EvolDir

July 1, 2025

Month in Review

Foreword

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

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

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

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Conferences

LinnSocSystAssn London ConservationMisinformation Jun12

Dear all,

We are please to announce this year's joint Linnean Society of London < https://www.linnean.org/ > and Systematics Association < https://systass.org/ > Policy 'lecture', Misinformation and the Threat to Conservation.

This year we will have a discussion between biodiversity experts and science communicators to explore how the current prevalence of polarised discourse and scientific misinformation threatens conservation efforts, and what can be done to combat it. Chaired by Clare Carlile (DeSmog), Professor Amy Dickman (University of Oxford) and Dr Alexander Lees (Manchester Metropolitan University) will draw on their unique experiences at the intersection of science, media, and policy.

To foster open and informed dialogue in an impartial setting, and promote audience participation, this event will be in-person only and will not be recorded.

The debate will be followed by a drinks reception in the Linnean Society's library.

When: June 12 6PM UTC+1

Where: The Linnean Society, Burlington House, London

Further details and registration can be found here: https://www.eventbrite.co.uk/e/misinformation-and-the-threat-to-conservation-tickets-1321236075669 We hope you will join us for this event.

Ana Serra Silva Communications Officer for the Systematics Association

Communications SystAss
<communications@systass.org>

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Online SORTEE Oct15-16

Dear Colleague,Registration is now open for the fifth annual SORTEE conference (The Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology). The conference will run continuously from 15 October 07:00 UTC to 16 October 10:0

Dear Colleague,

Registration is now open for the fifth annual SORTEE conference (The Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology). The conference will run continuously from

15 October 07:00 UTC to 16 October 10:00 UTC to cover all time zones.

To register, please visit: https://www.sortee.org/-upcoming/ We are thrilled to announce the 2025 plenary presenters: 1) Prof. Simine Vazire 2) Dr. Israel Borokini

We are working on delivering a fantastic program filled with interactive events such as unconferences, hackathons and workshops. Stay tuned for the program updates on the

SORTEE webpage.

The conference is a forum to discuss and develop ideas, while also exploring current practices for advancing research in fields related to ecology and evolutionary biology. If these topics interest you, please consider becoming a member of SORTEE https://www.sortee.org/join. Membership includes FREE access to the conference.

We are trying our best to make this conference as inclusive as possible. We encourage individuals with questions regarding accessibility when facilitating a session or attending the conference to reach out to us at conference@sortee.org.

Nominations are still open for the SORTEE Commendation Awards! These awards celebrate projects that support open, reliable and transparent practices in eco-evo research. Nominations are open until August 15, 2025. Submit a nomination or learn more on the SORTEE Awards website.

We hope to see you in October.

Sincerely, The SORTEE Conference Committee

SORTEE Conference Committee <conference@sortee.org>

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Padova Italy Poeciliid Jul15-18

We are excited to announce the 12th International Conference of Poeciliid and Goodeid Biologists, to be held next 16-18 July 2026 at the University of Padova, Italy. Padova is a beautiful, lively city to discover, a major train hub with nonstops throughout Europe and beyond from the nearby Venice airport. We will have optional excursions before and after the meeting. The conference is timed right before the International Society for Behavioral Ecology conference, which starts July 20 in Torino. Please go tohttps://groups.google.com/g/poeciliidae2026 to receive updates.

Dr. Ingo Schlupp Presidential Professor of Biology School of Biological Sciences, University of Oklahoma

Director of the International Stock Center of Livebearing Fishes: https://international-stock-center-for-livebearing-fishes.oucreate.com/blog/ Webpage: https://ingoschlupp.com/ Book: https://global.oup.com/academic/product/male-choice-female-competition-and-female-ornaments-in-sexual-selection-9780192872586?lang=en&cc=us "Schlupp, Ingo B." <schlupp@ou.edu>

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SmokyMountains SEPEEG EvolGenet Oct3-5

SouthEastern Population, Ecological, and Evolutionary Genetics (SEPEEG) brings together scientists from institutions in the Southeastern US to discuss their research on ecology, population biology, evolution, and genetics. It will be held in the Great Smoky Mountains the weekend of Oct 3-5. We will have research talks and a poster session. The meeting is student-friendly and fun. See the link for more information:

https://sepeeg2025.blogspot.com/ Benjamin M. Fitzpatrick Ecology and Evolutionary Biology University of Tennessee https://fitzpatrickabc.blogspot.com "Fitzpatrick, Benjamin (Ben Fitzpatrick)" <benfitz@utk.edu>

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SwissAlps EvolArtSelection Aug12-15

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

Where: in a remote mountain hotel in the Jungfrau-Aletsch-Bietschhorn UNESCO World Heritage.

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

We invite PhD students, postdocs, and researchers to join us for a high-level CUSO course exploring how wild populations are being unintentionally shaped by artificial selection often with unforeseen consequences. While natural and sexual selection are well-studied, less is known about how human activities (e.g., non-random exploitation) alter selection regimes and increase genetic load, ultimately affecting population fitness and evolutionary potential. This workshop will address these pressing questions in the context of global environmental change and rapid evolution.

Further information & registration: https://www.unil.ch/dee/en/home/menuinst/research/research-groups/wedekind-group/workshop-evolutionary-consequences-2025.html Claus Wedekind, PhD

Full Professor Department of Ecology and Evolution, Biophore, University of Lausanne, 1015 Lausanne, Switzerland. Tel. +41 21 692 42 50 https://www.unil.ch/dee/wedekind-group Claus Wedekind <claus.wedekind@unil.ch>

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Tours France EvolEntomology Jun29-Jul3

Hello everyone,

We are delighted to announce that the next European Congress of Entomology will take place in Tours (France) from June 29 to July 3, 2026. Visit our website now: www.ece2026.org/ The plenary lectures will be given by Jérôme Casas (France), Cleo Bertelsmeier (Switzerland), Martin Kaltenpoth (Germany), Bregje Wertheim (Netherlands), and Francesco Pennachio (Italy).

The scientific committee has already planned over 50 symposia across the following topics:

Biodiversity Ecology and Behavior Genetics, Genomics and Evolutionary Biology Global Change Insect Vectors Insects and Society Insects as Solutions Insects Through Time Physiology and Biochemistry Social Insects

We are confident that everyone will find a space to present their work, expand their network, and quench their thirst for knowledge about insects of all kinds!

Registration and submissions will open on July 10, 2025.

We hope many of you will join us for this conference!

Elisabeth Herniou and David Giron On behalf of the ECE2026 Organizing Committee

Dr Elisabeth Herniou Directrice de Recherche CNRS

Institut de Recherche sur la Biologie de l'Insecte UMR 7261 CNRS - Université de Tours Faculté des Sciences Parc Grandmont 37200 Tours Tel: +33 247 367381 Mail: elisabeth.herniou@univ-tours.fr Bluesky: @hernioue.bsky.social

Co-Chair of the XIII European Congress of Entomology 2026 - ece2026.org

"Elisabeth Herniou (Univ)" <elisabeth.herniou@univ-tours.fr>

Warsaw PolishEvolutionaryConf Sep8-10

We are happy to invite you to the 11th Polish Evolutionary Conference.

Polish Evolutionary Conference (PEC) in annual meeting of the broad-sense evolutionary biologists. This year, PEC conference is aimed at integrating micro- and macro worlds. Besides traditional topics such as evolutionary ecology, there will be sessions on evolutionary processes at the cellular scale, such as endosymbiosis, adaptation of microbial organisms to the changing environment, host-microbial interactions, and many more.

PEC in relatively small conference with several sessions of contributed talks, and long breaks facilitating networking. We particularly encourage young researchers to come and present their work in a friendly atmosphere.

The invited speakers include:

*Krystyna Nadachowska-Brzyska, Jagiellonian University, Krakow, Poland Investigates the influence of extreme fluctuations in population size of outbreaking species on the dynamics of neutral and adaptive genetic variation using genome-wide datasets and novel analytical approaches.

* Gytis Dudas, Vilnius University, Lithuania Studies RNA virus evolution at both short (genomic epidemiology) and long (metagenomic virus discovery) timescales.

* Stevens, Lewis, Wellcome Sanger Institute, UK Interested in genome evolution in animals, with a particular interest in nematodes.

* Michael Westbury, University of Copenhagen, Denmark Interested in the production and analysis of genomic data from modern, historical, and palaeontological specimens. Uses population and comparative genomic analyses to better understand their respective evolutionary histories and relationships.

When:8-10 September 2025 Where: Warsaw, Poland Fee:

only 450PLN (~100 euro) Abstract submission deadline: 15.06.2025 More info: https://pec2025.biol.uw.edu.pl/ On behalf the organising committee,

dr hab. Agnieszka Kloch, prof. UW ZakÂ³ad Ekologii, WydziaÂ³ Biologii Uniwersytet Warszawski Âwirki i Wigury 101, 02-089 Warszawa

Agnieszka Kloch <a.kloch@uw.edu.pl>

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GradStudentPositions

HongKongU AvianCognitionBehaviour

*** PhD Positions in Bird Cognition, Intelligence, and Behaviour ***

We are looking for highly motivated candidates for PhD positions to work on bird cognition, intelligence, senses, and communication. A key focus of this project is to understand how birds communicate and interact in a social environment, and how their mental capacities help them to survive and reproduce. The lab has established a study system and is routinely conducting animal behaviour experiment. The PhD will have extensive opportunities to interact with other lab members and collaborators and involve in different projects.

Duration: This is a four-year full-time PhD position.

Start Date: 2025 or 2026.

Qualifications and requirement: - BSc/MPhil degree in biology or related fields (or will have completed a BSc/MPhil before the position start); - High motivation and strong interest for animal behaviour and evolutionary biology; - Proficiency in English; - Background in animal behaviour, molecular ecology, behavioural ecology, evolutionary biology, chemical analysis, bioinformatics, engineering, computer science, or related disciplines is desirable; - Willingness to learn new skills in AI, etc.

Study Environment: The University of Hong Kong is an English-speaking institute and one of the most international universities in Asia. It has a rank of 35 according to the Times Higher Education World University Rankings 2025.

