstate.edu/locations/science-laboratory/ >) School of Biological Sciences < https://biology.illinoisstate.edu/ > Illinois State University Normal, IL 61761 Email: xlopezg@ilstu.edu Website: https://goldarlab.weebly.com/

MountainLakeBiolStation EarlyCareerResearchOpportunity

Mountain Lake Biological Station (MLBS) welcomes applications to our Early Career Research Opportunity program! Join our vibrant and dynamic research community where you will gain access to an extensive range of facilities, equipment, databases, and other resources to support your career development. Funding is based on the length of your residency at the station, but recipients may receive up to 10 weeks of financial support that covers lodging, meals at our on-site dining hall, and lab/facility fees. Salaries are not covered. This is a great opportunity to collect pilot data for a grant proposal, develop new collaborations with other station users, and/or explore possibilities for a long-term research program at MLBS.

Applications are accepted on a rolling basis. To apply, please email the following documents to sandyk@virginia.edu:

1. Cover letter that includes the desired length of time and time of year you would like to visit MLBS 2. Short research plan (maximum of two pages) 3. Curriculum vitae 4. If you are conducting research on live vertebrates, a copy of an approved IACUC protocol from your home institution/organization

Please visit our website to learn more about MLBS (https://mlbs.virginia.edu/). Questions may be directed to the Associate Director, Sandy Kawano (sandyk@virginia.edu).

Sandy Kawano, PhD Associate Director of Mountain Lake Biological Station (MLBS) Director of MLBS Research Experience for Undergraduates (REU) program Assistant Professor of Biology, General Faculty she / her / hers

E brr3ph@virginia.edu

University of Virginia Department of Biology 485 McCormick Road P.O. Box 400328 Charlottesville, VA

22903

“Kawano, Sandy (brr3ph)” <brr3ph@virginia.edu>

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OmennPrize BestArticle EvolutionMediccine

Nominations for the $5000 Gilbert S. Omenn Prize are open now. The deadline is March 15, 2026. The nomination form takes only a minute to complete. Details at https://isemph.org/Omenn-Prize Please forward this invitation to all who might know about excellent articles in the area of evolution, medicine, and public health.

The Omenn Prize is awarded by the International Society for Evolution, Medicine, and Public Health https://isemph.org for the best article published in the previous calendar year on a topic related to evolution in the context of medicine and public health. The first author is invited, expenses paid, to present a plenary talk at the Society’s annual meeting. This year’s meeting will be July 28-31 in Kiel Germany. Abstracts for the meeting are welcome and due March 1.

The deadline for nominations for the Omenn Prize is March 15, 2026, but sooner is better. A direct link to the nomination form is below. https://airtable.com/appBV61kAMPLS9JU6/pagV3oO6FX9hian6y/form The winning article is announced in May and the prize is awarded to the first author of the article at the ISEMPH annual meeting. The prize includes travel, lodging, and an invitation to present at talk at the ISEMPH annual meeting. All peer-reviewed articles that use evolutionary principles to advance understanding of a disease or disease process are eligible. The prize committee will give priority to articles with implications for human health, but many basic science or theoretical articles have such implications. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome.

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

Randolph Nesse <nesse@asu.edu>

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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>

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Software AdmixturePopulationGenomics

Genome polarisation for admixture genomics

This is to announce the first official release of *diempy*, a python package for fast and reference-free genome polarisation.

The package is available on PyPi and easily installed using pip. A brief introduction, installation instructions, and API documentation are available on *read the docs*: https://diempy.readthedocs.io/en/latest/intro.html We provide an extensive and interactive tutorial that showcases all the features of *diempy* and outlines the basic workflow in Jupyter Notebook: https://github.com/-DerekSetter/tutorial-DiemPy. We recommend starting there.

The code for *diempy* is available open-source on gitHub: https://github.com/Studenecivb/diemPy Please, DO NOT REPLY to this email (of course). If you have any issues with the software or tutorial, please open an issue on github using the appropriate link above.

The associated manuscript is available as a preprint on bioRxiv https://doi.org/10.64898/2026.02.18.706591 Best regards,

Derek Setter

Konrad Lohse

Stuart J.E. Baird

StuartJEBaird <stuartj.e.baird@gmail.com>

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Software PopGeneJS BrowserBasedPopGeneticSimulator

Hello

PopGeneJS is a free web-based platform for teaching population genetics, offering 32 interactive modules covering drift, selection, mutation, migration, linkage, and mating systems.

Students and instructors can explore Wright-Fisher dynamics, F-statistics, De Finetti diagrams, and molecular summary statistics through real-time visualizations. No installation required?¿‘runs in any modern browser.

PopGeneJS modernizes PopGene.S (2005), expanding from 6 to 32 modules. Each includes help panels with formulas and references. A Python port is available for computational workflows.

Web: https://popgenejs.bioinformat.org Code: https://-/github.com/Bioinformat/popgenejs Paulo Nuin nuin@genedrift.org

nuin@genedrift.org

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UAberdeen EarlyCareerRecruitment Bursary

The Ecology < https://www.abdn.ac.uk/sbs/-research/clusters/ecology/ >, Evolution < https://-/www.abdn.ac.uk/sbs/research/clusters/evolution/ >, and Ecophysiology < https://www.abdn.ac.uk/-sbs/research/clusters/ecophysiology/ > Research Clusters within the School of Biological Sciences < https://www.abdn.ac.uk/sbs/ >, University of Aberdeen < http://abdn.ac.uk/ > (Scotland) are pleased to offer an Early Career Recruitment Bursary. We are specifically looking to attract talented early career researchers (ECRs) to enable travel for development of competitive fellowship applications. The University of Aberdeen, founded in 1495, is among the top 1% of oldest Universities worldwide, boasting excellence in environmental research and a location rich in cultural heritage and natural beauty.

What we are offering: We are offering bursaries to facilitate travel of ECRs to Aberdeen for a period of 1-3 weeks, to facilitate co-development of competitive fellowship proposals in collaboration with our existing researchers. We will support return travel and subsistence costs and invite applicants to submit a fully costed budget.

Application due date: 15 March 2026 for priority consideration; consideration will continue on a rolling basis afterwards.

Eligibility: You must be eligible for a target fellowship opportunity that you have identified and plan to pursue in Aberdeen. Potential fellowship opportunities include but are not limited to: NERC IRF < https://www.ukri.org/what-we-do/-developing-people-and-skills/nerc/nerc-fellowships/ >, Royal Society URF < https://royalsociety.org/grants/-university-research/ >, MSCA Postdoctoral Fellowships < https://marie-sklodowska-curie-actions.ec.europa.eu/-calls/msca-postdoctoral-fellowships-2026 >, among numerous other potential funders to be discussed with potential hosts (see below). You must furthermore be eligible to travel to the UK and to arrange any required visas prior to your visit. We can provide guidance on accommodation options and costs in Aberdeen.

Application process: Prior to submitting an application, you should reach out to at least one member of staff within the Ecology and Evolution or Ecophysiology Research Cluster (full list of eligible hosts can be found: here < https://www.abdn.ac.uk/sbs/research/clusters/ecology/ > and here < https://www.abdn.ac.uk/sbs/research/clusters/ecophysiology/ >) to establish a potential collaboration idea. You must then submit (1) your fellowship idea in writing (approximately 1 page), (2) an indicative budget for travel and subsistence, and (3) a copy of your CV, as email attachments in word or pdf format to the cluster chair, Prof Lesley Lancaster (lesleylancaster@abdn.ac.uk) on or before the deadline, using the subject heading "Cluster Bursary" when you submit.

Outcomes: We envisage supporting 2-4 bursaries this financial year subject to the availability of funding and the extent of interest. Outcomes will be communicated by the last week in March, and the planned travel must take place before June 30, 2026. Applications for later visits or which are received after the deadline will continue to be considered on a rolling basis, as future budgeting allows.

Informal inquiries can be directed to any eligible host (please follow links above) or to lesleylancaster@abdn.ac.uk.

The University of Aberdeen is a charity registered in Scotland, No SC013683.

Tha Oilthigh Obar Dheathain na charthannas clàraichte ann an Alba, Ã. SC013683.

"Fisher, David" <david.fisher@abdn.ac.uk>

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PostDocs

BCM Houston BioinformaticsEducation

Postdoc at Baylor College of Medicine (Houston, Texas)

Description: Baylor College of Medicine (BCM) has a postdoctoral position available in the laboratory of Dr. Erik Wright, who recently joined the Department of Molecular Virology and Microbiology (MVM). The length of the fellowship is for four years. As part of the Fundamentals in Bioinformatics (FunInBio) program, the Postdoctoral Associate will develop and present innovative bioinformatics educational materials to postdoctoral scientists and early career faculty in biological fields. The FunInBio curriculum surrounds a community science project about the environmental component of antibiotic resistance. This position provides an exceptional opportunity to hone teaching skills, master bioinformatics, and benefit the scientific community.

More information about FunInBio can be found here: https://reporter.nih.gov/project-details/11144035 Job Duties: - Develops and conducts a curriculum tailored to training biologists in bioinformatics. - Participates in iterative content revision based on participant feedback. - Hones teaching through in-person cohort sessions, at the Texas Medical Center or in the regional area. - Creates compelling online documentation for teaching bioinformatics. - Prepares survey reports, summaries, lesson plans, and perform quantitative analyses of outcomes. - Contributes to preparation of scientific articles reporting program findings, and present results at conferences such as ISMB (Education/Outreach tracks). - Maintains high level professional expertise through familiarity with the current scientific literature. - Interacts with facilitators in related programs, such as the Bioconductor project, EvolvingSTEM, or SEA-PHAGES. - Supports the FunInBio program and lab. - Performs other job-related duties as assigned.

Minimum Qualifications: - MD or Ph.D. in Basic Science, Health Science, or a related field. - No experience required. Preferred Qualifications: - MD or Ph.D. in biology, bioinformatics, computational biology, biomedical engineering, genomics, genetics, biotechnology, evolution, ecology, systems biology, epidemiology, biomedicine, or a related field. - Experience as an instructor or teaching assistant. - Strong interest in teaching and adult pedagogy is desired. - Demonstrable programming abilities is a plus.

To Apply: Informal inquiries can be directed to Dr. Erik Wright (Erik.Wright@bcm.edu). Formal applications can be submitted here: https://jobs.bcm.edu/job/Postdoctoral-Associate-Bioinformatics-Education/24335-en_US "Wright, Erik Scott" <Erik.Wright@bcm.edu>

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Eawag Switzerland AquaticEcologyEvolution

The call for the prestigious "Eawag-Postdoc", a 2-year postdoctoral fellowship at Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is open:

https://apply.refline.ch/673277/1335/pub/2/index.html

The deadline for applications is 5 April 2026. Please refer to the advert for details. The call is open for researchers in any field within the area of aquatic sciences, and we strongly encourage ecologist and evolutionary biologists to apply.

Information on Eawag's research departments can be found here: https://www.eawag.ch/en/about-us/portrait/organisation/research-departments/ Interested candidates have the opportunity to define their own research project at Eawag. The followship includes research support. Feel free to contact any of Eawag's research group leaders to discuss possibilities.

*** Christoph Vorburger Eawag, Swiss Federal Institute of Aquatic Science and Technology & Institute of Integrative Biology, ETH Zï¿½rich ï¿½berlandstrasse 133 8600 Dï¿½bendorf Switzerland

Phone: +41 58 765 5196 e-mail: christoph.vorburger@eawag.ch or vorburgc@ethz.ch group homepage: http://homepages.eawag.ch/~vorburch/ ***

"Vorburger, Christoph" <Christoph.Vorburger@eawag.ch>

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Edinburgh UK GenomicsAndBreeding

Hi,

We have two active applications for 3 year post-doc positions at The Roslin Institute in very exciting area with lots of opportunities for internal and external collaboration! Details below:

Postdoctoral Research Associate in quantitative genomics https://elxw.fa.em3.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1001/job/13616 Postdoctoral Research Associate in quantitative genetics and breeding https://elxw.fa.em3.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1001/job/13615 With regards!

Prof Gregor Gorjanc Chair in Selective Breeding, HighlanderLab Head, Quantitative Biology Division The Roslin Institute, University of Edinburgh, UK Industry Fellow, Royal Society edin.ac/highlander-lab | edin.ac/qb-division | roslin.ed.ac.uk

Apply to our new online MSc programme and individual courses in Data-Driven Breeding and Genetics edin.ac/pgt-data-driven-breeding-genetics

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

Gregor Gorjanc <Gregor.Gorjanc@roslin.ed.ac.uk>

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ETH Switzerland AdaptiveEvolution

A Postdoc position in Genomic signatures of adaptive evolution along the fast-slow life history continuum is open at the Swiss Federal Institute of Aquatic Science and Technology, an internationally networked aquatic research institute within the ETH Domain (Swiss Federal Institutes of Technology).

The position is part of the ERC Starting Project "Tipping dynamics and resilience in adapting ecological systems" aimed to understand how the capacity of populations to adapt influence ecological resilience. Within this project, the postdoctoral researcher will investigate how genomic signatures of selection vary along the fast-slow life-history continuum, with a particular focus on disentangling the relative contributions of coding and regulatory evolution to adaptive potential. To address this question, the postdoc will combine comparative genomic and phylogenetic approaches with exploratory analyses of both proximal and distal regulatory elements, including the use of emerging sequence-based genomic foundation models (e.g. DNABERT, AlphaGenome, etc).

We are looking for a motivated early-career researcher with a PhD in computational evolutionary biology or related field. Experience with comparative genomics and phylogenetic methods is required. The candidate should be comfortable working with large multi-species genomic datasets and have a strong conceptual background in evolutionary theory. Experience analyzing noncoding regulatory regions and an interest in regulatory evolution and life-history theory would be advantageous. Experience with, or interest in, modern sequence-based machine-learning approaches and genomic foundation models is an asset. The working language in the group is English; fluency in speaking and writing is required. The position is fully funded for two years (with possibility of extension to one more year) and is expected to start in Q2 of 2026.

Deadline for applications is 10 March 2026 or until the position is filled. Your application should include a letter explaining your research background and motivation to apply for this position, a CV, university diplomas, and the names and contact information for three references (all in one pdf file). For details about the position and how to apply, follow this link https://apply.refline.ch/673277/1341/pub/1/index.html Catalina.Chaparro@eawag.ch

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ETH Switzerland EvolDynamicsResilience

A Postdoc position in Experimental eco-evolutionary dynamics of resilience is open at the Swiss Federal Institute of Aquatic Science and Technology, an internationally networked aquatic research institute within the ETH Domain (Swiss Federal Institutes of Technology).

The position is part of the ERC Starting Project "Tipping dynamics and resilience in adapting ecological systems" aimed to understand how the capacity of populations to adapt influence ecological resilience. In this project, the postdoctoral researcher will design, conduct, and analyze an experimental evolution study to examine how adaptation contributes to demographic, population- and community-level resilience. Using plankton communities as a model system, the project will examine how plastic and evolutionary changes in life-history traits affect population and community resilience across a gradient of environmental stress.

We are looking for a motivated early-career researcher with a PhD in evolutionary biology, ecology, or a closely related field. Experience with experimental evolution is highly desirable, including lab work with micro/macro-organisms. A strong conceptual background in ecological and evolutionary theory, as well as strong data analysis skills are expected. The working language in the group is English; fluency in speaking and writing is required. The position is fully funded for two years (with possibility of extension to one more year) and is expected to start in Q2 of 2026.

Deadline for applications is 10 March 2026 or until the position is filled. Your application should include a letter explaining your research background and motivation to apply for this position, a CV, university diplomas, and the names and contact information for three references (all in one pdf file). For details about the position and how to apply, follow this link https://apply.refline.ch/673277/1340/pub/1/index.html Catalina.Chaparro@eawag.ch

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Freiburg ForestGenetics

The Professorship of Forest Genetics seeks to hire a *Postdoctoral Researcher (m/w/d)*

* Application deadline: March, 10th 2026 * Starting data: as soon as possible * Fulltime position

Our research team for Forest Genetics at the Albert-Ludwigs-Universität Freiburg investigates the genomic and epigenetic basis of adaptation and acclimation in temperate and tropical tree species. Our research is carried out in natural populations as well as in greenhouses and climate chambers, and we have experience collecting and analyzing genetic, genomic, phenotypic, and environmental data. We value collaborative, open, and respectful communication within our diverse and international team.

For our team, we are seeking a postdoctoral researcher with experience analyzing genomic datasets in non-model species and the motivation to work in tree genetics for the next 4-6 years. The postdoctoral researcher will have the opportunity to establish his/her own profile in forest genetics research and teaching and will be integrated into some of our ongoing research projects (https://uni-freiburg.de/enr-forgen/). After a training phase, you will also support the working group with data management on DataPlant (https://www.nfdi4plants.org/).

The position has a teaching obligation of four semester hours per week. This includes a course on bioinformatic analysis of genetic datasets for MSc students, which should be coordinated and taught independently. Contributions to a course on forest genetics lab and data analysis skills for MSc students and a lab practical course for BSc students are also expected.

Your profile

* You hold a very good Master's degree in biology, forest sciences, bioinformatics, or related fields, and have completed a Ph.D. in forest genetics or a closely related area. * You have experience in analyzing genomic data, especially RNAseq and whole-genome sequencing datasets. * You are experienced in lab work (e.g., DNA/RNA extractions) and ideally in running and analyzing qPCRs. * You are proficient in bioinformatic analyses (including HPCs), comfortable in Unix environments, and experienced with R; Python knowledge and willingness to learn new analysis pipelines are a plus. * Ideally, you are familiar with the challenges of working with non-model species. * You can carry out scientific work independently, as demonstrated by your publications. * You thrive in teamwork, collaborate effectively in diverse and international groups, and communicate openly and respectfully with colleagues. * You have experience teaching and supervising BSc and MSc theses, with good to very good teaching evaluations. MSc-level lectures and group communication are in English, so excellent English skills are required; good German skills are an advantage for administrative and BSc-level teaching tasks.

What we offer You will be integrated into our working group at the University of Freiburg. We are broadly interested in the adaptation and acclimation processes of trees, and in the genetic diversity and gene flow in tree populations in temperate and tropical regions. With several recently started large collaborative projects, including the Cluster of Excellence "Future Forests," the University of Freiburg is becoming a hub for forest science with many opportunities for national and international collaborations.

The position offers the possibility of scientific qualification. The postdoctoral researcher will be supported in writing his/her own research proposals. The salary follows the standard postdoctoral scale in Germany, including social security and health insurance.

Your application

Your application should include a letter of motivation, an academic CV (including an overview of your research and teaching activities, an overview of data analysis and software skills, and a publication record), copies of academic transcripts, and contact details for two academic references. Please upload the applicants as a single document to the application portal of the University of Freiburg (https://uni-freiburg.de/-stellenangebot/00004860).

Prof. Dr. Katrin Heer Forest Genetics Eva Mayr-Stihl Stiftungsprofessur für Forstgenetik Albert-Ludwigs-Universität Freiburg Fakultät für Umwelt und Natürliche Ressourcen

Bertoldstraße 17, 79098 Freiburg i. Br., Germany Phone: +49 761 203 3647 www.forestgenetics.uni-freiburg.de

Katrin Heer <katrin.heer@forgen.uni-freiburg.de>

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JohnInnesCentre UK HerbivoreMicrobeInteractions

Postdoctoral Researcher Salary:37,500 - 45,350 per annum depending on qualifications and experience. Contract:3 years, full-time Location:John Innes Centre,Norwich, UK. Closing date: 25 March 2026 Reference: 1006056

An opportunity has arisen for a Postdoctoral Researcher to join the newly appointed group of Dr Hassan Salem at the John Innes Centre in the Department of Molecular Microbiology.

About the John Innes Centre:

The John Innes Centre is an independent, international centre of excellence in plant and microbial sciences. We nurture a creative, curiosity-led approach to answering fundamental questions in bioscience, and translate that knowledge into societal benefits.Our strategic vision,Healthy Plants, Healthy People, Healthy Planet,sets out our ambitious long-term goals for the game changing impact of our science globally.

Our employees enjoy access to state-of-the-art technology and a diverse range of specialist training opportunities, including support for leadership and management.Click here to find out more about working at the John Innes Centre.

About the Salem Group:

The Salem Group studies the evolution, function, and adaptive consequences of herbivore-microbe symbioses. Our research focuses on how extracellularbacterial symbionts upgrade host digestive physiology, enable dietary specialization, thereby facilitating herbivory.

By integrating comparative and population genomics, symbiont transcriptomics, functional genetics, microscopy, and biochemical assays, we investigate how streamlined symbiont genomes maintain host-beneficial functions, how symbiont gene expression dynamically matches host nutritional demands, and how digestive symbioses originate and persist over deep evolutionary time. Our work aims to uncover general principles governing the emergence, maintenance, and evolutionary impact of obligate mutualisms.

We seek a postdoctoral researcher to lead mechanistic and multi-omics studies of obligate symbiosis, building directly on our recent work.

The Role:

Working as part of a team led by Dr Hassan Salem, and in collaboration across the Department of Molecular Microbiology, and the research groups of Dr.Aileen Berasategui (The Sainsbury Laboratory) and Dr. Tatsuya Nobori (The Sainsbury Laboratory) you will investigate the developmental basis of symbiosis in beetles.

This role will include:

Designing and conducting symbiont- and host-focused transcriptomic and genomic analyses, including tissue- and cell-type-specific approaches targeting symbiotic organs. Applying functional genetic tools to manipulate symbiont or host pathways (e.g., RNAi, heterologous expression). Reconstructing and testing symbiont-encoded metabolic pathways, linking gene content and expression to host physiology and performance. Using confocal microscopy, fluorescence in situ hybridization (FISH), and immunostaining to localize symbionts, host tissues, and gene expression patterns. Integrating evolutionary, ecological, and functional data to understand how symbiosis shapes host diet breadth, adaptation, and diversification. Disseminating results through high-impact publications, conference presentations, and mentoring of students.

The ideal Candidate:

You will have a PhD (or equivalent) in evolutionary genomics, molecular biology, microbiology, entomology, chemical ecology, or a related discipline.

The successful candidate will have:

Experience with RNA-seq, comparative genomics, or pathway-level analyses, ideally in host-microbe systems. Experience with or strong interest in functional genetic manipulation of insects (e.g., RNAi, CRISPR). Familiarity with confocal microscopy, FISH, and/or interest in spatial gene expression methods. Strong computational skills for biological data analysis (preferably R and/or Python). Demonstrated ability to develop independent, hypothesis-driven research at the interface of evolution and mechanism. You will also have excellent communication skills, experience mentoring students or visitors, and the ability to work both independently and collaboratively in an interdisciplinary research environment.

Additional information:

For further information and details of how to apply, please visit our website http://jobs.jic.ac.ukor contact the Human Resources team on 01603 450814 ornbi.recruitment@nbi.ac.ukquoting reference 1006057.

This role meets the criteria for a visa application, and we encourage all qualified candidates to apply. Where the successful applicant requires a visa, we will fund the costs for their visa and the Immigration Health Surcharge. Please contact the Human Resources Team if you have any questions regarding your application or visa options. We are an equal opportunities employer, actively supporting inclusivity and diversity. As a Disability Confident organisation, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this

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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 Investigacïï¿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>)

McMasterU Marine sedaDNA

Call for Applications Postdoctoral Fellowship in Sedimentary Ancient DNA (Marine sedaDNA Postdoctoral Fellow)

We invite applications for a full-time Postdoctoral Fellow (PDF) position associated with a new NSERC Alliance-funded collaboration between the McMaster Ancient DNA Centre and the Hakai Institute (Tula Foundation). This position will join a coordinated program to improve sedimentary ancient DNA (sedaDNA) methods and reconstruct past ecosystems from terrestrial permafrost and marine sediment archives, while helping to build the Canadian Ancient DNA (Can-aDNA) Network. This position will be a joint appointment between McMaster University (Hamilton, Ontario, Canada) and the Hakai Institute???s Ancient DNA Lab on Quadra Island, BC (Canada). You will work closely with Dr. Hendrik Poinar (McMaster University) and Dr. Tyler Murchie (Hakai Institute), alongside collaborators Dr. Duane Froese at the University of Alberta, Cooper Stacey at Natural Resources Canada, and other partner institutions such as the Yukon Government, the University of Victoria, and the University of British Columbia.

Project overview Our program aims to: - Experimentally improve/optimize sedaDNA workflows (extraction/purification, library preparation, capture enrichment, and metagenomic analysis) for terrestrial permafrost and marine sediments. - Use these improved methods to reconstruct long-term terrestrial and marine ecosystem dynamics across the Quaternary, focusing on Canadian relic permafrost deposits and Pacific marine cores around Vancouver Island and the Canadian Arctic. - Build the Canadian Ancient DNA (Can-aDNA) Network, a national platform for methodological sharing, training, and coordinated method comparisons/validation across Canadian ancient DNA labs.

Focus: Marine sediment cores from Barkley Canyon (deep sea) and Saanich Inlet (nearshore, varved sediments) among other sites with available cores (such as Howe Sound and seamounts in Queen Charlotte Sound) to reconstruct long and short-term marine biodiversity and food-web dynamics, and to develop improved marine sedaDNA protocols.

Example activities: - Lead sedaDNA work on archived cores from the Institute for Ocean Sciences and related repositories, spanning the late Pleistocene and Holocene. - Combine DNA metabarcoding, ddPCR, and hybridization capture to track changes in plankton, macrophytes, and fish communities through time. - Link sedaDNA signals to known oceanographic records (e.g., productivity, oxygenation, carbon cycling) and physical core stratigraphy. - Help benchmark and refine marine sedaDNA workflows for broader use in palaeo-oceanography and conservation applications.

Responsibilities - Lead an independent but collaborative research program within your thematic area (permafrost, marine, or bioinformatics), including experimental design, data generation, analysis, and manuscript preparation. - Mentor and collaborate with PhD candidates and other trainees working on related sedaDNA projects (with 1-2 PhD and/or MSc students). - Contribute to the Can-aDNA Network, including organizing and moderating online seminars, helping coordinate annual symposia, and engaging with the national community through the online forum. - Spend time at both the Hakai Institute Biodiversity Genomics facilities on Quadra Island, BC (near the city of Campbell River on Vancouver Island) and McMaster University (Hamilton, Ontario), and other collaborating institutions as needed. - Present research at national and international conferences and contribute to open, reproducible data and method sharing.

Qualifications Required: - PhD (completed or near completion) in a relevant field such as ancient DNA, molecular ecology, biomolecular archaeology, evolutionary genomics, bioinformatics, marine science, Quaternary science, or a related discipline. - Demonstrated experience with ancient or environmental DNA and/or high- throughput sequencing data, with contamination control for the wet-lab- heavy roles, or with large-scale sequence data analysis and pipelines for the bioinformatics role. - Strong quantitative, analytical, and writing skills, with evidence of peer-reviewed publications commensurate with career stage. - Ability to work collaboratively within a multi-institution, interdisciplinary team and to mentor junior trainees.

Preferred: - Background in marine ecology, oceanography, marine genomics, or sedimentary records; familiarity with metabarcoding, ddPCR, or marine monitoring data is an asset.

Terms and compensation - Appointment length: 2 years (with the possibility of extension subject to funding - Annual salary: CAD $70,000 plus benefits (provided in accordance with McMaster University guidelines.) - Postdoctoral fellows will be employees of McMaster University, working closely with and spending time at the Hakai Institute. - normal hours of work are 35 hours per week.

How to apply

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McMasterU PermafrostAncientDNA

Call for Applications Postdoctoral Fellowship in Sedimentary Ancient DNA (Permafrost sedaDNA Postdoctoral Fellow)

We invite applications for a full-time Postdoctoral Fellow (PDF) position associated with a new NSERC Alliance-funded collaboration between the McMaster Ancient DNA Centre and the Hakai Institute (Tula Foundation). This position will join a coordinated program to improve sedimentary ancient DNA (sedaDNA) methods and reconstruct past ecosystems from terrestrial permafrost and marine sediment archives, while helping to build the Canadian Ancient DNA (Can-aDNA) Network.

This position will be a joint appointment between McMaster University (Hamilton, Ontario, Canada) and the Hakai Institute's Ancient DNA Lab on Quadra Island, BC (Canada). You will work closely with Dr. Hendrik Poinar (McMaster University) and Dr. Tyler Murchie (Hakai Institute), alongside collaborators Dr. Duane Froese at the University of Alberta, Cooper Stacey at Natural Resources Canada, and other partner institutions such as the Yukon Government, the University of Victoria, and the University of British Columbia.

Project overview Our program aims to: - Experimentally improve/optimize sedaDNA workflows (extraction/purification, library preparation, capture enrichment, and metagenomic analysis) for terrestrial permafrost and marine sediments.

- Use these improved methods to reconstruct long-term terrestrial and marine ecosystem dynamics across the Quaternary, focusing on Canadian relic permafrost deposits and Pacific marine cores around Vancouver Island and the Canadian Arctic.

- Build the Canadian Ancient DNA (Can-aDNA) Network, a national platform for methodological sharing, training, and coordinated method comparisons/validation across Canadian ancient DNA labs.