A Postgraduate Scholarship will be offered, in addition to annual leave and medical benefits

How to apply: Please send (1) a CV (including a list of publications), (2) motivation letter describing research interests and skills, (3) transcripts, and (4) contact details for 2-3 references to Dr. Simon Sin (sinyw@hku.hk). Review of applications will begin immediately and continue until the position is filled.

Simon Sin Assistant Professor School of Biological Sciences Kadoorie Biological Sciences Building The University of Hong Kong Pok Fu Lam Road, Hong Kong Lab website: www.simonywsin.com <sinyw@hku.hk>

Yung Wa Sin <sinyw@hku.hk>

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HongKongU Two EvolAvianPopGenomics

*** PhD Positions in Evolutionary Genomics or Population Genomics ***

We are looking for highly motivated candidates for PhD positions to work on evolutionary genomics or population genomics. Key focuses of the project are to understand genotype-phenotype association, and the selective forces that shape genetic and phenotypic variation. Example research areas include genetic basis of avian coloration and population genomics of birds. The PhD will have extensive opportunities to interact with other lab members and collaborators and involve in different genomics projects.

Duration: This is a four-year full-time PhD position.

Start Date: 2025 or 2026.

Qualifications and requirement: - BSc/MPhil degree in biology or related fields (or will have completed a BSc/MPhil before the position start); - High motivation and strong interest for genomics and evolutionary biology; - Proficiency in English; - Background in genomics, bioinformatics, evolutionary biology, molecular genetics, or related disciplines is desirable; - Willingness to learn new skills in bioinformatics, molecular lab work, etc.

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Simon Sin Assistant Professor School of Biological Sciences Kadoorie Biological Sciences Building The University of Hong Kong Pok Fu Lam Road, Hong Kong Lab website: www.simonywsin.com <sinyw@hku.hk>

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Simon Sin Assistant Professor School of Biological Sciences Kadoorie Biological Sciences Building The University of Hong Kong Pok Fu Lam Road, Hong Kong Lab website: www.simonywsin.com <sinyw@hku.hk>

Yung Wa Sin <sinyw@hku.hk>

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IllinoisStateU PlantInsectInteractions

WHAT: PhD and/or MSc positions in Evolutionary Ecology of plant-insect interactions

WHERE: Goldar Lab (https://goldarlab.weebly.com/). School of Biological Sciences at Illinois State University.

WHEN: Starting in Spring, Summer or Fall 2026

Description:

PhD and/or MSc positions are available in the Goldar Lab in the School of Biological Sciences at Illinois State University to start in Spring, Summer or Fall 2026. The positions are broadly focused on how chemical ecology, environmental gradients and climate change shape plant-insect interactions. Our lab seeks harnessing classic hypotheses of Plant Defense Theory to investigate how plant-insect interactions vary in an organ-dependent manner across environments, and to predict changes in magnitude and direction of performance of plants, insects and their interactions in response to simultaneous stresses of global change. The work will employ greenhouse, lab and/or field experiments and will involve the use of biotic interactions with herbivores and pollinators.

I am looking for a highly motivated PhD and/or MSc candidate to join the lab. We offer a vibrant, collaborative and respectful working environment with high-quality supervision. You should have a degree in any field of Biology and a strong interest in evolutionary ecology. Proficiency in English, both orally and written, is also required. Prior experience with plants and/or insects, chemical ecology, population genetics and genomics, and foundations in statistics are an advantage.

If you are interested, please contact me at xlopezg@ilstu.edu and include in a single PDF file 1) a brief description of research interests (for PhD or MSc), experience and career goals, 2) CV/Résumé, 3) writing sample (publication, manuscript in preparation, thesis), and 4) names and email addresses of 3 references maximum. The deadline is June 30th.

The School of Biological Sciences at ISU hosts many labs with access to molecular and ecological tools, spanning diverse scientific disciplines, including neuroethology, microbiology or conservation. Opportunities for collaborations between labs are also possible. Also, it has access to greenhouses, growth chambers and field sites for plant cultivation and experiments. The School of Biological Sciences provides funding for graduate students through Teaching Assistantships and Research Assistantships. More information on the department, application procedures, and requirements can be found for Master's (https://biology.illinoisstate.edu/academics/behavior-ecology-evolution-and-systematics-masters/) and Doctoral (https://biology.illinoisstate.edu/academics/-behavior-ecology-evolution-and-systematics-doc/) programs. The city of Normal also offers an excellent quality of life, attractive surroundings for outdoor sports and nearby iconic cities and places.

Please feel free to contact me if you have any questions. I am looking forward to receiving your application!

Xosé López Goldar Assistant Professor in Evolutionary Ecology xlopezg@ilstu.edu

Dr. Xosé López Goldar (@XGoldar) Assistant Professor in Evolutionary Ecology 125 S. Fell Avenue, Science Laboratory Building (SLB) School of Biological Sciences < https://biology.illinoisstate.edu/ > Illinois State University Normal, IL 61761 Email: xlopezg@ilstu.edu Website: https://goldarlab.weebly.com/ "Lopez Goldar, Xose" <xlopezg@ilstu.edu>

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INRAE ToulouseFrance DemographyInferenceInLivestock

We (Pierre Faux and Bertrand Servin) are looking for candidates to work on population genomics of livestock populations and infer their past demographic histories. Key focus of the project is to evaluate recent methods for demographic inference (based on Ancestral Recombination Graphs or Deep Learning) on large datasets of livestock species. This evaluation will be facilitated by knowledge of deep pedigrees for some of these populations, giving access to their recent dynamics. Applications are anticipated in Sheep and Goat.

Duration: This is a three year full-time PhD position.

Start Date: Before Dec 2025

Qualifications and requirements: - Masters' degree in genetics, bioinformatics or applied statistics (needs to be completed before start) - Strong interest in genomics and evolution - Knowledge in programming in Python, R or similar language. Experience with scientific computing and/or deep learning libraries would be a plus. - It is not required to speak French in the work environment

More information about the position and application can be found at : https://jobs.inrae.fr/en/ot-25908 bertrand.servin@inrae.fr https://genphyse.inrae.fr

Bertrand Servin <bertrand.servin@inrae.fr>

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LarlstadU Sweden FlySexDimorphism

I have openings for a PhD student to work on questions related to the evolution of sexual dimorphism in flies, as well as a postdoc to work on related questions either using flies or comparative methods.

PhD add: https://kau.varbi.com/en/what:job/-jobID:828774/iframeEmbedded:0/where:4 Postdoc add: https://kau.varbi.com/en/what:job/jobID:828768/-iframeEmbedded:0/where:4 Deadline is June 15 for both Email stephen.de.lisle@kau.se for more information or questions. All the application materials have to be submitted on the online portal varbi

N?r du skickar e-post till Karlstads universitet behandlar vi dina personuppgifter < https://www.kau.se/gdpr >.

When you send an e-mail to Karlstad University, we will process your personal data < https://www.kau.se/-en/gdpr >.

Stephen De Lisle <stephen.de.lisle@kau.se>

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SimonsFoundation Evolution

The Simons Foundation's Life Sciences division is now accepting applications for its Simons Graduate Fellowships in Ecology and Evolution awards (https://www.simonsfoundation.org/grant/simons-graduate-fellowships-in-ecology-and-evolution/). *The deadline for fellowship applications is July 31, 2025, at 12:00 p.m. (noon) Eastern time.*

The purpose of these awards is to provide support for students entering U.S.-based Ph.D. programs with a plan to perform research in ecology and evolution. While we will consider all projects in ecology and evolution, we are particularly interested in interdisciplinary research that jointly considers processes on both ecological and evolutionary timescales or that links studies of ecology and evolution to other STEM fields, including physics, computer science, mathematics, chemistry and other areas of biology, especially genetics.

Among other eligibility requirements, applicants must be entering or applying for Ph.D. programs in biology or a subfield of the life sciences to study ecology and evolution, with matriculation to start no later than fall 2026. It is permissible for applicants to hold a master's degree and encouraged that they hold a master's degree in physics, mathematics, computer science or engineering. Individuals who already hold a Ph.D. or other terminal degree, or who have enrolled in a Ph.D. program prior to fall 2025, are not eligible. Fellowships must be hosted at United States institutions, at a campus within the United States. There are no citizenship requirements.

For any questions, please contact lifegrants@simonsfoundation.org.

Molly Potter <mpotter@simonsfoundation.org>

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SZN Italy EvolutionGenomicsRangeShifts

Fully funded PhD opportunity - Stazione Zoologica Anton Dohrn, Italy

Dear all,

We are excited to announce a fully funded 3-year PhD position at Stazione Zoologica Anton Dohrn (Naples, Italy)! This project will investigate the evolutionary processes driving range shifts in a cool marine snail, offering a unique opportunity to work at the intersection of evolution, genomics, ecology, conservation, and marine biology.

The successful candidate will join a dynamic, international, and transdisciplinary research team, benefiting from excellent training, collaboration opportunities, and cutting-edge scientific resources.

Find full details and application instructions here: raffinifrancescalab.weebly.com/join.html

Application deadline: June 14th, 2025, at 12:00 CET

If you know talented students who might be interested, we'd greatly appreciate it if you could share this opportunity with them!

Thank you for your support we look forward to welcoming a new team member!

Best wishes, Francesca

Francesca Raffini, PhD Full Scientific Researcher

Department of Biology and Evolution of Marine Organisms Stazione Zoologica Anton Dohrn Villa Comunale 80121 Naples Italy

Centre for Marine Evolutionary Biology Department of Marine Sciences Tjärnö Marine Laboratory University of Gothenburg Laboratorievägen 10 SE 453 96 Strömstad Sweden

Lab: https://raffinifrancescalab.weebly.com/ Littorina Research Community: https://littorina.at.biopolis.pt/ WinkleWatch - a community science project on snail color: https://littorina.at.biopolis.pt/winklewatch SZN: https://www.szn.it/index.php/en/ CeMEB: https://www.gu.se/en/cemeb-marine-evolutionary-biology Francesca Raffini <francesca.raffini3@gmail.com>

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TechUMunich ParasitoidEvolution

PhD position: Evolution of Chemoreception in Parasitoids

Project description: Chemical signaling, the most ancient and widespread form of communication, can play a crucial role in maintaining species boundaries through exclusive communication channels that potentially drive speciation. Cuticular hydrocarbons (CHCs), long-chained lipids found on the surface of insects, serve as an excellent example of this. CHCs have been shown to encode species-specific sexual signals across various chemical communication systems in insects. However, how insects perceive, discriminate, and process the biological information encoded in CHC profiles is still poorly understood. This PhD project aims to address these knowledge gaps by focusing on Nasonia, a species complex of parasitoid wasps that serves as an evolutionary and ecological model system.