Focus: Metagenomic analyses of terrestrial permafrost cores from the Yukon, Alaska, and other regions of northern Canada, using sedaDNA to reconstruct Quaternary ecosystems and test methodological optimizations for DNA recovery and authentication.

Example activities: - Work with permafrost cores from Canadian permafrost archives, including subsampling, DNA extraction, library preparation, and capture enrichment under strict ancient DNA protocols.

- Optimize workflows for DNA release from organo-mineral complexes, inhibitor removal, and library preparation efficiencies for highly degraded, low-abundance DNA.

- Apply and refine targeted capture approaches for plants, vertebrates, and other taxa to reconstruct past ecosystems and ecological transitions, including building in-house baits.

- Integrate sedaDNA results with stratigraphic, geochronologic, and palaeoenvironmental data to address questions about biodiversity change, extinction, and adaptation through glacial-interglacial cycles.

Responsibilities - Lead an independent but collaborative research program within your thematic area (permafrost, marine, or bioinformatics), including experimental design, data generation, analysis, and manuscript preparation.

- Mentor and collaborate with PhD candidates and other trainees working on related sedaDNA projects (with 1-2 PhD and/or MSc students).

- Contribute to the Can-aDNA Network, including organizing and moderating online seminars, helping coordinate annual symposia, and engaging with the national community through the online forum.

- Spend time at both the Hakai Institute Biodiversity Genomics facilities on Quadra Island, BC (near the city of Campbell River on Vancouver Island) and McMaster University (Hamilton, Ontario), and other collaborating institutions as needed.

- Present research at national and international conferences and contribute to open, reproducible data and method sharing.

Qualifications Required - PhD (completed or near completion) in a relevant field such as ancient DNA, molecular ecology, biomolecular archaeology, evolutionary genomics, bioinformatics, marine science, Quaternary science, or a related discipline.

- Demonstrated experience with ancient or environmental DNA and/or high-throughput sequencing data, with contamination control for the wet-lab-heavy roles, or with large-scale sequence data analysis and pipelines for the bioinformatics role.

- Strong quantitative, analytical, and writing skills, with evidence of peer-reviewed publications commensurate with career stage.

- Ability to work collaboratively within a multi-institution, interdisciplinary team and to mentor junior trainees.

Preferred: - Experience with permafrost, Quaternary geology, palaeoecology, or sedimentary archives; prior work with sedaDNA or ancient DNA strongly preferred.

Terms and compensation - Appointment length: 2 years (with the possibility of extension subject to funding.) - Annual salary: CAD $70,000 plus benefits (provided in accordance with McMaster University guidelines.) - Postdoctoral fellows will be employees of McMaster University, working closely with and spending time at the Hakai Institute.

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McMasterU SedimentaryAncientDNA

Call for Applications Postdoctoral Fellowship in Sedimentary Ancient DNA (Computational / Bioinformatics Postdoctoral Fellow)

We invite applications for a full-time Postdoctoral Fellow (PDF) position associated with a new NSERC Alliance-funded collaboration between the McMaster Ancient DNA Centre and the Hakai Institute (Tula Foundation). This position will join a coordinated program to improve sedimentary ancient DNA (sedaDNA) methods and reconstruct past ecosystems from terrestrial permafrost and marine sediment archives, while helping to build the Canadian Ancient DNA (Can-aDNA) Network. The position will be a joint appointment between McMaster University (Hamilton, Ontario, Canada) and the Hakai Institute's Ancient DNA Lab on Quadra Island, BC (Canada). You will work closely with Dr. Hendrik Poinar (McMaster University) and Dr. Tyler Murchie (Hakai Institute), alongside collaborators Dr. Duane Froese at the University of Alberta, Cooper Stacey at Natural Resources Canada, and other partner institutions such as the Yukon Government, the University of Victoria, and the University of British Columbia.

Project overview Our program aims to: - Experimentally improve/optimize sedaDNA workflows (extraction/purification, library preparation, capture enrichment, and metagenomic analysis) for terrestrial permafrost and marine sediments. - Use these improved methods to reconstruct long-term terrestrial and marine ecosystem dynamics across the Quaternary, focusing on Canadian relic permafrost deposits and Pacific marine cores around Vancouver Island and the Canadian Arctic. - Build the Canadian Ancient DNA (Can-aDNA) Network, a national platform for methodological sharing, training, and coordinated method comparisons/validation across Canadian ancient DNA labs.

Focus: Cross-cutting analytics and method development across permafrost and marine components, with an emphasis on metagenomics, de novo assembly, classification accuracy, and reproducible and sensitive pipelines. Develop AI or machine learning classification tools for low read abundance data and model accuracy and robustness of palaeoecological reconstructions (using serially sampled temporally discrete isolates).

Example activities: - Test and optimize pipelines for shotgun, capture-enriched, and metabarcoding sedaDNA data, including quality control, taxonomic assignment, phylogenetics, and community analyses. - Evaluate and compare metagenomic classifiers using simulated and empirical data to quantify false-positive and false-negative rates. - Explore machine-learning approaches for improved sedaDNA identification and ecological dynamics reconstructions. - Work with McMaster and Hakai's in-house high-performance computing infrastructure systems and bioinformatics teams to support the project's analytical needs.

Responsibilities - Lead an independent but collaborative research program within your thematic area (bioinformatics), including experimental design, data generation, analysis, and manuscript preparation. - Mentor and collaborate with PhD candidates and other trainees working on related sedaDNA projects (with 1-2 PhD and/or MSc students). - Contribute to the Can-aDNA Network, including organizing and moderating online seminars, helping coordinate annual symposia, and engaging with the national community through the online forum. - Spend time at both the Hakai Institute Biodiversity Genomics facilities on Quadra Island, BC (near the city of Campbell River on Vancouver Island) and McMaster University (Hamilton, Ontario), and other collaborating institutions as needed. - Present research at national and international conferences and contribute to open, reproducible data and method sharing.

Qualifications Required - PhD (completed or near completion) in a relevant field such as ancient DNA, molecular ecology, biomolecular archaeology, evolutionary genomics, bioinformatics, marine science, Quaternary science, or a related discipline. - Demonstrated experience with ancient or environmental DNA and/or high-throughput sequencing data, with contamination control for the wet-lab- heavy roles, or with large-scale sequence data analysis and pipelines for the bioinformatics role. - Strong quantitative, analytical, and writing skills, with evidence of peer-reviewed publications commensurate with career stage. - Ability to work collaboratively within a multi-institution, interdisciplinary team and to mentor junior trainees.

Preferred: - Strong skills in programming (e.g., Python, R, Bash, Machine Learning), high-performance computing, and metagenomic analysis; prior work with classifier benchmarking or machine-learning approaches is an advantage.

Terms and compensation - Appointment length: 2 years (with the possibility of extension subject to funding.) - Annual salary: CAD $70,000 plus benefits (provided in accordance with McMaster University guidelines.)

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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>)

Montpellier,Polyploidy

I am hiring a Postdoc to study how polyploidy affects sex chromosomes in the plant Silene latifolia, using bioinformatic analyses of RNA-seq and DNA-seq data.

Contract starting date: Between May and July 2026.

Contract duration: 18 months.

Deadline for application: March 24th, 2026.

Full details available on Euraxess: https://euraxess.ec.europa.eu/jobs/412961

For inquiries, please contact me at: aline.muyle@cnrs.fr

Thanks for your help in spreading it.

Best wishes,

Aline Muyle CNRS researcher Website < https://sites.google.com/view/muyle-lab/home > ÃÂquipe Stratégies Reproductives des Plantes (SRP) BÃÂtiment 22, Institut des Sciences de l'ÃÂvolution de Montpellier (ISEM) Université de Montpellier, campus Triolet, cc065 2 Place Eugene Bataillon 34095 Montpellier cedex 05 France ISEM Webpage < https://isem-evolution.fr/en/membre/muyle/ > Researchgate < https://www.researchgate.net/profile/Aline_Muyle > Linkedin < https://www.linkedin.com/in/aline-muyle-07157170/ >

<aline.muyle@cnrs.fr>

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NatlInstHealth VirusEvolution

Postdoctoral Fellow in Virus Evolution and Spillover

Organization

National Library of Medicine, Bethesda, MD and surrounding area

The Division of Intramural Research (DIR) at the National Library of Medicine (NLM) invites applications for a position as a Postdoctoral Fellow supervised by Dr. Martha Nelson.

About the position

The NLM is one of the 27 institutes at the National Institutes of Health (NIH). The NLM is the worldï¿½s largest biomedical library and a leader in research, development, and training in biomedical informatics and health information technology. The DIR within the NLM has two primary research areas: computational health research and computational biology. In computational health research, our efforts center on natural language processing (NLP), clinical image analysis, biomedical ontologies, information modeling, and clinical data analytics. In computational biology, we emphasize transcriptional regulation, chromatin and network biology, structural and functional analysis, sequence statistics, and evolutionary genomics. The post-doctoral scholar will study how rapidly evolving RNA viruses (e.g., H5N1 avian influenza, coronavirus) transmit and evolve at the human-animal interface, using advanced Bayesian phylodynamic approaches and large-scale genomic data. The post-doctoral scholar will perform data analyses within an interdisciplinary team of international scientists who conduct fieldwork, experimental studies, and statistical analyses on emerging pathogens. This position is strictly computational (no fieldwork or lab work required). This project is part of a longstanding government-academic partnership spanning multiple Federal agencies and academic institutions to study disease spillover between humans, wildlife, and livestock and identify successful intervention strategies to break transmission in real-world settings.

Position Overview: This is a full-time postdoctoral fellow position. The initial appointment will be for one year, and is renewable on a yearly basis, with extensions up to 5 years total. The NIH offers a competitive salary (based on postdoctoral experience, see stipend tables: https://www.training.nih.gov/stipends/) and comprehensive health insurance.

The NIH is dedicated to the continued education and career development of all its research staff. Candidates are subject to a background investigation. Additional information about NIH postdoctoral fellowships: https://www.training.nih.gov/research-training/pd/ Apply for this vacancy

What you'll need to apply

Prospective candidates should include "Post-doctoral Inquiry" and their last name in the email subject line. Applicants must submit the following materials to Dr. Martha Nelson at nelsonma@mail.nih.gov.

* Updated CV * Statement of research interest * Contact information for 3 references (please include the full name with titles, institute, email address and phone

number of each reference).

Application Deadline: Applications will be accepted until the position is filled.

Contact name

Dr. Martha Nelson

Contact email

nelsonma@mail.nih.gov

Qualifications

* Candidates should have or be close to obtaining a Ph.D. or equivalent degree in computational biology, computer science, bioinformatics, molecular biology, or a closely related field. * Candidates with experience using Bayesian approaches to phylodynamic analysis of virus populations (specifically BEAST software) are particularly encouraged to apply. * Fluency in R, python, or another programming language is essential. * Experience working with genomic data from pathogens (especially RNA viruses, e.g., influenza A virus) is essential. * Applicants must possess good communication skills and be prepared to work collaboratively on a fast-paced team of international scientists to inform time-sensitive outbreak responses.

Disclaimer/Fine Print

U.S. citizens and permanent residents are eligible to apply. NIH welcomes foreign nationals with the exception of individuals from this list < https://www.state.gov/countries-of-particular-concern-special-watch-list-countries-entities-of-particular-concern/
>.

"Nelson, Martha (NIH/NLM) [E]" <nelsonma@mail.nih.gov>

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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)

NorthCarolinaStateU PopGenetics

The Guerrero Lab at North Carolina State University has an open postdoc position. Research in the lab is focused on computational approaches to evolutionary genetics, with current interests in sex chromosome evolution, structural variation, and the genetic basis of sexual dimorphism. More information can be found at rguerrer.org

While the project will be shaped in part by the candidate's expertise, this position is ideal for someone with experience in quantitative approaches (programming, command-line bioinformatics, population genetics). The work will likely involve computational and mathematical modeling as well as the analysis of population genomic datasets.

Compensation will follow NIH pay scale. The initial appointment is for one year with expected renewal contingent on performance. The offer will include $3K/year for travel and up to $10K for independent research. The start date is flexible (Summer/Fall 2026).

To apply, please email (1) a CV and (2) a single paragraph describing how your research interests align with the lab to rfguerre@ncsu.edu by March 10, 2026. Review of applications will begin immediately after the deadline.

Rafael F. Guerrero Department of Biological Sciences North Carolina State University

Rafael Guerrero <rfguerre@ncsu.edu>

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PalackyU Czechia EvolutionaryBiogeography

Postdoc in BIOGEOGRAPHY and MACROECOLOGY (Olomouc, Czech Republic)

Dear all, We are seeking a highly motivated, productive and cooperative postdoctoral researcher to study biogeography and macroecology of species pools across biomes. We combine large-scale databases, citizen science data, fieldwork, and advanced computational approaches to analyze regional and local diversity of birds in forests and savannahs worldwide. We are keen on macroecology, biogeography, macroevolution, and modelling. We are seeking an ambitious postdoctoral researcher to strengthen our science and complement our team at the Department of Zoology, Palacky University in Olomouc, Czechia.

YOUR TASKS - Independent research: biogeographic, comparative, and phylogenetic analyses of global datasets of birds, linked to environmental, climatic, and geohistorical data - Lead writing and publishing high-quality papers - Active participation in shaping the collaborative effort of the project team

WE OFFER - Participation on an exciting eco-evo project, fully funded by the Czech Science Foundation - Work-life balance respecting and supportive environment, flexible working hours - Health insurance, employee benefits, and life in a pleasant and safe city - Competitive salary

YOUR QUALIFICATION AND SKILLS Essential - Ph.D. in evolutionary biology, ecology, zoology or a related discipline - Strong publication record in high-quality journals in biogeography, evolutionary biology, ecology or a related field (appropriate for a career stage) - Experience in state-of-the-art analysis of ecological and evolutionary data - Scientific curiosity, independent and conceptual thinking, and team spirit - Excellent command of English, both written and spoken - Proficiency in R language programming and strong quantitative skills

Desirable - Demonstrated knowledge of advanced biogeographic, comparative, and phylogenetic methods, quantitative methods in biodiversity studies, GIS in R, and spatial statistics - Experience with process-based models in ecology and biogeography - Knowledge of other programming languages (Julia, Python) and cluster- based computing

APPLICATION PROCEDURE For informal enquiries and application, email to prof. Vladimir Remes at vladimir.remes@upol.cz. To apply, send one PDF file (max. 5 MB) including your CV, list of publications, a short cover letter stating your previous work, qualification and motivation, and names and e-mails of two references. Please, state “Postdoc search” in the subject line of your e-mail.