PhD Position: The PhD candidate will investigate the chemoreception networks involved in CHC perception, particularly in the context of prezygotic reproductive isolation within the Nasonia species complex. Our previous research has already deciphered the patterns of sexual attractiveness in Nasonia CHC profiles. Expanding on this foundation, the PhD candidate will employ a suite of advanced techniques single-sensillum recording (SSR), gas-chromatography/ mass-spectrometry (GC-MS), electro- antennographic detection (EAD), RNAi knockdowns, and behavioral olfactometer assays to elucidate how divergence in CHC perception has potentially contributed to prezygotic reproductive isolation. This will largely advance our still limited knowledge on the intricate mechanisms of CHC perception in particular and on speciation mechanisms mediated by chemosensory evolution in general. The successful candidate will join the newly established Heisenberg group "Evolution of chemical communication" (PD Dr. Jan Buellesbach) at the Plant-Insect Interactions group (Prof. Sara D. Leonhardt) as part of the TUM Department of Life Science Systems. Starting date is fall 2025. The position is fixed-term (36 months). Salary scale: TV-L 13, 65%. As part of the assigned duties, there will be ample opportunity to conduct the independent scientific research necessary for the completion of a doctorate. The limitation complies to ç 2, 1 WissZeitVG.

Job profile - We require: - Strong interest and motivation in conducting evolutionary and chemical ecological research at different levels. - MSc/diploma in a relevant field (e.g., evolutionary biology, chemical ecology, sensory biology). - Strong experience with chemoreception and sensory biological techniques (SSR, GC-EAD, EAG). - Experience in analytical chemistry (GC-FID, GC-MS). - Experience in or willingness to learn statistical data analyses, data processing and analytical chemical analyses. - Excellent command of English language (written & oral) and experience with scientific writing.

We offer: - Friendly and inspiring working atmosphere in a highly international young research group, as part of a vivid ecological department. - Graduate Education at an excellent university ranked number 1 in Germany and 12th worldwide. - Free access to transferable skill and statistical courses as part of the TUM Graduate School and the Biodiversity Exploratories.

Salary & Conditions: TUM strives to raise the proportion of women in its workforce and explicitly encourages applications from qualified women. Applications from disabled persons with essentially the same qualifications will be given preference. As part of your application, you provide personal data to the Technical University of Munich (TUM). Please view our privacy policy on collecting and processing personal data in the course of the application process pursuant to Art. 13 of the General Data Protection Regulation of the European Union (GDPR) at https://portal.mytum.de/kompass/datenschutz/Bewerbung/. By submitting your application you confirm to have read and understood the data protection information provided by TUM. Find out more about us at www.tum.de .We invite applications from highly motivated candidates with passion for and experience in chemical ecological research, and ideally with experience in chemoreception and chemical analyses. Please send your application via eMail to Jan Buellesbach (jan.buellesbach@tum.de) as a single PDF document until the 3rd of July 2025. Applications should include a motivation letter, a short summary of research interests and experience, CV, and contacts of two potential referees.

PD Dr. Jan Buellesbach Evolution of Chemical Communication Life Science Systems Technical University of Munich Hans-Carl-von-Carlowitz-Platz 2 D-85354 Freising 100004, Germany

E-mail:jan.buellesbach@tum.de

Jan Buellesbach <buellesb@uni-muenster.de>

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UAlberta ComputationalEvolBiol

Graduate Student Opportunities: AI Foundation Models for Organismal Biology Fully Funded MSc and PhD Positions with Dr. Russell Dinnage Department of Biological Sciences, University of Alberta

Start Date: January 2026 or September 2026 (flexible)

Funding: Competitive funding packages available through University of Alberta assistantships and fellowships. Additional funding opportunities available through external scholarships and awards.

Research Focus

The Dinnage Lab develops foundation models for organismal biology - artificial intelligence systems that learn from and help us understand living systems from molecules to ecosystems. Our work bridges computational innovation with fundamental biological questions, creating new approaches that integrate biological principles into AI architecture design.

Students will have opportunities to engage with three major research themes:

1. AI-Driven Simulation-Based Inference Develop novel AI foundation models for population genomics and phylogenetic comparative methods using Prior-Data Fitted Networks (PFNs) and other cutting-edge approaches. Projects may involve creating systems that can infer demographic histories from genomic data or model complex trait evolution across phylogenies.

2. High-Throughput Phenomics Work with museum collections and citizen science datasets to develop AI frameworks for automated phenotype extraction and analysis. Students can develop methods for creating “digital-first specimens”, develop new approaches to large-scale morphological analysis, or leverage AI to connect different species’ data sources using multimodal models, to create ’vector databases’ for comprehensive biodiversity analysis.

3. AI-Biology Cross-Disciplinary Inquiries Explore AI systems as model organisms for evolutionary research, develop biology-inspired explainable AI methods, or create in silico evolutionary simulations using AI models as representations of complex phenotypes. This cutting-edge work examines how evolutionary principles can inform AI development and vice versa.

Students may also propose projects outside these themes in the area of computational or quantitative organismal biology, or at the intersection between organismal biology and machine learning or artificial intelligence methods.

Qualifications

Minimum Requirements: * BSc in biology, ecology, evolution, computer science, statistics, mathematics, or related field * Strong interest in both organismal biology and computational methods * Admissible to University of Alberta graduate programs

Competitive Applicants Will Have: * Experience with programming in R, Python, or similar languages * Background in machine learning, deep learning, or advanced statistical methods * Experience with large datasets or computational biology approaches * Strong written and oral communication skills * Interest in interdisciplinary collaboration and open science practices

The Advisor

Dr. Russell Dinnage is an Assistant Professor whose research develops AI foundation models for understanding organismal biology. He works at the intersection of the fields of ecology, evolutionary biology, statistics and computer science. His work has been published in leading journals including Nature Ecology & Evolution, Science Advances, and Evolution. He currently serves as Associate Editor at Methods in Ecology and Evolution. His research program emphasizes ethical AI development, open science principles, and collaborative approaches to complex biological questions.

The Environment

The University of Alberta's Department of Biological Sciences offers world-class research facilities and a collaborative environment for interdisciplinary work. Students will have access to high-performance computing resources, extensive natural history collections, and opportunities to collaborate with the Alberta Machine Intelligence Institute (Amii). Edmonton provides an excellent quality of life with abundant outdoor recreation opportunities and a vibrant cultural scene.

Application Process

Applications are reviewed on a rolling basis. For full consideration for a Jan 2026 start, submit by July 15, 2025 (to allow time for application preparation before the University of Alberta deadline of August 1, 2025).

Before contacting me, please: * Review our recent publications and research themes on the lab website * Familiarize yourself with University of Alberta Biology Department admission requirements (https://www.ualberta.ca/en/biological-sciences/graduate-studies/for-applicants/index.html) * Explore funding opportunities and program details (https://www.ualberta.ca/en/biological-sciences/graduate-studies/for-applicants/program-funding.html) * Consider additional scholarship opportunities (

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UExeter UK SalmonParasiteResistanceGenomics

Funded PhD at the University of Exeter on Leveraging Genomic Technologies to Investigate the Molecular Basis of Sea Lice Resistance

Link to Application and Detailed PhD Description: https://www.exeter.ac.uk/study/funding/award/?id=5542 The University of Exeter's Department of Biosciences is inviting applications for a PhD studentship funded by CEFAS and the Faculty of Health and Life Sciences to commence on 22 September 2025 or as soon as possible thereafter.

Our research broadly applies cutting-edge genomic tools to understand the molecular, evolutionary, and ecological underpinnings of trait variation in aquatic species, generating insights that support aquaculture innovation, fisheries management, and biodiversity conservation.

This PhD project will focus on tackling the threat of sea lice parasitism in wild and farmed salmonids by uncovering the molecular and cellular mechanisms that drive natural resistance within and between salmonid species. The project will involve molecular lab work (e.g., preparing tissue samples for transcriptomic sequencing), and bioinformatic analysis of newly generated and existing datasets, including bulk RNA sequencing, single-nuclei RNA sequencing, and spatial transcriptomics. The outcomes of this research will directly inform the development of biotechnological solutions to enhance sea lice resistance in salmonids, improving sustainability and animal welfare, while also providing fundamental insights into the evolution of parasite resistance.

The successful student will receive extensive training in molecular biology, bioinformatics, immunology, and parasitology, under the supervision of an interdisciplinary team from the University of Exeter, University of Stirling, and CEFAS (Centre for Environment, Fisheries and Aquaculture Science). This strong collaboration between government and academia will provide the student with access to cutting-edge lab facilities and a dynamic research environment.

The ideal candidate will have a strong interest in fish and/or parasite biology, experience in designing and conducting independent research, and excellent written and oral communication skills. They should also have experience using bioinformatics tools to analyse data (particularly within R and Linux environments), writing and debugging code, and conducting molecular lab work (e.g., DNA/RNA extraction, PCR). Experience working with large genomic datasets and/or high performance computing will also be considered an asset.

For eligible students the studentship will cover Home tuition fees plus an annual tax-free stipend of at least ?20,780 for 3.5 years full-time, or pro rata for part-time study and a research budget of ?21,000 for conferences, lab, field and research expenses. The student would be based in the Faculty of Health and Life Sciences at the Streatham Campus in Exeter.

Please see the PhD advertisement page on the University of Exeter website for further details: https://-www.exeter.ac.uk/study/funding/award/?id=3D5542 Applications must be received through the University of Exeter website (link above) by June 20.

For any informal inquiries regarding the position, please email S.Salisbury2[@]exeter.ac.uk.