APPLICATION DEADLINE AND STARTING DATE Review of applications will start 15 March 2026. Selected applicants will be interviewed in late March. The starting date is August 2026, and the position is available for up to 28 months (until the end of 2028).

Best regards,

Vladimir Remes Department of Zoology Palacky University in Olomouc Czech Republic https://vladremes.github.io Vladimír Reme <vladimir.remes@upol.cz>

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PennsylvaniaStateU PopulationFunctionalGenomics

A Postdoctoral Scholar appointment is available in the López-Uribe lab (www.lopezuribelab.com) at The Pennsylvania State University to work on an NSF-funded project investigating sensory biology evolution in pollinators. The person in this position will be responsible for genome assembly and annotation, as well as the detection of signatures in olfactory receptors. The postdoc is expected to complete the work and disseminate results via peer-reviewed publications within the timeframe of the position. There will also be opportunities to engage in outreach and to transfer research outputs from this project to the general public. Evidence of bioinformatic skills is required for the position. The candidate should demonstrate a strong publication record, as well as evidence of effective teamwork and student mentoring.

Qualified candidates are required to have a Ph.D. in biology, evolutionary biology, bioinformatics, or related fields of study. The successful candidate must have completed all PhD degree requirements by the appointment date. The applicant must have strong bioinformatics skills and experience analyzing genomic data. The person in this position will be involved in grant writing, mentoring graduate and undergraduate students, and outreach activities. The position is open to anyone with the legal ability to begin working in the US. This position will be located at Penn State in University Park, PA (Penn State's main campus). Applications will be reviewed by March 1st, 2026.

Interested applicants should submit the following documents:

(1) a brief statement (up to 2 pages) describing relevant previous research experience and interests in working in the lab and as part of this project. Please address point-by-point how your previous experience relates to the responsibilities detailed in the job description.

(2) curriculum vitae (include experience in both research and outreach/extension)

(3) contact information for three references willing to provide letters of recommendation.

Please send any questions regarding the position to Margarita López-Uribe (mml64@psu.edu) with the subject line: "Postdoctoral Scholar Appointment in Population and Functional Genomics". This position will be open until a suitable candidate is found.

To apply and find more details about the position, please visit this website:

REQ_0000075202 Postdoctoral Scholar in Population and Functional Genomics < https://psu.wd1.myworkdayjobs.com/en-US/PSU_Academic/job/Postdoctoral-Scholar-in-Population-and-Functional-Genomics_REQ_0000075202-1 >

For

Margarita M. López-Uribe Preferred pronouns: she/her/hers Associate Professor Department of Entomology Lorenzo L. Langstroth Early Career Professor Pollinator Health Extension Specialist Intercollege Graduate Degree Program in Ecology Institute of Energy and the Environment Fellow The Pennsylvania State University

website: http://www.lopezuribelab.com/ twitter: @lopezuribelab

If you would like to set up a time to meet, here < https://calendar.app.google/MpHQ19CFChgB3iEH8 > is my availability

"I acknowledge that Penn State University occupies the ancestral lands of the Susquehannock peoples. In acknowledging this, I reaffirm my commitment to dismantling the legacies of settler colonialism and the exclusion and marginalization of Indigenous peoples from this land."

Margarita M Lopez-Uribe <mml64@psu.edu>

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SLU Umea ForestComputationalGenomics

Postdoctoral opportunity in forest tree genomics and population genetics

Join us in uncovering the evolutionary genomics of forest tree species through cutting-edge computational approaches.

About the position

UmeÃ¥ Plant Science Center is offering a 2-year postdoctoral scholarship in the newly established McEvoy Lab to study the genomics of forest trees with a focus on evolution and adaptation using computational approaches. We seek a candidate with strong computational aptitude and an interest in developing and applying innovative approaches to forest genomics.

The primary project involves identifying selective sweeps in multiple forest tree species maintained in genetic conservation units across Europe. This is an opportunity for a first author paper in population genomics, working with well-established European colleagues and a broad international audience. SNPs filtered from target-capture sequence data are ready and available for analyses. The position provides access to a high-performance computing cluster and bioinformatic support where needed.

Other secondary projects are available depending on the time and interest of the applicant. These projects range from assembly and annotation of genomes, development of an angiosperm tree pan-genome, gymnosperm phylogenetics, comparative genomics across forest tree species, or population genomics of forest trees. Development of projects and proposals of your own interest are encouraged and supported.

Beyond research, you will be expected to contribute to writing manuscripts, presenting research at UPSC and at conferences, and contributing to the UPSC community via journal clubs, seminars, etc.

The McEvoy lab is looking for its founding members (https://www.upsc.se/susan_mcevoy). Initial work will be in close collaboration with the PI. We will soon hire a doctoral student, so there will be additional opportunities for cooperation and mentoring over time. UPSC is a diverse organization, and we welcome applicants from all backgrounds and are committed to fostering an inclusive research environment.

Your profile

We seek a highly motivated candidate who can take initiative and work both independently and collaboratively. Excellent communication skills are required, with strong written and oral English.

Requirements:

- Doctoral degree in biology or equivalent at the time of starting the position - Knowledge in the topics of population genetics and/or plant genomics - Demonstrated interest and experience in computational work - Familiarity with installing and running bioinformatic tools in a Linux environment - Familiarity with scripting (Bash, R, etc)

Desired:

- Background in relevant focal areas such as plant stress response, adaptation, conservation - Publication record in relevant research areas

Compensation

This position is funded by a stipend from the WIFORCE program. At SLU, fellows receive a tax-free stipend for research purposes and are not considered employees. The stipend provides financial support, but it is not a salary and does not include employee benefits such as paid vacation, sick leave, or pension. Non-EU/EEA citizens must apply for and be granted a residence permit for research before entering Sweden and starting the work. You will be provided a Swedish coordination number for public benefits provided to residents such as medical care.

Research environment

The Department of Forest Genetics and Plant Physiology is part of UmeÃ¥ Plant Science Centre (UPSC, https://www.upsc.se) which is a centre of excellence for experimental plant research and forest biotechnology in Northern Sweden. Our mission is to perform excellent and innovative basic research and generate knowledge that benefits forestry, agriculture, environment and society. We work across a wide range of disciplines in plant science reaching from cell biology to ecophysiology and from basic research to industrial applications. Our common goal is to understand the plants' ability to grow, adapt and acclimate to a changing world and how we can breed better plants.

Postdocs at Umea Plant Science Center

UmeÃ¥ has a strong postdoc community organized in the UmeÃ¥ Postdoc Society (UPS). UPS fosters networking amongst postdocs, organizes social and career development events and works towards improving the postdoc experience in UmeÃ¥. Do not hesitate to get in contact with them early on at https://umeapostdocs.com/ The Wallenberg Initiatives in Forest Research (WIFORCE)

Biodiversity and the role of forests in climate change are now key social issues that require more knowledge. WIFORCE was created as a coherent basic science research program to address large and complex issues and develops new analytical tools in order to both sustainably

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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>

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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-pa-su/att-soka-en-anstallning .Stockholm University contributes to the development of a sustainable democratic society through knowledge, enlightenment and the search

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Tokyo TheoreticalBiology

Dear Colleagues,

The RIKEN Centre for Interdisciplinary Theoretical and Mathematical Sciences (iTHEMS; ithems.riken.jp), located near Tokyo, Japan, is currently accepting applications for the 2027 Special Postdoctoral Researcher (SPDR) programme. These are highly competitive 3 year positions, with an expected start date between April 1st, 2027 and March 31st, 2028.

SPDRs are fully independent researchers and are expected to design and lead their own research projects. In addition to a monthly salary of 550,000 JPY and other benefits, each SPDR receives a research budget of 1,000,000 JPY per year, with further funds available (see site for details). SPDRs are also eligible to apply for their own internal and external, domestic and international grants and other funding opportunities.

Complete details about RIKEN's SPDR programme can be found here: https://www.riken.jp/en/careers/programs/spdr/career2027/ Within RIKEN, iTHEMS promotes interdisciplinary collaborations among theoretical and computational scientists from diverse fields including mathematics, physics, biology, computer science, etc. Interactions are encouraged through daily activities such as journal clubs, seminar series, study/working groups, workshops, and international research collaborations. Any iTHEMS researcher can propose new collaborative activities around any topic of common interest.

SPDR candidates interested in being hosted in iTHEMS should contact their potential host prior to submitting their application. Of most relevance to this mailing lists are the iTHEMS laboratories of:

Catherine Beauchemin (biophysics/math biology/infectious diseases) https://ithems.riken.jp/en/members/catherine-beauchemin cbeau@riken.jp

Leo Speidel (mathematical genomics) https://ithems.riken.jp/en/members/leo-speidel leo.speidel@riken.jp

Yohsuke Murase (mathematical social science/game theory) https://ithems.riken.jp/en/members/yohsuke-murase yohsuke.murase@riken.jp

Your proposed research does not necessarily need to align with that of your host, but you should identify strong potential for collaborations with members of the host laboratory. You are encouraged to directly contact iTHEMS members whose research is close to your own, to establish a direct connection and explore possible collaborations. This will strengthen your application. Consider, for example, Gen Kurosawa (circadian rhythms), Kyosuke Adachi (biophysics/active matter), Eiryo Kawakami (medical mathematics/AI), Jos? Said Guti?rrez-Ortega (evolutionary biology/ecology), Isaac Planas Sitja (social insect modelling) or other iTHEMS researcher.

A full list of iTHEMS researchers can be found here:

https://ithems.riken.jp/en/members A full list of RIKEN researchers able to host SPDRs within and beyond iTHEMS can be found here:

https://www.riken.jp/medialibrary/riken/careers/programs/spdr/career2027/host_lab.pdf Deadline for registering basic information 2026, April 2, Thursday, 5 p.m. (JST)

Deadline for revising/uploading documents & letters of reference 2026, April 9, Thursday, 5 p.m. (JST)

Catherine Beauchemin

Deputy Director, iTHEMS, RIKEN, Saitama, Japan https://ithems.riken.jp/en/members/catherine-beauchemin Professor, Physics, Toronto Metropolitan University, Toronto, Canada https://www.torontomu.ca/physics/our-people/catherine-beauchemin/ thomas.hitchcock@riken.jp

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UCalifornia LosAngeles PopulationGenetics

Postdoctoral research position at UCLA in population genetics and/or microbiomes

The Garud Lab at UCLA is recruiting a postdoctoral researcher in population genetics and/or microbiomes 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 of Human Genetics, David Geffen 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>

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UCalifornia SantaCruz EcolEvolutionaryBiology

POSTDOCTORAL FELLOW in Ecology and Evolutionary Biology

POSITION DESCRIPTION

With generous funding from the Moore Foundation, the Department of Ecology and Evolutionary Biology (EEB) at the University of California, Santa Cruz (UCSC) invites applications for a postdoctoral fellow in EEB, broadly defined to include ecology, conservation biology, ecophysiology, behavior, phylogenetics, comparative organismal biology, population genetics, and evolution, as well as discipline-based education research. The Fellow will have a collaborative research program that bridges the interests of two or more EEB faculty research groups. Candidates should contact appropriate faculty sponsors before applying.

The Fellow will play a leadership role in our community, serving as a resource, collaborator, and role model to our graduate students. In service of that role, the Fellow will lead a workshop, seminar, or similar activities that contribute to community-building at UC Santa Cruz. These activities may focus on broad research techniques or topics, career development, or broadening opportunities in our field. Fellows should discuss leadership possibilities with their prospective faculty sponsors.

The hiring unit will not sponsor employment-eligible immigration statuses for this position.

Ecology and Evolutionary Biology: https://eeb.ucsc.edu/ QUALIFICATIONS

Ph.D. (or equivalent foreign degree) in Ecology and Evolutionary Biology or related fields. Ph.D. must be conferred before July 1, 2026.

APPLICATION REQUIREMENTS

All documents and materials must be submitted as a single PDF titled "Lastname_Firstname" and emailed to eebrecruitment@ucsc.edu with the subject "EEB postdoctoral fellowship".

Interested candidates should submit the following:

-Cover letter (1 page): Letter of application that summarizes the candidate's research experience, qualifications,interest in the position, and confirms the candidate's ability to start in person no later than July 1, 2026

-CV

-Research Statement: A short description of research accomplishments (1 page maximum)

-Description of proposed research with at least 2 EEB faculty mentors (2 page maximum, including figures;references may be in addition to the page limit)

-Description of proposed community-building leadership (1 page maximum)

-PDF of two manuscripts (published, preprints, or drafts)

-Letters of Recommendation (2; Letter writers should submit letters as PDFs named "Candidate Last Name_LetterWriter Last Name" directly to eebrecruitment@ucsc.edu)

We encourage candidates to discuss how they have expanded the reach and impact of their scientific activities in any or all of their documents.

APPLICATION WINDOW

Full consideration will be given to applications completed by March 15, 2026. Applications received after this date will be considered only if the position has not been filled.

Anticipated start: July 1, 2026

General questions about this position may be directed to the Department Chair, Dr. Rita Mehta at rmehta2@ucsc.edu

Kathleen Kay Professor Department of Ecology and Evolutionary Biology UC Santa Cruz

Kathleen Kay <kmkay@ucsc.edu>

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UColorado Boulder ComputationalPopulationGenetics

Postdoc in computational genomics to study archaic introgression in American populations

The laboratory of Fernando A Villanea in the Department of Anthropology at The University of Colorado Boulder is seeking applications for a postdoctoral scholar. The postdoc will have the opportunity to lead multiple population genetics and computational biology studies on Neanderthal and Denisovan ancestry in Indigenous and Latino American populations, through computational approaches. This includes mastering the existing computational architecture developed by the lab. Additional research project opportunities in human population genomics, in animal domestication, or in other areas based on individual interests, are also possible. For more information about our lab visit: https://www.villanealab.com/ Successful candidates will be expected to analyze ancient and modern genomic data, prepare and collaborate on manuscripts, mentor graduate and undergraduate students, and assist with grant preparation. There will also be opportunities for postdocs to develop their own research projects and apply for grants. The scholar's duties will be 100% research (no teaching or service load).

In addition to a demonstrated record of publication, the ideal candidate will have expertise with population genetics/computational biology and interest in applying these techniques to the study of human evolution. Candidates with genomics/bioinformatics expertise and other computational biology experience will also be considered. This position comes with a salary following NSF pay scales, university benefits, and funding for research/conference travel. The position is funded for three years, with annual renewal, and a possibility of continuing the position pending funding availability. The position will start between May and August 2026. A qualified candidate must hold a Ph.D. degree or have completed all of the requirements for a Ph.D. by the time of appointment.

Qualifications:

Applicants should have a Ph.D. in anthropology, genetics, evolutionary biology, or a related field with knowledge of population genetics. Applicants should have some experience with analyzing genomic data.