Dr. Sarah Salisbury Lecturer in Sustainable Aquaculture Dept. of Biosciences University of Exeter

S.Salisbury2@exeter.ac.uk

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UGroningen ManagementBirdPopulations

PhD: Multi-dimensional population projections and management of wild bird populations

Job description

The Groningen Institute for Evolutionary Life Sciences (GELIFES - https://www.rug.nl/research/gelifes/) offers a 4-year M20 Program funded PhD position for a project on “Multi-dimensional population projections and management of wild bird populations in times of climate change”, with the Seychelles warbler (Acrocephalus sechellensis) as a model system.

The project is supervised by Prof. Hannah L. Dugdale, Dr Viktor A. Venhorst and Dr Stephen A. Adaawen. The project is in collaboration with Profs Jan Komdeur, Terry Burke and David Richardson, as part of the Seychelles warbler research group. The candidate will join a lively and highly international team of PhD and Master students working on human demography, and ecology and evolution in wild animals, supported by laboratory and analytical technicians.

Massive human-mediated habitat loss over the last century has elevated vertebrate extinction rates up to 100 times higher than the background level. Species confined to islands that have nowhere else to go in the event of habitat loss are at particular risk of extinction. Demographic analyses of wild vertebrate populations on small islands are now urgently needed to inform direct intervention and management to save many endangered species from extinction. This project will conduct state-of-the-art multidimensional projection modelling to project the impact of climate change and age structure on population size.

The once critically endangered species Seychelles warbler is a small insectivorous passerine bird confined to five small islands in the Seychelles. The project will use the unique long-term Seychelles warbler dataset (spanning 40 years) to conduct detailed multidimensional projection modelling. It will contrast projections for the five islands to inform management decisions. The project will specifically address whether additional translocations are required to establish new populations on other islands, or to mix genetic variation between already established populations, to protect the species from extinction.

The project works with government agencies, NGOs, and private islands owned by local families and businesses to inform and implement conservation action plans.

The candidate will be required to:

- Design, plan and conduct a programme of investigation, in consultation with the three supervisors. - Produce a PhD thesis, written in English, consisting of four data chapters, an introduction and discussion at the level of international scientific journals. - Disseminate the research through publication in leading peer-reviewed journals, presentations at international conferences, outreach, social media etc. - Conduct fieldwork over three field seasons, of up to three months each season. - Collaborate with other researchers on the long-term project and other relevant groups. - Work interdisciplinarily with ecologists, conservation biologists and demographers. - Contribute to teaching 10% of the time, by supervising BSc and MSc students, and assisting on courses.

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

Qualifications

We are looking for a candidate who:

- Holds a Master degree (or will graduate before appointment date), ideally with distinction and one year of research during the Master. - Is curiosity-driven and passionate about fundamental research in the context of demography, ecology and conservation biology. - Has strong quantitative skills (analyses of long-term data, modelling and statistical analyses, ideally in the R environment) . - Is proficient in English and meets the university's English language requirements (https://www.rug.nl/(...)requirements?lang=3Den).

The ideal candidate will also have:

- Data wrangling experience in extracting data from databases (e.g. Access) or large datasets. - Fieldwork experience on birds (mist-netting, colour-ring reading, behavioural observations) in a harsh environment. - Written at least one scientific publication - Strong communication skills, and is motivated to disseminate results to both scientific peers and a broad audience. - Excellent teamwork skills, and is willing to work with a diverse group of researchers and technicians, and can also work independently.

Organisation

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UGroningen NL OmicsAdaptationEnvironmentalDisease

The Jones Lab at the University of Groningen invites applications for a fully-funded 4 year PhD position in molecular, functional and population genomics of vertebrate adaptation.

The position involves decoding how variation in genome function in natural populations influences gene regulation, phenotype and environmentally-dependent fitness. We aim to identify molecular mechanisms in natural populations that provide evolutionary solutions to environmentally-mediated disease.

We leverage the unique advantages of natural and laboratory studies of adaptively diverging ecotypes of threespine stickleback fish - now a classical model of evolution at the molecular and functional genetics level. This project has the potential to combine diverse 'omic datasets (e.g. ChIP-, ATAC-, RNA-, DNA- and single-cell multiomics); studies of diverse wild-derived strains at different developmental stages and under different environmental conditions in a state-of-the-art fish facility; and natural population hybrid zones studies of divergently adapted ecotypes.

These project will build upon our research into the following areas, e.g., molecular basis of adaptation (Jones et al (2012) Nature, Verta and Jones (2019) Elife), recombination variation (Venu et al 2024 Nature Ecology and Evolution, Dreau et al 2019 Nature Communications), and evolutionary processes that facilitate and constrain rates of adaptation in natural populations (e.g. Kirch et al 2021 Current Biology; Schluter et al 2021 PNAS).

GELIFES at the University of Groningen, the Netherlands is a unique institute dedicated to evolutionary biology. Its members' research spans from ecosystems through organismal biology to neurobehaviour. Our group members are embedded with the Evolutionary Genetics and Developmental Biology (EGDB) expertise cluster, and enjoy close interactions with the lab of Frank Chan.

Groningen is vibrant and lively; it is the youngest city in the Netherlands. It ranks among the highest for living standards, happiness and student satisfaction. All seminars and communications are in English.

To apply: We seek a motivated candidate with experience in bioinformatics, gene regulation and/or development whose interests span functional and evolutionary genomics. Please e-mail a cover letter, CV, academic transcripts with names and contact information of referees to Associate Professor Felicity Jones (f.c.jones@rug.nl).

Felicity C Jones <f.c.jones@rug.nl>

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UGroningen OriginOfLife

Interested in the emergence of life on Earth, and in doing a PhD project? We have a PhD position available on Modelling the emergence of information transfer in prebiotic self-replicating systems! (https://www.rug.nl/about-ug/work-with-us/job-opportunities/?details=00347-02S000BBOP) - applications still welcome until June 11 - as one of the 15 PhD projects in the PRELIFE consortium (https://www.originscenter.nl/prelife/).

The origin of life remains one of the greatest mysteries in science. While many theories have been proposed, no single explanation has yet gained universal agreement. That's where the PRELIFE consortium comes in. PRE-

LIFE unites experts across a wide range of disciplines from astronomy, biology, chemistry, computer science, earth and planetary sciences, education, mathematics, to physics. Together we will explore two fundamental questions: How did life emerge on Earth, and how common are the conditions elsewhere in the universe?

To answer these profound questions, we will take an interdisciplinary approach, bringing together diverse perspectives to unlock new insights. But we believe this question is not just for scientists, it is for everyone. That's why we will invite teachers, students, and the public to join us, through educational programs, artistic collaborations, and museum partnerships. We're searching for answers to life's biggest questions, and we need your help. As part of the PRELIFE program we offer 15 exciting research projects which can be found at http://www.prelife.originscenter.nl of which the research project of the current PhD position is one.

This project aims at uncovering how the capacity for Darwinian evolution may have first arisen. While parts of this puzzle have been solved, an important open question is the emergence of information transfer (inheritance), one of the three key ingredients for Darwinian evolution. Interestingly, for evolution to function, information transfer must be near-perfect, but not flawless: with perfect replication, no variation will be generated for natural selection to act on. In this joint PhD project between the University of Groningen (promotors Prof. Martijn Egas, martijn.egas@rug.nl, and Prof. Rampal Etienne, r.s.etienne@rug.nl) and Utrecht University (co-promotor Dr. Bram van Dijk, b.vandijk@uu.nl), we aim to uncover the conditions that allow near-perfect information transfer to arise from simple interactions between simple building-blocks in early prebiotic systems.

In this project, you will use computational models to explore the minimal functional requirements for self-replication to emerge from polymerising molecules. Instead of simulating specific chemistries in full detail, we will build abstract, spatially explicit models of interacting molecules to examine which properties (features of both the building blocks and the environment) enable replication with sufficient variation and inheritance. Using an open-ended model, we will explore molecular structures of life as we know it (DNA), as well as other potential polymerisation rules. These models will also help interpret and guide experiments, e.g. the stacking fiber system pioneered by Prof. Sijbren Otto at the University of Groningen.

Martijn Egas <martijn.egas@rug.nl>

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WoodsHole ClimateConference Nov7-9

Dear all,

We are pleased to announce that MIT and the Woods Hole Oceanographic Institution will be hosting the 19th Annual Graduate Climate Conference (GCC) on November 7-9, 2025, at Woods Hole, MA. This conference is fully funded, with additional travel funding available for select recipients. Applications < https://urldefense.com/v3/__https:/-docs.google.com/forms/d/e/1FAIpQLSdZfJbW-OYd61ulhxa4zt5YeS330qmzyQUsb6CG4Ss9qmztBg/-viewform?usp=header__;!!IaT_gp1N!2jKHlbSlaZIpgg8SNo3lX7HVr37AC dSGygPpHlpyqo9uW0Ugxjhuk1oq-f81goeWZjxa3CA$ > are due in about a week on June 15th. More information can be found below.

The GCC is an annual interdisciplinary climate conference run by graduate students, for graduate students, featuring panel discussions, presentations, workshops, social events, and more. More information about the organizers, conference history and logistics can be found on the GCC website < https://urldefense.com/-v3/__https:/graduateclimateconference.github.io/-__;!!IaT_gp1N!2jKHlbSlaZIpgg8SNo3lX7HVr37ACVRGKZnnIRO2LN4-dSGygPpHlpyqo9uW0Ugxjhuk1oq-f81goeUU6zvgug$ >.

GCC highlights climate research from a variety of disciplines within the physical, natural, and social sciences and humanities. The organizers strive to feature a diverse representation of students and research topics to create a broader, more inclusive community for emerging leaders in climate-related fields. We encourage students from all backgrounds and stages of their graduate careers to apply.

The deadline for abstract submission is June 8th. The application link is attached above and can be found on the website as well. There is no fee to register or apply. Acceptances will be emailed in July. Limited funding to cover any costs incurred by attending the conference will be awarded on an as-needed basis to as many participants as possible.