Preference will be given to individuals with experience using computational clusters for data analysis, experience with ancient DNA or large human genomic datasets, and experience programming in python or R. Strong candidates will be able to work independently, have effective oral and written communication skills, and be able to collaborate with and mentor both undergraduate and graduate students.

Application Instructions:

To apply, visit: https://jobs.colorado.edu/jobs/JobDetail/?jobId=69938 For full consideration, applications should be submitted by March 30th. Review will continue until the position is filled.

Applicants should submit the following items:

A cover letter describing relevant research experience and motivation, as well as interest for current position.

A curriculum vitae (CV).

Contact information (telephone number and email address) of three people who can be contacted for letters of reference.

Up to three of your publications.

Fernando Villanea Guevara <Fernando.Villanea@colorado.edu>

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UCopenhagen PopulationGeneticsStatistics

Postdoc position in population genetics at the University of Copenhagen.

A 2 year postdoc position is available jointly at the Dept of Mathematical Science and at the Dept of Biology, commencing according to arrangement. The position is open until filled.

The project is concerned with the development of statistical and computational tools to understand the genetic exchange across species boundaries through migration and introgression, which today is recognized as a common phenomenon in evolution. Understanding how different species are connected in evolutionary networks is of fundamental interest in biology, but current methods to infer the evolutionary relationship among closely related species fall often short.

The project seeks to develop new statistical and computational methods to disentangle the genetic relationship between species based on data from wild and domestic cattle (the Bos genus), with a special emphasis on detecting selection acting on genes that have crossed species boundaries. How do we measure and quantify exchange? Current methods are typically discrete, and based on a graphical representation. The new methods might be based on modelling, for example by extending the concept of Admixture Graphs to allow for continuous events or movements in space, or by applying Deep Learning as well, for example using generative diffusion models.

The ideal candidate has a quantitative background within (applied) math, statistics, engineering, computer science or quantitative biology. You need not have experience in population genetics but a keen interest to develop and apply your skills in a real-world context.

If you're interested, send me (Carsten Wiuf, wiuf@math.ku.dk) an email with your CV and publication list, and a short motivation for applying.

Carsten Wiuf <wiuf@math.ku.dk>

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UHelsinkiFinland PigmentCellEvoDevo

Postdoctoral Researcher in Integrative Evolutionary Cell Biology (ERC Project IntEvoCell) University of Helsinki (Finland) - Helsinki Institute of Life Science (HiLIFE) / Faculty of Biological and Environmental Sciences

The research group of Assoc. Prof. Claudius Kratochwil at the University of Helsinki, Finland (www.intevobio.fi) invites applications for two Postdoctoral Researcher positions in integrative evolutionary cell biology. Our ERC-funded project uses pigment cells in tropical cichlid fishes as a powerful model to uncover how complex cellular phenotypes and developmental programs evolve (EvoDevo focus). We integrate single-cell sequencing with high-throughput cell phenotyping and comparative evo-devo across species and developmental stages to link molecular cell states to quantitative phenotypes and evolutionary change.

We are building an integrative framework that links (i) high-dimensional single-cell molecular profiles to (ii) quantitative cellular phenotypes and (iii) evolutionary and developmental variation. The project already includes existing datasets and established pipelines, and the successful candidates will contribute both by analyzing and extending these resources and by developing new data and approaches where needed. You will join an international, collaborative team with access to excellent core facilities and computational infrastructure in Helsinki.

LINK TO JOB AD: https://jobs.helsinki.fi/job/-Helsinki-Postdoctoral-Researcher-in-Integrative-Evolutionary-Cell-Biology-%28ERC-Project-IntEvoCell%29/1353550057/ THE POSITIONS We are hiring two postdoctoral researchers whose expertise is complementary. Applicants may be primarily experimental or computational. We are especially interested in candidates who can cover a strong combination of skills (not necessarily all) from the lists below.

The preferred start date is between 1 May 2026 and 1 January 2027, or upon agreement. The positions are full-time and fixed-term for two years, with a possibility for a two-year extension. A six-month probationary period will be applied (standard in Finnish university employment contracts).

MAIN RESPONSIBILITIES Depending on expertise and mutual interests, the postdoctoral researchers will: - Lead and carry out research aligned with the project goals, contributing intellectually, methodologically and empirically - Generate and/or analyze single-cell and phenotyping data; develop robust, reproducible workflows - Write manuscripts for peer-reviewed journals and present findings at international conferences - Participate in mentoring of students and research trainees - Contribute to coordination of project activities, data management, collaborations and shared lab responsibilities

The work may include teaching and supervision duties (up to 10% of annual working time). A more detailed work plan will be crafted based on the selected candidates' strengths and interests.

WHAT KIND OF EXPERTISE ARE WE LOOKING FOR? Applicants must hold a doctoral degree by the start of employment and have the ability to conduct independent scholarly work. We encourage applicants with a strong profile in at least one of the tracks below, and ideally a combination across tracks:

Track A: Single-cell & computational analysis (choose a combination) - Single-cell RNA-seq analysis (e.g., Seurat/Scanpy, QC, integration/batch correction, clustering, annotation) - Multimodal integration and/or feature engineering (linking phenotypes, imaging, cytometry, or other readouts to transcriptomics) - Statistics / machine learning for biological inference (model validation, differential state testing, embeddings/classifiers) - Reproducible research software (Git, workflow tools, documented pipelines; HPC/cluster use)

Track B: High-throughput cell-phenotyping & cell sorting (choose a combination) - Flow cytometry / spectral cytometry, gating strategy development, and cell sorting - Sample preparation and dissociation protocols for nuclei and/or cells, ideally across multiple tissues including challenging tissues (e.g., skin) - High-throughput imaging or microscopy-linked phenotyping; quantitative image analysis - Robust experimental QC and data/metadata handling across many samples and conditions

Track C: Evo-devo / functional genetics (choose a combination) - Experimental evo-devo in fish or other vertebrate systems; developmental staging and phenotyping - Genetics of pigmentation and patterning; comparative developmental analyzes - Functional follow-up (e.g., CRISPR/Cas9 strategy, genotyping workflows, mutant/variant assessment) - Comparative frameworks (orthology-aware thinking, cross-species mapping, or phylogenetic reasoning)

GENERAL EXPECTATIONS - Strong written and spoken English

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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>

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UMaryland QuantitativeBiology

Postdoctoral Positions in Quantitative Biology

The Department of Biology at the University of Maryland, College Park seeks applications for three quantitative biology postdoctoral fellow positions as part of its newly established Quantitative Biology Initiative (QBI). Department research spans ecology, evolution, behavior, developmental biology and sensory neuroscience, leveraging insights made possible via quantitative approaches, including dynamical systems analysis, agent-based modeling, stochastic processes, machine learning, and recurrent and deep neural networks. QBI Fellows will have two departmental faculty co-mentors, at least one of whom is quantitatively focused (including Bruns, Butts, Cummings, Fagan, Johnson, Karatayev, Maltas, Simon, Sukharev, Weitz). Faculty mentors will support QBI Fellows in developing a research program at the intersection of their interests as well as building and teaching an undergraduate quantitative biology course to be offered once a year in either summer or winter term. The cohort of fellows will also jointly organize an annual QBI symposium in collaboration with the

Department of Biology community.

Applicants should reach out to potential mentors to discuss research ideas before applying. Applications should include 1) CV, 2) research statement (3 pages) describing past and current research directions along with proposed research including proposed faculty mentors, 3) teaching statement (1-2 pages) including a possible course idea with brief outline of topics and course activities, 4) contact information for three references.

We expect to hire three fellows each for a three-year term at a salary of $65-75,000 per year depending on experience. For best consideration, submit application materials by March 14, 2026. Start date is slated for summer or fall 2026.

https://umd.wd1.myworkdayjobs.com/en-US/-UMCP/job/University-of-Maryland-College-Park/-Post-Doctoral-Associate_JR103315 plfj@umd.edu

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UNewSouthWales MathematicalPhylogenetics

Postdoc at UNSW Sydney

A 3-year postdoctoral position in mathematical phylogenetics is available at the University of New South Wales in Sydney, Australia. The postdoctoral fellow will contribute independently and as a team member in collaborative research on the mathematics associated with encodings of phylogenetic trees and networks, on outcomes linked to a grant from the Australian Research Council (CIs Andrew Francis, Mark Tanaka, Michael Hendriksen).

About the role - Level A - $113K - $121K AUD plus 17% superannuation and annual leave loading - Fixed term - 3 years full-time (35 hours per week)

The role reports to Professor Andrew Francis and has no direct reports.

Applications close: March 5th, 2025

For details, see https://external-careers.jobs.unsw.edu.au/cw/en/job/537899/-postdoctoral-fellow-mathematics-statistics Please apply online - applications will not be accepted if sent directly to the contact listed.

Contact: Andrew Francis Email: a.francis@unsw.edu.au

This email and any files transmitted with it may contain confidential information. If you believe you have received this email or any of its contents in error, please notify me immediately by return email and destroy this email. Do not use, disseminate, forward, print or copy any contents of an email received in error.

Mark Tanaka <m.tanaka@unsw.edu.au>

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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>

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UPennsylvania PlantInsectInteractions

Postdoctoral Researcher in Eco-Evolutionary Dynamics of Human-Altered Environments at Penn

The Comerford Lab, newly established in the Department of Biology at the University of Pennsylvania, is seeking a highly motivated Postdoctoral Researcher to join our team in the Summer of 2026. This is a foundational role in a brand-new lab. The successful candidate will not only lead cutting-edge research but will also play a key role in the “unboxing” and development of our physical lab space and the cultivation of an inclusive, high-achieving lab culture. Together, our lab will investigate how plant-insect ecology and evolution respond to human-altered environments. We utilize a full-stack holistic approach that combines large-scale field experiments, molecular genomics, and theoretical modeling in order to better understand the rules of life in a changing world. The Postdoc will help to lead two primary initiatives:

1. Diet Breadth & Resilience: Investigating the role of insect herbivore diet breadth in tolerating and adapting to environmental perturbations (e.g., extreme weather, host shifts).

2. Mechanistic Spatial Sorting: Utilizing controlled lab-based microcosm experiments to elucidate the underpinnings of spatial sorting; a critical but under-described evolutionary driver in the wake of anthropogenic disturbance.

Required Qualifications

Education: A Ph.D. in Ecology, Evolutionary Biology, or a related discipline.

Expertise: Demonstrated aptitude in plant-insect interactions and the design/implementation of complex field or lab experiments.

Technical Skills: Proficiency in molecular techniques or computational modeling (e.g., R, Python) is highly preferred.

Mindset: We are looking for a scientist who is excited by the prospect of building something from the ground up, someone who is as comfortable designing a genomic pipeline as they are helping to set up a new microcosm array.

Position Details

Start Date: Summer 2026 (preferred), with some flexibility.

Duration: Initial 1-year appointment, with the potential for extension contingent on performance and funding.

Location: University of Pennsylvania, Philadelphia, PA.

Applicants will be considered starting March 10th and continue until the position is filled

How to Apply

Interested applicants should submit the following materials as a single PDF to mattheauc@gmail.com with the subject line “Postdoc Application - [Your Name]”:

Please include:

Curriculum Vitae

Research Statement (1-2 pages): Detailing past achievements and how your interests align with the Comerford Lab’s goals of testing eco-evo dynamics in a human-altered world.

Publications: 2-3 representative reprints.

References: Contact information for three professional references.

For more information on our research and philosophy, please visit: mattheaucomerford.weebly.com or our Penn Faculty Page https://www.bio.upenn.edu/people/mattheau-s Mattheau Comerford <mattheauc@gmail.com>

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UTurku Three HumanDiversity

Postdoctoral researcher (2 yrs) and a Doctoral researcher (4 yrs) in Evolutionary Language Sciences in the field of linguistics. Apply for these positions here; deadline 26 February 2026 at 16:00 (Europe/Helsinki). https://ats.talentadore.com/apply/tutkijatohtorin-ja-vaitoskirjatutkijan-projektitutkijan-maaraaikaiset-tehtavat-evolutiivisen-kielentutkimuksen-alalla/ZzJpkl?lang=en&UTUID!251 Postdoctoral researcher in Evolutionary Demography (3 yrs) in the field of evolutionary biology. Apply for this position here; deadline 27 February 2026 at 16:00 (Europe/Helsinki). https://ats.talentadore.com/apply/maaraaikainen-tutkijatohtorin-tehtava-evolutiivisessa-demografiassa/mexlxW?lang=en&UTUID!249 There is also this position in Finnishï¿½ Project researcher or Research assistant (1 yr) in the field of evolutionary biology (In Finnish). Apply for this position here; deadline 26 February 2026 at 16:00 (Europe/Helsinki). https://ats.talentadore.com/apply/datanhallinnan-projektitutkijan-tai-tutkimusavustajan-maaraaikainen-tehtava-biologian-laitoksella/DGykOg?UTUID!274 More info: https://sites.utu.fi/humandiversity/news/positions-open-in-human-diversity-consortium/

Jenni Santaharju Project coordinator of Human Diversity consortium Evolution through Contact and Communication Networks; Prof7 Human Diversity Through Contacts Centre of Excellence University of Turku Finland

https://sites.utu.fi/humandiversity/-
jenni.santaharju@utu.fi

Jenni Santaharju <jenni.santaharju@utu.fi>

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UValparaiso EvolGenomicsBioinformatics

Postdoctoral Position in Evolutionary Genomics and Bioinformatics, at the Center for Interdisciplinary Neuroscience at University of Valparaiso, Valparaiso, Chile.

The Center for Interdisciplinary Neuroscience of Valparaiso (CINV) in Valparaiso, Chile, invites postdoctoral researchers to apply for a Postdoctoral Fellowship focusing on understanding the evolution of genes and molecular pathways that play a role on inflammatory processes driving diseases affecting the central nervous system.

The postdoctoral researcher will contribute to this project using a combination of evolutionary and comparative genomics, as well as a diverse set of bioinformatic approaches for data analysis and integration (e.g., transcriptomics, genomics, phenotypic data). This position offers a unique opportunity to integrate diverse state-of-the-art genomic and phenotypic datasets across different model organisms to understand the role of genes, molecular pathways in the origin of complex diseases.

CINV provides a highly collaborative and multidisciplinary environment using a variety of computational and experimental approaches, including genetically tractable animal models as well as expertise in genetics, behavior, glia-neuron communication, metabolism, biophysics, genomics, bioinformatics, host-microbe communication, and biomolecular modelling. The new postdoc will be part of one of our labs which focuses more generally on the intersection between molecular evolution and disease biology.

Required qualifications are a PhD in evolutionary biology, computational biology, bioinformatics, or closely related fields. Candidates must have excellent verbal and written communication skills (working language is English), 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 bioinfomatics, computational biology, population genetics or evolutionary genomics are strongly preferred. Ideal candidates should have experience in analyzing genomic and phenomic data, performing comparative evolution or population genomic analyses, as well as in collaborating with experimentalists.

Interested candidates should first contact Evandro Ferrada at <evandro.ferrada@uv.cl>. 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 of at least 2 references. A short online interview will follow to discuss specific proposals. Candidate materials will be reviewed as soon as possible until the position is filled.

For further information, please visit: https://cinv.uv.cl/-cinv-postdoctoral-fellowship-program-2026/ Dr. Evandro Ferrada Associate Profesor

Centro Interdisciplinario de Neurociencia (CINV)

Facultad de Ciencias, Universidad de Valparaï¿½so.

Pasaje Harrington 287, Playa Ancha, Valparaï¿½so, Chile.

Tel. +56 (32) 250 8453

www.cinv.cl Evandro Ferrada <evandro.ferrada@uv.cl>

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

UWarsaw PDF PhD PlantEvolution

Post-doc position

A newly established lab at the Institute of Evolutionary Biology, University of Warsaw, invites applications for a postdoctoral-level Assistant Professor position funded by the Polish National Science Centre (SONATA project).

The project "How changes in meristem patterning drive evolutionary innovations: insights from syncephalia in the sunflower family (Asteraceae)" investigates the developmental and genomic basis of morphological innovation in plants using comparative genomics, developmental transcriptomics, and gene expression analyses. We seek candidates with experience in plant evolutionary developmental biology (e.g. in situ hybridization, regeneration/transformation approaches) or comparative genomics/transcriptomics in evolutionary research.

The position is full-time, starting October 2026 (initial 12-month contract with possible extension).

Application deadline: 30 April 2026

For more details, visit: https://www.biol.uw.edu.pl/-wp-content/uploads/sites/19/2026/02/ogloszenie-WB-KG-1-2026-EN.pdf ---

Doctoral position

A newly established lab at the Institute of Evolutionary

Biology, Faculty of Biology, University of Warsaw invites applications for a PhD student position funded by the Polish National Science Centre (NCN, SONATA-20 project).

Project desciption: The sunflower family (Asteraceae), with more than 32,000 species, owes much of its evolutionary success to the capitulum, a complex, flower-like inflorescence that has undergone repeated modifications. One such innovation is syncephaly, in which capitula are composed of smaller, often highly reduced capitula. The project aims to uncover the evolutionary-developmental mechanisms underlying the formation of these fractal-like blossoms.

The PhD project will integrate: - comparative genomics - transcriptomics - in situ gene expression analyses - functional and developmental approaches

The successful candidate will conduct research within the project, prepare scientific publications, and present results at national and international conferences.

Position details - Number of positions: 1 - Project duration: 36 months - Expected start: October 2026 - Monthly scholarship: ~3700 PLN net/month (years 1-2), increasing to ~4900 PLN net/month after midterm evaluation - Possibility to additionally apply for funding through the University of Warsaw Doctoral School

Candidate requirements - MSc degree in biology, biotechnology, environmental science, or a related discipline - Basic background in plant biology - Either: laboratory experience (e.g. DNA/RNA isolation, PCR, electrophoresis), or computational experience (Unix environment, R and/or Python) - Good command of English (spoken and written)

Application materials - Academic CV including research experience and skills - Copy of MSc diploma - One recommendation letter from a previous supervisor

Applications should be sent directly to: j.baczynski@uw.edu.pl

Selected candidates will be invited for short online interviews in the second half of April 2026.

Application deadline: 17 April 2026 Expected decision date: 1 May 2026

Jakub Baczyn̄ski, PhD Institute of Evolutionary Biology, Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw ul.Âwirki i Wigury 101, 02-089 Warsaw, Poland e-mail:j.baczynski@uw.edu.pl website:ibe.biol.uw.edu.pl

Jakub Baczyn̄ski <j.baczynski@uw.edu.pl>

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Vienna PolygenicAdaptation

Postdoc Polygenic Adaptation Vienna

A postdoc position is available at the Institute of Population Genetics, Vetmeduni Vienna. The position is available from April 1st with up to two years of guaranteed funding. Later starting dates are negotiable.

Requirements:

- Familiarity with polygenic adaptation and/or quantitative genetics

- Keen interest to either analyze experimental time series data available at the Institute or to further develop theoretical concepts of polygenic adaptation

- Strong motivation to interact with faculty, postdocs and students of the FWF funded priority program on polygenic adaptation (link) aiming to connect ongoing experimental and theoretical work.

The successful candidate will have considerable freedom to develop an independent research project within the framework of polygenic adaptation. The position comes with some priority program associated administrative duties aiming to connect the teams at different institutions. Successful candidates with an empirical research interest would have the opportunity to take some of the experimental Drosophila populations, which have evolved for up to 350 generations, to their next career step.

Vienna is an internationally recognized hub of empirical and theoretical population geneticists, with a strong research focus on understanding polygenic. Beyond this, Vienna is home to many research groups with a keen interest in evolutionary biology (This results in fantastic training and network opportunities:

- weekly seminar series () provide the opportunity for one to one interaction with internationally renowned evolutionary biologist

- regular meetings and exchanges with the members of the priority program as well as associate faculty (e.g. N. Barghi, Plön and K. Swarts)

- Evolvienna meetings bringing the Viennese community of evolutionary biologists together

- Regular journal clubs and progress reports, frequently joined by member of other research teams

Postdoctoral Position in Polygenic Adaptation

Institute of Population Genetics, Vetmeduni Vienna

A postdoctoral position is available at the Institute of Population Genetics, University of Veterinary Medicine Vienna (Vetmeduni). The position is available from April 1st, with up to two years of guaranteed funding. Later starting dates are negotiable.

Research Focus

The postdoc will work in the broad area of polygenic adaptation, with substantial freedom to develop an independent research project. The position is embedded in an FWF-funded priority program on polygenic adaptation, aiming to closely connect experimental and theoretical approaches across institutions.

Depending on interests and expertise, the successful candidate may:

* Analyze existing experimental time-series data available at the Institute, and/or

* Further develop theoretical frameworks of polygenic adaptation.

Importantly, candidates with an empirical research focus will have the opportunity to take long-term experimental Drosophila populations which have evolved for up to 350 generations with them to their next career stage, providing a unique platform for establishing an independent research program.

Requirements

* Background in polygenic adaptation and/or quantitative genetics

* Strong motivation to pursue independent research within the field of polygenic adaptation

* Keen interest in active collaboration with faculty, postdocs, and students within the FWF priority program

* Willingness to contribute to limited program-related administrative and coordination tasks aimed at strengthening collaboration across institutions

Research Environment

Vienna is an internationally recognized hub for empirical and theoretical population genetics (www.evolvienna.at), with a strong research focus on polygenic traits and evolutionary genomics. The city hosts a vibrant evolutionary biology community, offering excellent training and networking opportunities, including:

* Weekly seminar series with internationally renowned evolutionary biologists, enabling close scientific exchange (www.popgen-vienna.at/news/seminars/)

* Regular meetings and exchanges with members of the priority program and associated faculty (e.g. N. Barghi, Plön; K. Swarts)

* EvolVienna meetings, bringing together the Viennese community of evolutionary biologists

* A Graduate School dedicated to population genetics (www.popgen-vienna.at)/

* Journal clubs and progress report meetings, often joined by members of other research groups

Application

Applications and informal enquiries should be submitted to Christian Schlötterer (schlotc@gmail.com) by February 25th for full consideration. The search will remain open until the position is filled.

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

Zoom:

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

WorkshopsCourses

Bath ComputationalAndExperimentalMicrobiomics Jul6-18

Computational and experimental microbiomics Bath, UK 6-18 July 2026

We are pleased to announce the EMBO Practical Course: Computational and experimental microbiomics, to be held at the University of Bath, UK from 6-18 July 2026.

Course website: https://meetings.embo.org/event/26-microbiomics Recent advances in computational approaches including metagenomics and multi-omits dataset integration are transforming understanding of microbiota composition and dynamics. At the same time, genetically tractable zebrafish have emerged as a powerful alternative to rodent models for sophisticated imaging-based characterisation of dynamic host-microbe relationships. This EMBO Practical Course is designed to give participants a comprehensive exposure to these cutting-edge approaches. You will learn how to sample, sequence, assemble and interpret metagenomes, quantify the host responses they elicit and study the evolution of their constituent taxa and host co-evolution - using a range of genomic, comparative genomic and phylogenetic methods. Concurrently, you will learn how to characterise the impacts of core members of the bacterial microbiome on metabolic signalling in zebrafish and determine the effects of modified bacterial communities on lipid metabolism using state of the art imaging approaches. This mix of computational and experimental skill training will be complemented by speakers who represent leading lights in microbiome studies using both computational and experimental approaches, as well as experts on microbial evolution.

Application deadline: 15th April (abstracts), 11 May (registration)

Travel grants and registration fee waivers are available for participants.

For more information and to apply, visit: https://meetings.embo.org/event/26-microbiomics Tom Williams <tw2316@bath.ac.uk>

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Bordeaux PhilosophyInBiologyMedicine Jun1-5

Bordeaux Summer School - Philosophy in biology and medicine June 1 - 5, 2026 in Bordeaux, France

Organized by the PhilInBioMed < https://urldefense.com/v3/__https://philinbiomed.cnrs.fr/__;!!BDUfV1Et5lrpZQ!X5hObnLQ_QKjlPhWBZcdhqKpwJUPM8IfRxk > network and the Conceptual Biology and Medicine Team < https://urldefense.com/v3/__https://immunoconcept.cnrs.fr/conceptual-biology-medicine/__;!!BDUfV1Et5lrpZQ!X5hObnLQ_QKjlPhWBZcdhqKpwJUPM8IfRxk > in Bordeaux.

PhilInBioMed is both an interdisciplinary institute located at the University of Bordeaux and an international network connecting groups and people working at the interface between philosophy, biology, and medicine, with the shared conviction that conceptual and philosophical approaches can make a critical contribution.

Over the course of a week, around 25 young researchers (Master students, doctoral candidates and post-doctoral fellows) from the fields of philosophy, life sciences and medicine will come together and learn to address conceptual questions in scientific research using interdisciplinary methods. Conceptually/theoretically-oriented biologists and MDs are strongly encouraged to apply!

Experienced researchers from philosophy and biomedical fields will be present to share practical examples of interdisciplinary collaboration from their careers and to advise and interact with participants throughout the week. An important part of the summer school is a research activity in which groups of participants work together with experts on the different steps of a "Philosophy in Science" project. The programme also includes social activities, "speed dating," and plenty of opportunity for informal discussions to promote exchange between participants.

This summer school is a unique opportunity for young researchers to develop new interdisciplinary approaches that will benefit them throughout their careers. Participants will not only learn about specific concepts and scientific advances, but also how to view their own field of research from a new perspective.

This year's course leaders and speakers:

- *Alan COHEN *(Health and aging, University of Columbia) - *Scott GILBERT* (EvoDevo, Swarthmore College) - *Elis JONES* (Philosophy of marine biology, Technical University of Munich) - *Adeline LE CABEC* (Dental anthropology, University of Bordeaux & CNRS) - *Maël LEMOINE* (Philosophy of aging, University of Bordeaux) - *Mathilde LEQUIN* (Philosophy of paleoanthropology, University of Bordeaux) - *Carlo MALEY* (Cancer and evolution, Arizona State University) - *Thomas PRADEU* (Philosophy of immunology and cancer biology, University of Bordeaux & CNRS) - *Lisa ROUX* (Neuroscience, University of Bordeaux & CNRS) - *Jonathan SHOLL *(Philosophy of nutritional science, University of Bordeaux) - *Christopher STEVENS* (Philosophy of neuroscience, University of Bordeaux) - *Marie VASSE* (Ecology and evolution, University of Bordeaux) - *Orsolya VINCZE *(Cancer and evolution, University of La Rochelle)

Organizers:

- *Fridolin GROSS* (University of Bordeaux) - *Jan Pieter KONSMAN* (CNRS & University of Bordeaux)

Information and application: https://bss-philinbiomed.u-bordeaux.fr/en/ Deadline for application: March 15th, 2026

Sincerely,

Thomas Pradeu.

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

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Brazil ConGen Aug3-13

[Conservation Genetics - ConGen Global - Brazil] [Extended deadline for early application] We are pleased to announce the 2026 edition of the international course 'Recent Advances in Conservation Genetics (ConGen Global)', which will take place at an Atlantic Forest natural reserve in Brazil.

The ConGen Global course is an intensive, hands-on training program in conservation genetics and genomics. Sponsored by the American Genetic Association (AGA) and directed by Dr. Stephen J. O'Brien since 1996, ConGen Global has trained conservation scientists from around the world for three decades to apply genetic and genomic tools to real-world conservation and management decisions.

In 2026, ConGen will be held in Brazil's Atlantic Forest, one of the world's great biodiversity hotspots and among its most threatened ecosystems. The course will take place at the Vale Natural Reserve (RNV) in Linhares, Espírito Santo, a ~23,000-hectare reserve. This setting where fragmentation, endemism, and restoration are conservation realities allows lectures, computational labs, and case studies to connect directly to on-the-ground priorities in Brazil and across South America.

Course format and curriculum ConGen2026 is a 10-day program built around: - Morning lectures and interactive discussions focused on study design, theoretical concepts and practical applications in the field of conservation genomics. - Afternoon hands-on computer tutorials on conservation genomics (genomic data quality control and filtering; SNP calling; genomic diversity; population structure and admixture; estimating and interpreting ROHs; estimating genetic load; estimating demographic history and conducting population genetic simulations; estimating adaptive Evolution) using reproducible pipelines. - Evening keynote lectures highlighting case studies that connect methods to conservation practice. - Practical workshop on generating and analyzing genomic data from wildlife species. - Poster presentations by students throughout the course, with constant feedback by faculty. - Rotating “faculty tables” at meals, mentoring hours, and project clinics embed networking into the daily routine. All teaching materials (slides, code pipelines, datasets) are shared openly for post- course reuse and capacity building.

Faculty and admissions ConGen2026 will be taught by 15-20 faculty, including global leaders of the field, and will admit 25-30 students. Selection will prioritize scientific merit, regional representation, gender balance, and need-based support.

Dates and location August 3-13, 2026 Vale Natural Reserve (RNV), Linhares, Espírito Santo, Brazil Fees and support

Application is free. Registration fees are due only after acceptance and confirmation.