For conference updates, please check the GCC website < https://urldefense.com/v3/-__https:/graduateclimateconference.github.io/-__;!!IaT_gp1N!2jKHlbSlaZIpgg8SNo3lX7HVr37ACVRGKZnnIRO2LN4-

dSGygPpHlpyqo9uW0Ugxjhuk1oq-f81goeUU6zvgug$ > or follow us on social media.

Please contact the Organizing Committee with any additional questions at gradclimateconference@gmail.com

We hope to see you this fall! Sincerely, The GCC 2025 Organizing Committee

Hanne Borstlap | Ph.D. Candidate Department of Environmental Science University of Virginia

tpv4jw@virginia.edu

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Jobs

AarhusU Denmark Biodiversity

The Center for Quantitative Genetics and Genomics (QGG)at Aarhus University(AU), Denmark, offers a position as a tenure-track assistant professor in population genetics, comparative genomics and/or bioinformatics applied to biodiversity monitoring and conservation biology.

https://www.au.dk/om/stillinger/job/tenure-track-assistant-professor-in-biodiversity-research-using-genetics Tenure-Track Assistant Professor in Biodiversity Research Using Genetics - Ledig stilling pï¿$\frac{1}{2}$ Aarhus Universitet

Ledig stilling ved Center for Kvantitativ Genetik og Genomforskning, Aarhus, Aarhus Universitet

www.au.dk Quentin Geissmann <qgeissmann@qgg.au.dk>

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KunmingInstZool China Multiple EvolutionaryBiol

Senior Principal Investigator, Junior Principal Investigator, and Postdoctoral Positions at the Kunming Institute of Zoology, Chinese Academy of Sciences (KIZ, CAS) Kunming, China; Competitive Salary + Benefits Packages

The Kunming Institute of Zoology in Kunming, China is recruiting Senior and Junior PIs and postdoctoral fellows across all its research fields, which include evolution, genetics, ecology, and conservation.

We have particular interest in recruiting a senior PI to develop scalable biodiversity monitoring, for both basic and applied science.

Kunming is a very liveable city with the ideal climate combination of high altitude (1900 m) in the subtropics. KIZ has no undergraduate teaching.

We will begin assessing applications on 12 August 2025.

To make informal queries regarding applications at the Senior and Junior PI levels, especially from non-Chinese nationals, please feel free to email me at dougwyu@mac.com.

I will post this announcement multiple times before the deadline. The formal announcement is below.

Douglas Yu

About the KIZ

The Kunming Institute of Zoology (KIZ) is directly affiliated to the Chinese Academy of Sciences (CAS). Located at the head of the Indo-Burma biodiversity hotspot, KIZ is dedicated to research in the fields of evolution, genetics, human disease mechanisms, ecology, and biodiversity conservation.

KIZ provides a fertile environment for scientific innovation and vibrant interactions, offering competitive remuneration packages and high-quality training programmes for graduate students and postdoctoral fellows. The Institute currently has 40 research groups and attracts postgraduate students from around the world. It is home to several major research platforms, including the State Key Laboratory of Genetic Evolution & Animal Models, the National Research Facility for Phenotypic and Genotypic Analysis of Model Animals (our primate facility), and the Kunming National High-level Biosafety Primate Research Centre (Level-3 Lab). For more information, see www.kiz.ac.cn or english.kiz.ac.cn < http://english.kiz.cas.cn/ >.

KIZ welcomes applications for (1) Senior Principal Investigators, (2) Junior Principal Investigators, and (3) Postdoctoral Fellows from interested individuals of all nationalities and ethnicities.

Positions: 1. Senior Principal Investigators (Level 2) To lead large research teams that tackle high-risk/high-reward questions in one or more of the research fields listed above. Level 2 PIs are equivalent to Full Professors in the western academic system.

Qualifications: - Candidates should have made significant contributions in one or more of the research fields listed above. - Candidates should have shown the ability to independently fund and lead a research team. - Candidates should have demonstrated a high degree of scientific integrity and interest in collaborative research.

Support: - Senior PIs will receive full support from KIZ to establish a research team of research technicians, postdoctoral fellows, and graduate students. In addition, KIZ will provide excellent research facilities, attractive start-up funding, and competitive salary, benefits, and housing subsidy.

2. Junior Principal Investigators (Level 4) - To establish independent research programmes in one or more of the research fields listed above. Level 4 PIs are equivalent to Assistant Professors in the western academic system.

Qualifications: - Candidates should have a PhD degree in a relevant field. - Candidates should have excellent scholastic achievements and exhibit the potential to develop into an independent scientist. - Candidates should demonstrate a strong team spirit and a high degree of scientific integrity.

Support: - Junior PIs will be supported with the resources necessary to establish an independent research programme, including start-up funds, laboratory space, and a salary and benefits, and housing subsidy. A mentorship committee of three senior PIs will provide guidance in research direction and laboratory management.

3. Postdoctoral Fellows To join one of the well-funded research laboratories in KIZ, contributing your expertise in evolutionary biology, genetics, molecular and cell biology, ecology, bioinformatics, and/or statistics.

Qualifications: - Candidates should have a PhD degree in a relevant field. - Candidates should demonstrate promising scholastic achievements, commitment to a high degree of scientific integrity, and be ambitious and self-motivated. - Candidates should have the ability to work both independently and as a team member and are encouraged to carry out independent research projects.

How to Apply (send to kizfsc@mail.kiz.ac.cn) - Cover letter (please specify your target position) - CV (include birthdate, nationality, and full publication list)

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LundU Sweden 2yr VisitingProf

Lund University has announced a number of visiting professorships, intended to attract international talent. The positions are for 2 years, at 20% of full time. The deadline to apply is August 17th. Please inform any international colleagues who might be interested!

Obs - only people with the title full professor are eligible. Women are particularly encouraged to apply.

Information and link to apply here: https://lu.varbi.com/en/what:job/jobID:835541/ Jessica.

Dr. Jessica K. Abbott Head of Biology department Lund University Phone: 046 222 3801 Website: https://www.biologi.lu.se/ Jessica Abbott <jessica.abbott@biol.lu.se>

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NORCE Bergen Norway PaleogenomicsLabEngineer

Open Engineer position in the Molecular Ecology & Paleogenomics Research Group at NORCE

Laboratory Engineer

Application via jobbnorge.no https://www.jobbnorge.no/en/available-jobs/job/282953/laboratory-engineer About the position

We are pleased to announce an opening for a permanent laboratory engineer position in the Molecular Ecology & Paleogenomics Research Group (MEP) at NORCE Climate and Environment in Bergen (https://www.norceresearch.no/en/research-group/mep-molecular-ecology-paleogenomics).

The Molecular Ecology and Paleogenomics Research Group (MEP) applies molecular tools to address basic ecological and climatic questions. Our research covers marine and fresh water, sediments, and sea ice and contribute to a better understanding, and a sound management, of marine and freshwater ecosystems. MEP has a project portfolio that includes research projects funded by the Norwegian Research Council (RCN), European Research Council (ERC) and EU-H2020. We are now seeking a highly motivated laboratory engineer to strengthen our research group and contribute to driving our research forward. The engineer will be involved in a range of different research tasks within MEP and have a major role in further development of our laboratory facilities, with a special responsibility for our ancient DNA laboratory, developing and applying molecular tools to address ecological research questions, as well as instructing and supporting students and guest researchers in the aDNA lab. In addition, we frequently go out to sea on research expeditions, and participation in field sample collection is encouraged.

Main RCN funded projects we currently work on are:

BIOCAP_Reconstructing the biological carbon pump with ancient plankton DNA PASTIME_Present and past climate change impacts on Norwegian Fjord ecosystems AEGIS_Assessing the interactions between microalgae, microbial grazers, and viruses in a changing ocean METABRIDGE_Metabarcode data in marine environmental monitoring - bridging the gap between science and management ARCHIE_Late Quaternary Antarctic cryosphere interactions Projects funded through the European Research Council include:

i2B (ERC-Synergy) Into the Blue - Resolving past Arctic greenhouse climate BIOcean5D (H2020) Marine biodiversity assessment and prediction across spatial, temporal and human scales Work tasks Your main task will be to develop and apply environmental DNA tools for ecologically related research questions both in modern environments and a paleo-context. Specific work tasks will include (but are not limited to):

Perform laboratory work to extract, quantify and quality-assess environmental and ancient DNA from water and sediment samples (mostly marine but also freshwater ecosystems). Organize and manage the laboratory (orders of consumables, equipment maintenance, planning) and responsibility for HSE tasks connected to lab, field and cruise activities Test and adjust new protocols Perform qualitative (NGS metabarcoding and metagenomics) and quantitative (ddPCR/qPCR) molecular analyses of environmental and ancient DNA. Instruct and support students and guest researchers in lab Contribute to scientific publications in relevant peer-reviewed journals. Participate in research cruise(s) if relevant. Give input on bioinformatic and statistical analyses of qualitative and quantitative DNA/RNA results if relevant Your profile, qualifications and skills Education

A MSc or PhD degree in biosciences, molecular biology, ecology, molecular ecology, bioengineering or other relevant field is required.

Qualifications and personal skills

Meticulous laboratory and organizational skills and keen interest in developing molecular lab methods is a requirement Advanced knowledge and experience in molecular biology work (i.e. DNA extraction, PCR amplification, purification) is required Experience in shotgun metagenomics is an advantage. Experience in bioinformatic analysis of high-throughput DNA sequencing data is an advantage, but not mandatory. Experience with field work planning and preparation and sample collection in the field during expeditions is an advantage Strong team player, who can also work independently but also collaborate well with researchers, students and external guests Excellent communication skills are required. The main language in the group is English, knowledge of Norwegian is an advantage. We offer: A unique opportunity to strengthen an enthusiastic, supportive and cross-disciplinary research group A stimulating and professionally challenging working environment in an emerging research field combining environmental DNA/ and ecosystem sciences in marine and freshwater settings. Diverse daily tasks Possibility to influence your own work, worktime and choice of solutions

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QuadramInst UK PlantMicrobiome

Applications are invited for a Research Scientist to join the Laboratory of Dr Hildebrand at the Quadram Institute Bioscience (QIB), Norwich, UK.

Background:

In this BBSRC-funded position, the impact of plant-based diets on the gut microbiome will be explored in metagenomes, including tracing bacterial strains, reconstructing their genomes and metabolic food-webs in the gastrointestinal ecosystem. This will be used to understand the impact a changing environment (food sources, immune system, invading pathogens) have on ecosystem stability. Questions we will be asking are, for example:

- How can food-derived pathogens be effectively prevented from colonizing the gastrointestinal tract?

- Does switching to a plant-based diet lead to a destabilised gut ecosystem (or reverse)?

- How can the gut microbiome supplement essential micronutrients to the human body?

To answer these questions, the postholder will be primarily working with metagenomic data from diet interventions, using machine learning to predict genomes, functions and ecosystem states (similar to previous work, see doi: 10.1038/s41531-025-00885-5, 10.1016/j.chom.2023.05.024, 10.1016/j.cgh.2024.11.006, 10.1111/1751-7915.14396).

The work will build on bioinformatic tools available in the group (www.falk.science/software, www.github.com/falklab), that will be further refined/ newly developed to enable cutting-edge bioinformatic approaches in the project. Long-term, this research will contribute to developing pre-/pro-biotic strategies to reduce autoinflammatory disease and enable healthy aging in a wide population. In addition, the postholder will be involved in organizing group tasks, such as helping in supervising junior researchers, submitting grants, developing new research programmes and organizing outreach events.

The environment:

The Hildebrand group (https://falk.science) uses metagenomics to research the diversity, community interactions, and evolution of microbes in communities using custom software solutions.

The Quadram Institute is based on the Norwich Research Park, which is one of the largest single-site concentrations of research in food, genomics, and health in Europe. The Park hosts 4 BBSRC Institutes (including Earlham), 17,000 students, 3,000 full-time researchers and clinicians, and over 115 companies. The outstanding reputation of our researchers is internationally recognised, with 10 of the Park's scientists in the top 1% of the "most highly cited" in the world, including Dr Falk Hildebrand.

The applicant will have direct access to established PacBio/ONT, Hi-C and single cell sequencing facilities, as well as one of UK's largest HPC cluster at the NRP.

The ideal candidate:

The applicant needs to hold a PhD (or equivalent) in biology, bioinformatics, computer science or a related discipline with a background and/or interest in at least one of the following subjects:

- Microbiomes, evolution & biodiversity

- Nutrition & patient cohorts

- Molecular biology & Metagenomics

The ideal candidate will have a keen interest in gut microbiology and nutrition, experience in conducting scientific experiments independently, writing papers, presenting work and grant writing. Basic statistics and programming skills (either R, python, Perl, C++, or equivalent) is expected. Specialized skills will be taught and developed through mentorship and collaborations.

Additional information:

Salary on appointment will be within the range 36,720 to 42,000 per annum depending on qualifications and experience. This is a full-time post contracted until the funding end date of 31 March 2028.

For further information and details of how to apply, please visit our website https://jobs.quadram.ac.uk or contact the Human Resources team on 01603 450814 or nbi.recruitment@nbi.ac.uk quoting reference 1004914. This role meets the criteria for a visa application, and we encourage all qualified candidates to apply. Please contact the Human Resources Team if you have any questions regarding your application or visa options.

Interviews will be held approximately 20 July 2025.

We are committed to equity, diversity and inclusion, and welcome applications from all sectors of society. The Institute values of Respect, Innovation, Collaboration and Excellence are at the heart of all we do, and we expect all employees to share and display these values. To support our commitment, we have a range of family, faith and diversity friendly working arrangements to help all staff achieve excellence in their area of work.

As a Disability Confident employer, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy.

About the Quadram Institute:

The Quadram Institute is a new interdisciplinary research institute dedicated to understanding how food and microbes interact to promote

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QuadramInst UK ResScientist SoilMetagenomics

Applications are invited for a Research Scientist to join the Laboratory of Dr Hildebrand at Quadram Institute, Norwich, UK.

Background:

This post is part of the NERC project "Identifying novel microbial drivers to mitigate atmospheric methane emission". Methane is a powerful greenhouse gas, and we aim to reveal the role of ammonia oxidizing Archaea in methane oxidation in the environment. The project will determine how methane affects soil microbial communities, and how specific soil microorganisms respond to methane and metabolise it. The postholder will work with sequencing data derived from cultivated and natural soil microbiomes, to understand the role of prokaryotes (Archaea and Bacteria) in mitigating greenhouse gas emissions.

The role:

The project holder will use metagenomics (similar to doi:10.1038/s41586-018-0386-6, 10.1111/1462-2920.15314, 10.1186/s40168-022-01365-1) to profile both taxonomic and functional compositions of for SIP-enriched metagenomic and metatranscriptomic sequencing and functional-targeted amplicon sequencing data, interpreting experiments conducted in the laboratory of Prof Laura Lehtovirta-Morley. The bioinformatic tools will be developed to analyse and correct these data types, the statistical workflows established to interpret and understand how microorganisms respond to methane in both pristine and laboratory-based soil communities, building on tools available in the Hildebrand group.

Long-term, this work will advance our understanding of biogeochemical cycling, contribute to reducing the impact of climate change by manipulating existing microbial communities, and understanding how healthy soil microbiomes are established, and maintained.

The environment:

The Hildebrand group uses metagenomics to research the diversity, community interactions, and evolution of microbes in communities using custom software solutions. The Lehtovirta-Morley group explores environmental microbiomes and biogeochemical cycling using both cultivation-independent and cultivation-dependent experiments. Both groups collaborate closely on microbial archaeal research in soils. The research is situated at the Norwich Research Park (NRP) UK, that encompasses the University of East Anglia, 4 BBSRC Institute, 15 companies, 3,000 researchers and clinicians, 17,000 students. Norwich ranked in the top 10 for UK cities with a beautiful, historical town centre and an active gastropub & coffee aficionado scene.

The applicant is expected to help in the supervision of junior group members and to represent the group at trainings. The applicant will have direct access to established PacBio/ONT, Hi-C and single cell sequencing facilities, as well as one of UK's largest HPC cluster at the NRP.

The ideal candidate:

The applicant needs to hold a PhD (or equivalent) in biology, bioinformatics, computer science or a related discipline with a background and/or interest in at least one of the following subjects:

- Microbiomes & biodiversity - Metagenomics & patient cohorts - Ecology & evolution

The ideal candidate will have a keen interest in soil microbiology and biogeochemical cycling, and experience in conducting scientific experiments independently, writing papers, presenting work and grant writing. Basic statistics and programming skills (either R, python, Perl, C++, or equivalent) is expected. Specialized skills will be taught and developed through mentorship and collaborations.

Additional information:

Salary on appointment will be within the range 36,720 to 42,000 per annum depending on qualifications and experience. This is a full-time post for a contract of 9 months, potentially extensible for a further 9 months.

For further information and details of how to apply, please visit our website https://jobs.quadram.ac.uk or contact the Human Resources team on 01603 450814 or nbi.recruitment@nbi.ac.uk quoting reference 1004912. This role meets the criteria for a visa application, and we encourage all qualified candidates to apply. Please contact the Human Resources Team if you have any questions regarding your application or visa options.

Interviews will likely be held around 14 July 2025.

We are committed to equity, diversity and inclusion, and welcome applications from all sectors of society. The Institute values of Respect, Innovation, Collaboration and Excellence are at the heart of all we do, and we expect all employees to share and display these values. To support our commitment, we have a range of family, faith and diversity friendly working arrangements to help all staff achieve excellence in their area of work.

As a Disability Confident employer, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy.

About the Quadram Institute:

The Quadram Institute is a new interdisciplinary research institute dedicated to understanding how food and microbes interact to promote

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StonyBrookU NewYork DirectorInstConservation

Stony Brook University seeks an Associate Director for the Institute for Conservation of Tropical Environments (ICTE)/Centre ValBio (CVB) to provide leadership and promote a productive environment that fosters innovation and excellence in CVB's research, education, and outreach programs. The Associate Director should have academic expertise in one or more core areas covered by CVB, which covers the natural sciences. (e.g., ecology, evolutionary biology, zoology, botany, organismal biology [e.g., entomology, herpetology, etc.], natural history, paleontology, primatology, ecology and evolution of infectious disease, ecology and evolution of behavior, tropical ecology and evolution), applied natural sciences (e.g., conservation biology, tropical forestry), or at the interface between science and society (e.g., anthropology, one health, biodiversity management). While holding a tenure home in an allied department at the main SBU campus on Long Island, the Associate Director is expected to reside at CVB in Madagascar for a great proportion of the first two-to-three years of their appointment, and at least one academic term each year thereafter.

Led by Stony Brook University's Institute for the Conservation of Tropical Environments, CVB is poised to become a leading biological field station, enabling unparalleled access to a global biodiversity hotspot in Madagascar. Located in Ranomafana National Park, Ifanadiana, Madagascar, CVB hosts a small community of visiting faculty (~5-15 annually), graduate students (~10-20 annually), postdoctoral scholars and academic specialists (~3-6 annually), and ~135 support staff, as well as three vibrant multi-season study abroad undergraduate programs.

CVB is unique in its ability to support integrated laboratory and field research in the eastern rainforests of Madagascar. Its large year-round expert staff, state-of-the-art laboratory, research and teaching facilities, and connections to researchers at dozens of global universities have no parallel in Madagascar. Major research facilities at CVB include: a genomics lab, ultracold freezers, liquid nitrogen generation, cell culture facilities, and an herbarium and insectarium. Centre ValBio's staff includes research technicians who specialize in identifying local plant and insect life, recording primate behavioral ecology, collecting specimens, and conducting biodiversity surveys. These staff provide research support services to visiting faculty and researchers for work both at Ranomafana National Park and expeditionary work across Madagascar, facilitating the production of new knowledge about some of the most threatened ecosystems on the planet. Additionally, Centre ValBio's education and reforestation teams work with local communities to promote conservation education, restore areas of disturbed and degraded forest, and improve educational opportunities in local communities. Additional information about CVB can be found at https://www.stonybrook.edu/commcms/centre-valbio/ For details and to apply: https://apply.interfolio.com/167803 For an Associate Director of CVB, we are searching for a near-mid- to mid-career biodiversity scientist with the drive to advance their research at a biodiversity hotspot while supporting global science and education. An ideal candidate will have had some administrative experience, however, such experience may take many forms (e.g., being graduate program director or department chair, administering or helping administer a collaborative project with >2 PIs, running international programs for researchers at any level).