Registration fee: $2,500 USD

Includes: tuition, shared lodging, meals, and local transportation Not included: airfare, visa costs, travel insurance, personal expenses

Scholarships: reserved primarily for participants from low-income countries. If awarded, scholarships cover expenses in Brazil (registration, room, and board) but do not cover international travel. Scholarships require a separate application and are available only to accepted participants.

Apply by March 10 to be considered in full. Applications submitted after March 10 may be subject to a $250 late registration fee.

Apply here: http://congenglobal.org/brazil2026/ Thank you for your interest we look forward to receiving your application.

Eduardo Eizirik, PhD Professor Titular Escola de Ciências da SaÃo̲de e da Vida - PUCRS Av. Ipiranga, 6681, prédio 12 Porto Alegre, RS 90619-900 Brazil Email: eduardo.eizirik@pucrs.br http://www.pucrs.br/researchers/eduardo-eizirik ORCID: https://orcid.org/0000-0002-9658-0999 Instituto Pró-Carnívoros www.procarnivoros.org.br Curriculum Vitae na Plataforma Lattes/CNPq: http://lattes.cnpq.br/3626004211018550 Eduardo Eizirik <eduardo.eizirik@pucrs.br>

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- Practical workshop on generating and analyzing genomic data from wildlife species.

- Poster presentations by students throughout the course, with constant feedback by faculty.

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EvolAnalysisForBiomechanists Jun21-27

****Workshop in phylogenetic comparative methods for early career biomechanists****

OVERVIEW OF WORKSHOP Do you study biomechanics, locomotion, or functional performance? Are you a primarily experimental biologist who would like to expand your work to multiple species? Have you heard about phylogenetic comparative methods but are unsure how they might apply to your research field? If the answer to any of these questions is “yes,” you may be interested in an upcoming summer workshop on phylogenetic comparative biology.

The Moen lab in the Department of Evolution, Ecology, and Organismal Biology at the University of California, Riverside, will hold a summer workshop on phylogenetic comparative methods in evolutionary biomechanics. This workshop is part of an NSF CAREER grant focusing on the evolution of locomotor mechanics. Phylogenetic methods for analyzing trait evolution will be covered, particularly those methods most directly related to the evolution of biomechanical systems. A key goal of the workshop is to expose early career researchers with more experimental, single-species experience to methods and perspectives helpful in studying the evolution of their study system by analyzing data from multiple species.

No previous experience with these methods is required. Most expenses for attending the workshop will be covered. As a consequence, participation is limited to a maximum of 16 participants. We expect applications to be competitive.

ELIGIBILITY Participants should be mid-level to advanced Ph.D. students or post-docs at any stage. We will also consider early-career faculty members if the fit of their research goals highly overlaps with the workshop material. Strong applicants will have experience in one or more of the following research areas: biomechanics, locomotion, muscle physiology, and functional morphology and performance. Prior work in R will be especially helpful, though less-experienced participants will be provided materials to learn more prior to the workshop. Because learning will be facilitated by having your own data to analyze, we are particularly looking for applicants who have an interspecific dataset they can analyze or those who plan to soon collect such a dataset. More generally, we seek highly motivated applicants with a desire to expand their research into studies of phylogenetic comparative biology.

WORKSHOP AND APPLICATION DETAILS Workshop format: Most days will include lectures on the theory of methods, followed by hands-on exercises with R tutorials. We may also discuss key research papers, which will be provided to participants in advance. The workshop will finish with participants analyzing their own datasets, using the methods they have learned. Participants without their own dataset will be provided with one.

Workshop dates: The workshop will take place at the Owens Valley Station of the White Mountains Research Center, near Bishop, CA, from 21-27 June. Most participants will be expected to arrive to the Ontario, CA, airport prior to the workshop, either late Saturday (20 June) or early Sunday (21 June). We will pick up participants from Ontario on Sunday, 21 June, and head to the reserve. Those from southern California may alternatively make arrangements to arrive at UC Riverside and ride with us to the workshop. And those from northern California or Nevada could drive directly to the workshop. Within reason, travel arrangements may be flexible.

Field station details: While close to Bishop, the Owens Valley Station is still a field station. The lodging is rustic with shared, dorm-like rooms and bunk beds. Bathroom facilities are likewise shared. There are no single rooms. Please do not register unless you are comfortable with the idea of being at a field station or sharing a room, though we are happy to provide more details if you are uncertain. Stays at the station include meals made by an on-site cook, though participants will occasionally help set up or clean up for meals. Dietary offerings are broad and can accommodate nearly any preferences or restrictions. Please see the station's website for more details: https://www.wmrc.edu/owens-valley-station/ Details of financial support: All participants will be eligible for reimbursement of up to $500 in travel expenses to Ontario. Additional travel support may be available given need. Travel to and from the field station will be provided by us. Lodging and meal expenses while at the station will be fully covered.

Application deadline: Review of applications will begin on 15 March 2026, though we will still consider applications until we have filled all available seats in the workshop.

Applications must include: (1) A cover letter answering the following questions: (a) Why do you want to participate and what do you hope to learn? (b) In which part of your current or future research do you

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Mertola Portugal ConservationGenetics Apr13-17

The Conservation Genetics course is a comprehensive 5-day workshop designed for postgraduate students to provide advanced understanding of genetic diversity in natural populations and its critical role in conservation of threatened species and populations.

This intensive course will be held from 13-17 April and feature expert- led lectures and practical group work, promoting informal discussions, on a range of topics including: - Genetic Variation & Conservation: Understand the importance of genetic diversity and explore cutting-edge molecular techniques for genetic monitoring. - Fundaments of Population Genetics: Understand concepts such as Hardy- Weinberg proportions, effective population size, inbreeding depression, genetic drift, selection. - Molecular Methods in Conservation: Learn about application of high- throughput sequencing methods in conservation, and methods for genetic monitoring using non-invasive sampling. - Anthropogenic Hybridization and Genetic Rescue: Methods for detecting anthropogenic hybridization, case studies, and use of genomics in conservation of highly threatened species.

Pre-requisites: Participants are expected to have completed an introductory genetics course or possess equivalent background knowledge. APPLICATION Deadline: 01 March 2026

The course will also feature a half-day field trip to Parque Natural do Vale do Guadiana. This is an excellent opportunity to gain valuable insights, collaborate with peers, and enhance your expertise in the field of conservation genetics.

More info here:

https://www.cibio.up.pt/en/events/conservation-genetics-fundaments-and-applications-2/ We look forward to your participation!

Soraia Barbosa <soraiabarbosa@cibio.up.pt>

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Online AIforGenomics Apr7-9

Dear all,

we are pleased to announce the online course "AI for Genomics: From CNNs and LSTMs to Transformers", taking place on 7-9 April . The course is designed for researchers interested in applying modern machine learning and deep learning approaches to genomic and metagenomic sequence data. Course website: (https://www.physalia-courses.org/courses-workshops/-ai-for-genomics/)

Through a strongly hands-on approach using interactive notebooks, participants will learn how to encode biological sequences, train and evaluate CNN, LSTM, and Transformer models, and interpret results in a biologically meaningful way. The course covers real-world applications such as genomic functional element prediction, sequence classification, metagenomic source tracking, and biological sequence generation, while also introducing attention mechanisms and NLP-inspired methods adapted to genomics. For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/ai-for-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/)

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Online AI-PoweredImageAnalysis

Hello EVOLDIR members

AI-Powered Image Analysis led by Nikolay Oskolkov (Group Leader (PI) at LIOS) is now available as an on-demand streaming seminar. This seminar on AI-powered image analysis offers powerful tools for researchers to quantitatively extract phenotypes, cell counts, and morphological features from diverse biological images. Evolutionary biologists and geneticists can leverage deep learning methods like semantic and instance segmentation to precisely delineate and measure traits, track developmental changes, or identify genetic markers across large datasets. Participants will gain hands-on experience with reproducible Python workflows, including uncertainty quantification and model interpretability, enabling them to generate robust, publication-quality data for their studies on adaptation, development, and genetic variation.

Access this seminar (https://instats.org/seminar/ai-powered-image-analysis-1) at your own pace and please share this with colleagues and students who might benefit!

Best wishes

Michael Zyphur Professor and Director Instats | instats.org

mzyphur@instats.org

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Online BayesianPhylogenetics Apr21-24

Dear all,

We are excited to offer the online course "A Hands-on Course in Bayesian Modelling and Evolutionary Analysis using RevBayes", taking place 21-24 April.

Course website: https://www.physalia-courses.org/-courses-workshops/bayesian-phylogenetics/ This 4-day course introduces stochastic modelling in evolutionary biology through Bayesian phylogenetic inference using RevBayes. You will gain hands-on experience specifying, running, and interpreting complex evolutionary models, including biogeographic history, diversification, and comparative biogeographic models.

Ideal for higher degree students and early career researchers with some background in phylogenetics, this course deepens understanding beyond standard methods by focusing on flexible, interpretable Bayesian approaches.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/)

Best regards, Carlo

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Online CancerGenomics Apr27-29

Dear all,

We are pleased to announce the upcoming Physalia online course Practical Somatic Variant Analysis in Cancer Genomics, taking place on 27-29 April .

Course website: (https://www.physalia-courses.org/-courses-workshops/cg26/)

This 3-day hands-on workshop is designed to provide practical skills in cancer genomics, with a strong focus on somatic variant detection, annotation, and interpretation. Participants will follow the complete analysis workflow, from raw sequencing data to the identification and prioritization of potentially pathogenic mutations relevant to cancer research and precision oncology.

The course combines theoretical lectures and hands-on sessions, using whole-exome sequencing (WES) data from matched tumor-normal samples. All reference resources (GRCh38, Panel of Normals, gnomAD, ClinVar, REVEL, and other cancer-relevant databases) will be pre-staged for participants.

Key topics include:

Quality control and preprocessing of sequencing data

Read alignment and assessment of alignment quality

Biological and computational differences between germline and somatic variants

Somatic variant calling using GATK4 Mutect2

Variant filtering strategies and use of population databases

Variant annotation with Ensembl VEP

Variant analysis, prioritization, and visualization in R
Best regards,

Carlo

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Online Epigenomics Apr13-17

Dear all,

We are pleased to announce an upcoming online training course on Epigenomics Data Analysis (4th edition), taking place 13-17 April.

Course website: .(https://www.physalia-courses.org/-courses-workshops/course59b/)

This hands-on course introduces regulatory epigenomics through real-world analyses of RNA-seq, ATAC-seq, ChIP-seq, MNase-seq, and Hi-C data, using Linux tools and R/Bioconductor. Participants will move from raw sequencing data to downstream analyses and multi-omics integration, gaining practical skills applicable to their own research.

We will cover: gene expression, chromatin accessibility, chromatin composition, 3D genome organization, and multi-omics data integration.

For the full list of our courses and workshops, please have a look at: (https://www.physalia-courses.org/-courses-workshops/course59b/)

Best regards, Carlo

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Online GenerativeAI Mar3

Hello EVOLDIR members

Instats is offering a new 1-day seminar Generative AI for Statistical Science (Free Seminar) livestreaming March 3, led by Lei Ding (Faculty of Statistics, University of Manitoba). This seminar introduces modern generative AI paradigms, including VAEs, GANs, and diffusion models, from a statistical perspective. Researchers in evolutionary biology and genetics can leverage these methods for tasks such as generating synthetic genomic data, imputing missing ancestral states, or modeling complex evolutionary trajectories. Understanding these advanced statistical tools can significantly enhance the analytical capabilities for exploring high-dimensional biological datasets and testing evolutionary hypotheses.

Sign up today (https://instats.org/seminar/generative-ai-for-statistical-science-fr) 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

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Online GenomeAssemblyAnnotation Mar9-13

Dear all,

We've finalised the invited speakers for the Assembly and Annotation of Genomes course (9-13 March), and we've also got a Teaching Assistant on board: Ying Chen from the Vertebrate Genome Lab.

Course website: (https://www.physalia-courses.org/-courses-workshops/course20/)

The course will cover genome assembly and annotation using a range of sequencing technologies like Illumina, PacBio, Oxford Nanopore, plus scaffolding methods like Hi-C. We'll focus on quality control, manual curation, and annotation using real tools and datasets.

It's perfect for beginners and more advanced users alike, and no prior sequencing experience is needed.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-course20/)

Best, Carlo

Carlo Pecoraro, Ph.D

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Online GSEAinR May11-15

Dear all,

We're happy to share an upcoming online course on Gene Set Enrichment Analysis in R, taking place 11-15 May.

Course website: [https://www.physalia-courses.org/-courses-workshops/gse-in-r/]

Gene set enrichment analysis is a cornerstone of modern transcriptomics, proteomics, and multi-omics studies - but it's also easy to misuse or over-interpret. This course is designed to help you really understand what enrichment results mean, how they are computed, and how to use them responsibly in your research.

The course is strongly hands-on and flexible. Alongside the core topics, we adapt the pace and focus to participants' interests, and you're very welcome to bring your own data to work on during the practical sessions.

During the course, attendees will learn how to:

Understand the biological and statistical logic behind enrichment analysis

Choose appropriate gene set databases and annotations

Run and interpret ORA, GSEA, CERNO, and other ranking-based methods

Deal with gene identifiers and annotation pitfalls

Reduce redundancy and make sense of overlapping results

Visualize and communicate enrichment results clearly

Apply advanced approaches, including topology-based, multivariate, single-cell, and spatial methods

Design and validate custom gene sets Course format

Fully online, to encourage international participation

Sessions run daily from 14:00 to 19:00 (Berlin time)

Short lecture blocks combined with hands-on exercises, discussion, and Q&A For the full list of our courses and workshops, please visit: [https://www.physalia-courses.org/courses-workshops/]

Best regards, Carlo

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Online IntroSpatialMultiplexedProteomics Jun1-5

Introduction to Processing and Analysis of Spatial Multiplexed Proteomics Data (SPMP02) https://www.prstats.org/course/introduction-to-processing-and-analysis-of-spatial-multiplexed-proteomics-data-spmp02/ Dates:1-5 June 2026 Format:Live online, 5 days Ã 5.5 hours per day Fee:450 Time zone:UK (GMT+1); all sessions are recorded and made available for 30 days

Why This Course Matters Spatial multiplexed proteomics techniques such as CODEX, CycIF, and MxIF/MACSIMA are revolutionising how we understand tissue microenvironments, cellular interactions, and spatial heterogeneity in biological systems. However, converting raw multiplexed imaging data into actionable biological insight requires expertise in image processing, spatial statistics, phenotyping, and bioinformatics pipelines. SPMP01bridges that gap. Over five intensive days, you will learn both the theoretical foundations and the hands-on computational skills needed to process, analyse, and interpret spatial multiplexed proteomics data. Whether your work lies in basic biology, cancer immunology, neuroscience, or spatial systems biology, this course equips you to handle complex image-based proteomics datasets.