Direct questions to: liliana,davalos@stonybrook.edu

Liliana M. Dávalos online < https://lmdavalos.github.io >, Google scholar publications < https://scholar.google.com/citations?hl=en&user=XSwScHgAAAAJ&view_op=list_works&sortby=pubdate > bluesky: @labdavalos.bsky.social office: 631.632.1554

"Liliana M. Davalos" <lmdavalos@gmail.com>

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UHelsinki ForestGenomicsAdaptation

Current climate change scenarios estimate the growth zones to shift approximately 80 km northwards in a decade, and the speed is likely to accelerate towards the end of the century. On the other hand, forest trees take decades to mature, meaning that the seedlings begin their growth in a different kind of environment compared to the one they face as adults. How will the current forest tree populations survive in the future climate? The change also brings about negative effects such as droughts, introduction of new pathogens and pests, as well as extreme weather conditions - how are the current forests adapted to these conditions? From a forestry perspective, it needs to be considered how well the current breeding and forest reproductive material is going to survive and grow in the future climate - should new material be brought in, and if so, which?

You will now have a chance to address these issues in a four year "Future Forests" research project, funded by Jane and Aatos Erkko foundation. You will use Finland-wide remote sensing resources from one of the consortium members, Finnish Geospatial Research Institute to monitor tree growth in Finland and combine this information with whole genome sequencing data from up to 10,000 trees. We are using birches (Betula) as our model organism, as they have a relatively small genome, they are adapted to their local environments and there are accelerated breeding procedures for testing hypotheses arising from the analyses.

Are you a technology wizard, determined to apply your skills in something that really matters? Or, alternatively, you have a solid background in population genetics and you've been looking for a project where you can study adaptation and trait architecture in high spatial and genomic resolution?

We are seeking two postdoctoral researchers or one postdoctoral and one doctoral researcher for: (i) Remote sensing advised country-wide genotype-phenotype linking, and (ii) Country-wide study of genetic adaptation and population structure dynamics in a changing climate. In the project, you will analyse whole-genome data from birches collected from Finnish forests. After selecting the individuals to be collected and sequenced, you will associate the data to remote sensing-based phenotypic and climate data. You will perform population genetic analyses and simulations to study the effect of adaptation, hybridisation and past demographic events on potential future persistence under climate change. Your findings will be readily transferred to the practitioners, as the Natural Resources Institute of Finland is a consortium member and the main tree breeder in Finland.

Skills, expertise and qualifications

For the doctoral researcher's position, the appointee is expected to have an applicable second-cycle degree and the right to pursue doctoral studies at the University of Helsinki. Other requirements include the ability and motivation, as demonstrated in previous degree studies or otherwise, to pursue postgraduate studies and a doctoral degree according to a study plan and research proposal.

For the doctoral researcher's position, the appointee must enroll as a PhD student at the University of Helsinki. The appointee should either already have the right to pursue a doctoral degree at the University of Helsinki by the start of the appointment or apply for the right and obtain it within the probationary period of six months of their appointment. If the appointee does not already have the right to pursue a doctoral degree at the University of Helsinki, it must be applied for separately, please see: https://www.helsinki.fi/en/research/doctoral-education/the-application-process-in-a-nutshell For the postdoctoral researcher's position, the appointee shall hold a doctoral degree and have the ability to conduct independent scholarly work as well as the teaching skills necessary for the position. In the postdoctoral researcher's position, the degree requirement (doctoral degree) must be met by the beginning of the employment.

The optimal candidates will have acquired a PhD in biology, forest sciences, environmental sciences, or data sciences. A strong background or motivation to learn ecological genetics and evolutionary biology as well as competence in bioinformatics and population genetics is required. You should be acquainted or capable of learning the modelling associated with genome-wide association studies (GWAS), landscape genomic analyses, and population genetic simulations. You are ambitious to work and communicate in fluent English in an international consortium. Furthermore, you have a well-structured and careful working attitude, and you demonstrate a high level of team spirit.

The duties of the doctoral researcher include conducting research in the project framework with the aim of achieving doctoral degree in accordance

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UMelbourne Australia PaidFieldAssist Fairywrens

Field assistant required for bird breeding season for 2 - 4 months (casual rate, Unimelb scale).

This is a great opportunity to gain valuable field skills, and experience in research and data collection. The focal species for the study is the iconic superb fairy-wren.

Field site: Mount Ainslie Nature Reserve (Campbell Park Woodland), located a 10-minute drive from the city centre in Canberra, Australia. Fieldwork has been conducted at this site for 20 years, so data collected will contribute to a long-term dataset.

Details: The field assistant will join two other researchers in the field between September 2025 and January 2026. The assistant will work 5 days per week, 5 hours per day in the field, but there is scope for flexibility. Most days will require independent data collection and communication of findings. The assistant must be physically fit, as they will be required to walk around the reserve, sometimes 10km per day.

There is also some flexibility around the duration of the work, which will be discussed with the candidates. However, the field assistant must be available during the period from the middle of October 2025 to the middle of December 2025.

Teamwork and communication skills are essential. The candidate must also be self-motivated, enthusiastic, reliable and have a good work ethic. Previous experience working with birds in the field is desirable but not essential as we will provide training in the field methods required. In addition, previous bird banding experience is an advantage but not mandatory.

This is a paid casual position, and the rate will be appropriate for the qualification level of the candidate (using the University of Melbourne casual rate salary scale). Please note airfares and visas cannot be paid for, as it is a paid position. Please check that you are able to travel to Canberra (Australia) before applying and also note that some visas have wait times for approval. Precautions for COVID-19 can be practiced during this work as social distancing can easily be implemented.

Main field duties: Finding nests, monitoring breeding attempts and documenting group dynamics throughout the breeding season. The field assistant will be required to identify individuals by their colour band code using binoculars.

If you are interested or require more information, please email me at <jessica.mclachlan@unimelb.edu.au> explaining a little about yourself, including interests, a CV with any prior experience and referees.

Jessica McLachlan Research Assistant BEAM group (https://www.ecomedina.com/), The University of Melbourne

jessica.mclachlan@unimelb.edu.au

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UNacionalAutonomaDeMexico SystematicEntomology

Faculty Position. Systematic Entomology Institute of Biology. Universidad Nacional Autonoma de Mexico https://tinyurl.com/2557avf6 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 Entomology, in the Department of Zoology.

CANDIDATE'S PROFILE We seek a scientist able to conduct research in systematic biology (e.g., species discovery and description, classification, phylogenetic analyses), extending to the application of innovative theoretical concepts and methodological tools to investigate one or more processes associated with their evolution above the species level (e.g., morphological diversity, species richness, distribution, evolution, diversification), with substantial experience of work and development of biological collections.

REQUIREMENTS 1. Doctorate or Ph.D. degree in zoology, entomology, systematics or evolution. 2. Preferably with postdoctoral experience. 3. Knowledge and professional experience of at least 3 years in research in phylogenetic systematics and evolution of insects, preferably in any of the following taxonomic groups: Diptera, Coleoptera (except Scolytinae), Odonata, Trichoptera or Psocodea. 4. Field work experience. 5. Experience in the use or development of biological collections. 6. 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. 7. Develop their own line of independent research, including procurement of funds for research and interaction and collaboration with other research groups. 8. Non-native speakers must be fluent in the Spanish language. 9. 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 no older than 39 years of age, and male applicants should be no older than 37 years of age 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 and evolution, preferably on the aforementioned taxonomic groups. 2. Description of research conducted during at least the past 3 years (maximum 2 pages). 3. Research proposal to be developed in three years, in the context of longer research plan, focused on the systematics and evolution of any of the aforementioned groups of insects, preferably with a focus on Mexican groups (maximum 15 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 date of birth. 6. Shortlisted candidates should provide academic recommendation letters from at least three persons.

DEADLINE Applications, accompanied by supporting documents, will be received from June 17th, 2025 until the close of this call, on August 04th, 2025 at 18:00 h (Mexico City time). Shortlisted candidates will be contacted to request recommendation letters, a seminar for the academic community of the Institute of Biology, 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.

Susana Magallón <s.magallon@ib.unam.mx>

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USalzburg Austria EvolEcol

New professorship “Zoological EvolEcol” available at the University of Salzburg Austria. More information here: https://www.plus.ac.at/personalwesen/stellenmarkt-en/universitatsprofessuren-en/universitaetsprofessur-%c2%a798-fuer-zoologische-oekologie/?lang=en Rüdiger Jens <jens.ruediger@plus.ac.at> Rüdiger Jens <jens.ruediger@plus.ac.at>

Other

EvolJLinneanSociety

Evolutionary Journal of the Linnean Society

Publish with us The Evolutionary Journal of the Linnean Society publishes open-access original papers on all aspects of the evolutionary biology of diverse organisms and ecological systems. We encourage submissions across disciplinary divides, from genetics, through palaeontology and systematics to behaviour. Find out more (https://academic.oup.com/evolinnean/pages/why-publish)

Funding Support for Open Access Publishing Explore automatic APC waivers for authors. Find out more (https://academic.oup.com/pages/open-research/open-access/charges-licences-and-self-archiving/apc-waiver-policy)

Call for Papers: Evolution on Islands: from genomes to communities This special issue will offer a synthesis of the latest research in island biology. It will be introduced by a joint perspective authored by Professor Rosemary G. Gillespie (University of California, Berkeley) and Professor Robert J. Whittaker (University of Oxford). We welcome original research articles, short reports, and invited perspectives. Contributions may focus on a single island or archipelago or span multiple scales and systems. Find out more (https://academic.oup.com/evolinnean/pages/evolution-on-islands)

Dom Notarangelo

Marketing Manager, Researcher Science | Academic Marketing

Oxford University Press

Dom Notarangelo <Dom.Notarangelo@oup.com>

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SiberianJay BirdResesarch FieldAssistant

Expenses paid field assistant position to assist fieldwork with Siberian Jays in Swedish Lapland

We are seeking one highly motivated field volunteer to support a long-term ecological research project on Siberian jays led by Dr. Michael Griesser (University of Konstanz) and Dr. Miya Warrington (Oxford Brookes University).