What You'll Learn Participants will move from foundational concepts to applied workflows across these core topics:

Overview and comparison of spatial multiplexed imaging platforms (CODEX, CycIF, MxIF / MACSIMA)

Image processing workflows: tile stitching, illumination correction, alignment, and region-of-interest generation

Handling multi-resolution image formats (e.g., .tif, .ome.tif, .ome.zarr), and visualization strategies

Single-cell segmentation: algorithms (e.g. Cellpose, Stardist, Mesmer), mask QC, and error diagnostics

Feature extraction and cell phenotyping (marker intensity gating, clustering, annotation)

Spatial neighbourhood and cell-cell interaction analysis: quantifying local and global neighbourhood statistics

Batch processing and scalable workflows (using Nextflow pipelines such as MCMICRO)

Best practices for reproducibility, data storage, workflow modularity, and integration with R/Python pipelines

Through guided coding sessions and worked examples, you will apply these methods to real multiplexed imaging datasets and gain experience interpreting spatial proteomics results.

Format & Support

Each day blends lectures, demonstrations, and hands-on practical work

Participants are encouraged to bring their own data for discussion (time permitting)

All course materials, scripts, and datasets are shared with attendees

Livestream sessions are recorded and made available the same day

Post-course email support is offered for 30 days to assist with implementation and troubleshooting

Who Should Attend This course is aimed at researchers, computational biologists, bioinformaticians, and technical scientists who work with or plan to work with spatial omics and proteomics imaging data. Prior experience with R or Python is advantageous. Basic knowledge of statistics and familiarity with image data (microscopy) will help, but are not strict prerequisites. A comfortable level of computing literacy (e.g. command line use) is expected.

Instructors Dr Victor Perez Meza an expert in fluorescence microscopy, image artefact correction, and multiplexed imaging workflows MSc Miguel Angel Ibarra Arellano specialist in reproducible bioimage analysis, neighbourhood spatial statistics, and spatial omics tools Their combined experience ensures a mix of methodological insight and practical, cutting-edge implementation.

Who Will Benefit (Use Cases) Participants in SPMP01 will be better equipped to:

Process and clean raw multiplexed imaging datasets

Segment individual cells reliably and assess segmentation quality

Assign cell phenotypes and derive per-cell morphological or marker statistics

Quantify spatial relationships and neighbourhood structure in tissue

Develop reproducible pipelines for spatial proteomics workflows

Integrate processed spatial data into downstream statistical or machine learning analyses

In fields such as cancer microenvironment analysis, immunology, neuroscience, and developmental biology, these capabilities are invaluable for linking cellular spatial patterns to functional and phenotypic insights.

Registration & Details Spaces are limited to ensure a high-quality interactive experience. The early bird rate (400) is available to the first five registrants. Standard registration is 450. Visit the course page for full schedule, registration, and further details: SPMP02 - Introduction to Processing and Analysis of Spatial Multiplexed Proteomics Data

Email oliver@prstats.org with any questions

Oliver Hooker PhD. PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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Online MachineLearningForBioImaging Mar10-12

Dear all,

We are excited about this online Physalia course on Machine Learning for Bio-Imaging, taking place from 10-12 March.

Course website: (https://www.physalia-courses.org/-courses-workshops/ml-for-bio-imaging/)

This course introduces machine learning and deep learning techniques for bio-imaging analysis. Over three days, participants will learn the fundamental concepts of bioimage analysis, explore modern machine learning workflows, and gain hands-on experience applying convolutional neural networks (CNNs) to real biological imaging problems.

Sessions run live online from 14:00 to 19:00 CET.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-ml-for-bio-imaging/)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

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Online MachineLearning RandPython

Learn how to apply modern machine learning methods to ecological time-series data in our live online course Machine Learning for Time Series Using R (METR01).

https://prstats.org/course/machine-learning-for-ecological-time-series-metr01/ This applied R training is designed for scientists who want practical skills for analysing, modelling, and forecasting time-series data using reproducible workflows. Participants will work through hands-on examples to understand how machine learning approaches can be used to detect patterns, make predictions, and interpret complex ecological dynamics. The course covers:

Preparing and structuring time-series data

Supervised and unsupervised machine learning approaches

Model training, validation, and performance assessment

Forecasting trends and dynamics

Interpreting machine learning outputs

The training is delivered via recordings available 30 days before the course and supported by 5 x live Q and A sessions from 13-17 April. You also have access for 30 days after the course to revisit any materials.

Course details Dates: 13'17 April 2026 Duration: 5 days, approximately 7 hours per day Format: Recorded sessions with live Q&A Fee: pounds 450 This course is suitable for postgraduate students, researchers, consultants, and professionals working with ecological monitoring data, population time series, sensor data, or environmental datasets who want to apply machine learning techniques in R.

Full details and registration: https://prstats.org/course/machine-learning-for-ecological-time-series-metr01/ Email oliver@prstats.org with any questions

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Oliver Hooker PhD.

PR stats

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Build practical deep learning skills in Python with our live online course Deep Learning Using Python(DLUP01). https://prstats.org/course/deep-learning-using-python-dlup01/ This intensive two-day workshop provides a structured introduction to deep learning and its implementation in Python using PyTorch. Participants learn both the theoretical foundations of neural networks and how to build modern deep learning models through hands-on coding exercises. The course covers:

Foundations of artificial neural networks and deep learning

Training networks using backpropagation and optimisation methods

Building multilayer perceptrons in PyTorch Convolutional neural networks for image data

Transformer architectures and minimal GPT-style models

Using pre-trained models with the Hugging Face Transformers library ()

Delivered live online with recordings available, participants receive course materials, datasets, and post-course support.

Course details Dates: 14-15 April 2026 Duration: 2 days, approximately 6 hours per day Format: Live online Fee: 300 This course is suitable for researchers, data scientists, and professionals who are comfortable with Python and want a clear, practical introduction to neural networks, CNNs, and transformer models for real research problems. ()

Full details and registration: https://prstats.org/course/deep-learning-using-python-dlup01/ Email oliver@prstats.org with any questions

–

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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Online Metatranscriptomics Apr27-29

Dear all,

We are pleased to announce our upcoming online course: Statistical Methods for Metatranscriptomics Dates: 27-29 April Course website: (https://www.physalia-courses.org/courses-workshops/metatranscriptomics/)

This three-day workshop provides an in-depth introduction to advanced statistical and computational methods for analysing metatranscriptomic data, which capture gene expression profiles from complex microbial communities. Participants will gain hands-on experience in R/Bioconductor to perform data normalization, differential expression analysis, network construction, functional interpretation, and multi-omics integration.

Daily live sessions will run from 14:00 to 18:00 Berlin time.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-metatranscriptomics/)

Best regards, Carlo

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Online MultilevelModeling Feb26-27

Hello EVOLDIR members

Last chance to join our 2-day seminar Multilevel Modeling in R livestreaming February 26?¿'27 with Scott Colwell (University of Guelph and Enablytics). This seminar provides a rigorous introduction to multilevel modeling in R, focusing on the conceptual foundations and practical estimation for clustered or nested data. Researchers in evolutionary biology and genetics can apply these advanced methods to analyze hierarchical structures, such as genetic variation within populations or phenotypic traits across species, ensuring robust inferences from complex datasets. Participants will master R workflows for model specification, diagnostics, and reproducible reporting, directly enhancing the methodological rigor of their empirical studies.

Sign up today (https://instats.org/seminar/multilevel-modeling-in-r) 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

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Online MultivariateDataAnalysis May4-7

Dear all,

registration are now open for the online Physalia course on Multivariate Data Analysis with R and vegan, 4-7 May, and gain practical skills to analyse and interpret complex multivariate datasets using R and the vegan package.

Course website: (https://www.physalia-courses.org/-courses-workshops/vegan/)

This hands-on course covers ordination methods (PCA, CCA, RDA, PCoA), PERMANOVA, and permutation-based inference with applications to ecological and high-throughput data such as shotgun sequencing (metabarcoding) and metagenomics.

Participants should be familiar with RStudio and have some fluency in programming R code, including being able to import, manipulate (e.g. modify variables) and visualise data. There will be a mix of lectures, and hands-on practical exercises throughout the course.

Format: fully online, 14:00-20:00 Berlin time, mixing lectures, discussion, and exercises.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-vegan/)

Best regards,

Carlo

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Online MultivariateTraitEvolution Apr27-May7

Dear colleagues,

Transmitting Science is offering a new edition of the course "Modelling and analysing multivariate traits evolution using R".

Course webpage: https://www.transmittingscience.com/courses/evolution/modelling-and-analysing-multivariate-traits-evolution-using-r/ The aim of this course is to introduce participants to multivariate phylogenetic comparative methods using the mvMORPH R package.

By the end of the course, students will be able to:

Understand multivariate trait evolution models. Apply comparative methods using R. Interpret evolutionary patterns in multivariate datasets.

For any questions, please write to 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>

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Online NaturalSelectionPopGenomics Apr13-21

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. The course addresses practical and conceptual challenges, such as demographic confounding, limited statistical power, and difficulties in biological interpretation.

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. 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>

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Online PalaeoproteomicsSpeciesIdentification May19-28

Dear evoldir members,

Transmitting Science is offering the course "Proteomic Methods for Species Identification of Archaeological and Palaeontological Materials" (3rd edition).

Learn more and register here: https://www.transmittingscience.com/courses/genetics-and-genomics/palaeoproteomics-and-zooarchaeology-by-mass-spectrometry-zooms/ In this course, participants will be introduced to proteomic methods for species identification, focusing on peptide mass fingerprinting by MALDI-ToF mass spectrometry and LC-MS/MS based approaches.

During the course, participants will first be introduced to some theory with illustrative examples (both from simulated data as well as some real datasets) and will then learn how to interpret the data, both MS1 (e.g., fingerprints) and MS2 (or MS/MS 'sequencing' spectra), as well as how to assess their reliability.

Instructor: Dr. Michael Buckley (University of Manchester, UK), author of ZooMS (Zooarchaeology by Mass Spectrometry)

If you have any questions do not hesitate to 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>

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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

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Online PythonMachineLearning May11-15

Machine Learning for Time Series using Python -Online recordings and live Q&A

This intensive five-day online course provides a practical introduction to machine learning techniques for modelling, analysing, and forecasting time-series data using Python. Designed for researchers, analysts, and data scientists who work with temporal datasets, the course focuses on hands-on workflows that can be applied directly to real-world problems.

Participants will learn how to prepare and visualise time-series data, implement machine learning models for forecasting and classification, evaluate model performance, and interpret results in a statistically sound way. The training combines structured teaching with guided exercises, giving attendees experience with modern Python tools and methods commonly used in time-series analysis.

All sessions are delivered live online and recorded for later review, with opportunities for questions and discussion during dedicated Q&A sessions.

Course details Dates: 11-15 May 2026 Format: Online recordings and live Q&A Fee: ï¿½450 This course is suitable for professionals and postgraduate researchers who have basic familiarity with Python or data analysis and want to develop practical machine learning skills for time-dependent data.

Register here: https://prstats.org/course/machine-learning-for-time-series-mltp01/ Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

(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>

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UConnecticut ComputationalBiol Feb20-Apr24

The Computational Biology Core at the University of Connecticut is hosting in-person data science workshops this spring! We still have space available in our Introduction to R Workshop (10 weeks, in person - Feb. 20-Apr. 24).

This hands-on workshop will introduce participants to the core principles of R for data analysis and visualization. You'll learn how to import and organize data, work with common data structures, wrangle and tidy datasets using the tidyverse, build functions and pipelines, create effective visualizations, and run basic statistical analyses?using real datasets and widely used R packages.

No prior programming experience is required. We will start with the basics and build skills week by week.

Learn more & register here: https://bioinformatics.uconn.edu/cbc-workshops/ WHERE: UConn Storrs Campus (room TBD) WHEN: Fridays, 1:00-2:00 PM EST COST: $500 (UConn affiliates) / $600 (External participants)

Registration is first come, first served.

Questions? E-mail: cbcsupport@helpspotmail.com

"Lambert, Karelyn" <zsc25001@uconn.edu>

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YosemiteNatlPark Symbiosis Apr17-19

The 14th Annual Yosemite Symbiosis Workshop 2026

An integrative meeting of biologists focusing on symbiosis research April 17-19, 2026 Sierra Nevada Research Station, Wawona, Yosemite National Park

Register here: https://snri.ucmerced.edu/form/symbiosis-workshop-2026 KEYNOTE SPEAKER: John McCutcheon, Arizona State University

Why: Our goal is to better integrate scientists who focus on symbiosis research, including researchers that study animal-microbe and plant-microbe systems, as well as broader topics related to microbiomes, cooperation, and mutualism. This will be our 14th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

Who: The meeting is small and intimate by design (45 participants). We typically cover a range of symbiosis topics from ecology and evolution to molecular mechanisms in different model and non-model systems. We are limiting registration to four people per lab, with priority for graduate students, postdocs, and PIs (undergraduate students are welcome to attend if we have space).

What: The meeting will consist of two half-days of talks and one poster session. Other than the keynote (~1 hour), talks are 15 minutes long (including time for questions). Posters are flexible for size, but the ideal poster should be no larger than ~4 feet square. When you apply for the meeting, you will provide your preference for a talk or poster. We usually strike a good balance but were a bit poster heavy in 2025, so talks are encouraged.

When: A welcome party will occur for everyone arriving on the evening of Friday April 17th. The talks and poster sessions will be held Saturday and Sunday April 18-19, 2026. Where: This is the best part! The meeting takes place at the Sierra Nevada Research Station, in Wawona California, within the border of Yosemite National Park!

What will it cost? Thanks to generous support from the Moore Foundation, this meeting is free for graduate students and postdocs –! We charge $300 for PIs and other types of participants (e.g. industry/foundation/journalist). PIs must pay a registration fee of $300. The registration deadline is March 15, 2026. We ask that graduate students and postdocs plan to present their work. Everyone who registers on time gets to present a talk or poster (your choice).

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

Unfortunately, we cannot accommodate guests The Yosemite field station is getting busier every year with researchers, and so must prioritize participants over guests. If you want to bring guests, we kindly ask that you make your own arrangements with the nearby Wawona hotel. If you are breastfeeding, we can try to accommodate your baby and partner, but there's no guarantee. Please email Carolin if this is your situation (cfrank3@ucmerced.edu).

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

Register here: https://snri.ucmerced.edu/form/-symbiosis-workshop-2026 Please direct any questions to the organizers:

Joel Sachs joels@ucr.edu

A. Carolin Frank cfrank3@ucmerced.edu

joel.sachs@ucr.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.