For the upcoming field season (1 Sept - 31 Oct 2025) we are looking for 1 assistant to help with our work on foraging ecology in Siberian jays. The assistants will help with catching and ringing birds, do behavioural observations, do field experiments, and assist with data management. Observe that temperatures in the end of the season can be as low as -15C, involves walking up to 10km per day. An overview over our past work can be found here: https://www.youtube.com/watch?v=-JaH6wjAYAiE Essential qualifications: 1) Bird ringing and mist-netting experience 2) Field work experience, involving behavioural observations and experiments 3) Ability to work in small teams and sociable personality 4) Driving license (manual transmission) 5) Fluent in English 6) Highly motivated

Applications received before 20 July 2025 will be given full consideration.

If you wish to apply, send a motivation letter, CV, and two contacts for references (as a single PDF) to michael.griesser@uni-konstanz.de

michael.griesser@uni-konstanz.de

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SMBE CareerAwardWinners

Society for Molecular Biology and Evolution is delighted to announce our 2025 Faculty Award Winners.

Please join us in congratulating their achievements!

2025 Early-Career Excellence Award winner: Alison Feder

Alison Federis an Assistant Professor of Genome Sciences at the University of Washington, and an Affiliate Investigator of the Herbold Computational Biology Program at the Fred Hutchinson Cancer Center. The Feder lab studies the rapid evolutionary processes undertaken by the viruses, bacteria and cancerous cells that live within us and cause disease. She earned her B.A. in Mathematics from the University of Pennsylvania, an M.Sc. in Statistics from the University of Oxford and a Ph.D. in Biology from Stanford working with Dmitri Petrov, before becoming a Miller Fellow at UC Berkeley with Oskar Hallatschek. The Feder Lab is currently supported by an NIH Director's New Innovator Award and grants from the Cystic Fibrosis Foundation.

2025 Mid-Career Excellence Award winner: Amanda Larracuente

Amanda Larracuente is the Nathaniel and Helen Wisch Professor of Biology at the University of Rochester. She received a BS in Biology from Canisius College in 2003. She received her PhD in Genetics from Cornell University in 2010 working with Dr. Andrew Clark on Drosophila genome evolution, population genetics, and sex chromosome evolution. Amanda's postdoctoral training was at the Whitehead Institute for Biomedical Research with Dr. David Page and the University of Rochester with Dr. Daven Presgraves, where she studied Drosophila evolutionary genetics. She opened her lab at the University of Rochester in 2015. The lab combines functional and evolutionary genomics, cytological, and molecular approaches to study how genetic conflicts shape genome evolution with a focus on genomic repeats in pericentromeres, centromeres, and on sex chromosomes. Her lab's work is currently supported by the National Institutes for Health (NIH) and the National Science Foundation (NSF). Amanda held a Stephen Biggar and Elisabeth Asaro fellowship in Data Science (2017-2020). She advises the undergraduate program in Computational Biology and co-directs an NIH-funded program in Genomic Intensive Data Science Research, Education and Mentorship at the University of Rochester. Amanda served on the Board of Directors for the Genetics Society of America (2022-2024), sits on their education committee, and is an Associate Editor for Molecular Biology and Evolution and for GENETICS.

2025 Lifetime Contribution Award winner: Chung-I Wu

Chung-I Wu's research spans a number of topics including meiotic drive, speciation genetics, molecular adaptation, microRNA evolution and, most recently, somatic cell evolution (that includes cancers). During COVID-19, he led a team to study the viral evolution as part of the duties of a scientist citizen.

His main works at the University of Chicago are about speciation genetics and molecular adaptation. He and his associates started the fine-scale genetic analysis of hybrid male sterility in 1990 which culminated in the cloning of the first "speciation genes", Odysseus, in Drosophila. He is proudest of the fine-scale genetics that shows the massive gene interactions underlying reproductive isolation. It is the genetic interactions that hold the key to understanding speciation. The cloning of the Odysseus gene complements the genetic analyses.

Beyond the genetics of speciation, Wu has made two important conceptual contributions. One is the genetic basis of Haldane's rule (Wu and Davis 1993) which points out that sexual selection in males may play a larger role than hemizygosity in H-rule. The Wu (2001) article on the genic view of speciation is now a classic, having been cited ~ 1500 times. This view lays the foundation for "speciation with gene flow".

In 2014, Wu started collaborating with Prof. Suhua Shi on speciation in natural populations, a task uniquely suited to mangrove trees. They identify important biogeographical mechanisms of speciation, in particular, the Mixing-Isolation-Mixing (MIM) mechanism.

In the last 10 years, Wu's major contribution to evolutionary biology is what they referred to as the ultra-microevolutionary processes, which is the evolution of somatic cells in multi-cellular organisms. Cancer and aging are two manifestation of this process. All these are summarized in the earlier Annual Review of Genetics article (2016) and the two recent eLife papers (Zhang et al. 2024a, b). In these two eLife papers, the potential contributions of evolutionary biology to cancer therapy are clearly laid out.

From 1998 to 2006, Wu served as the chair of the Department of Ecology and Evolution at the University of Chicago where he was a faculty member for 29 years. Between 2008 and 2014, he served as the guest director of Beijing Institute of Genomics (BIG). BIG was effectively a new institute that needs to be built up quickly. It indeed achieved that goal. Since

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Survey CoinfectionStudies

Inquiry Title: Inquiry for Coinfection Studies in Non-Human Biological Systems

Hello everyone,

We are currently conducting a survey to document the range of experimental and observational studies of nonhuman biological systems exhibiting pathogen coinfection. We are particularly interested in how scientists have detected and tracked the abundances of coinfecting pathogens (e.g., presence/absence data or viral load/intensity data over time).

If you work on any biological system with documented coinfections, we would greatly appreciate it if you could share relevant information about the system, including the diseases involved, the methods used to study coinfection, and how disease monitoring has been conducted.

You can contact me at: jing.jiao@cos.name

Best wishes, Jing Jiao Assistant Professor Department of Biology College of Science & Engineering Texas Christian University

Jing Jiao <jing.jiao@cos.name>

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PostDocs

Bethesda MD ViralGenomics

Computational Biologist (Postdoctoral Fellow)

Organization

National Library of Medicine, Bethesda, MD and surrounding area

Join a dynamic and interdisciplinary team pushing the frontiers of genomics and pandemic virus research under the leadership of Dr. Martha Nelson in the Division of Intramural Research (DIR) at the National Library of Medicine (NLM).

About the position

The NLM is one of the 27 institutes at the National Institutes of Health (NIH). The NLM is the world's 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. 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. Specific tasks and responsibilities include:

Phylodynamic analysis of virus genome data Writing papers for publication in peer-reviewed journals Presenting data at conferences and seminars Leading projects involving international collaborators Working collaboratively with other lab members

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 "Computational Biologist (Postdoctoral Fellow)" and their last name in the email subject line. Applicants must submit the following materials to Martha Nelson atnelsonma@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

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 a background in Bayesian approaches to phylodynamic analysis of virus populations are particularly encouraged to apply. - Programming skills (e.g., R, python) and an ability to learn how to use new software and quickly apply it to genomic data are essential. - Experience developing new software for genomic analysis - 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.

Martha Nelson, PhD Staff Scientist Division of Intramural Research National Library of Medicine National Institutes of Health Building 38A, Room 6N609C 301-480-6924 Martha.Nelson@nih.gov

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

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Bolzano Italy InsectSymbiontGenomics

A postdoctoral position is available at the Free University of Bozen-Bolzano (Italy) in the lab of Hannes Schuler. This project, funded for two years, aims to study bark beetles and psyllids and their associated microorganisms.

The European spruce bark beetle (Ips typographus), one of Europe's most destructive forest pests, relies on tight symbiotic associations with fungi and bacteria. In this project you will dissect those partners to discover how they shape the beetle's biology. In parallel, you will characterise the endosymbionts of phytoplasma-vectoring psyllids and test how these microbes influence host fitness and the acquisition and transmission of phytoplasmas. Comparing these two contrasting systems will let you probe universal versus host-specific rules of insect-microbe cooperation and uncover microbial targets for sustainable pest control.

The successful candidate will:

* Collect insect samples * Conduct amplicon-sequencing and whole genome sequencing for bacteria and fungi. * Analyze bacterial and fungal communities associated with insects using bioinformatic tools.

We are seeking an enthusiastic candidate with:

* A strong background in molecular biology. * Experience with bioinformatic analyses of bacterial and/or fungal communities associated with insects. * A PhD (or soon to be completed) in Biology, Evolution, or related fields.

The Free University of Bozen-Bolzano is situated in one of the most fascinating regions in Europe, at the crossroads between German-speaking and Italian cultures. The university is renowned for its trilingualism in teaching and research, its high level of internationalization, and its ideal research environment, guaranteed by excellent facilities. These attributes consistently place unibz at the top in both national and international rankings. Our lab is part of the newly funded Competence Centre for Plant Health within the Department of Agricultural, Environmental and Food Sciences. We are a young and dynamic research group dedicated to studying various aspects of insect-microbe interactions in a collaborative atmosphere http://hschuler.people.unibz.it If you are passionate about molecular biology, fascinated by insect-microbe interactions, and eager to join a vibrant research community, we encourage you to apply for this position.

General requirements for the position: A PhD (or soon to be finished) in Biology or Evolution or related fields. The candidate should have excellent communication skills and should be fluent in English. The project is expected to start as soon as possible, but the starting date is negotiable.

Application deadline is 27.06.2025 (noon). All documents for the application procedure can be found at: https://www.unibz.it/en/home/position-calls/-positions-for-academic-staff/7744-pflanzenpathologie-und-entomologie-prof-schuler-hannes?groupt For informal inquiries, and for questions about the hiring process, please contact Hannes Schuler hannes.schuler@unibz.it

Prof. Hannes Schuler Competence Centre for Plant Health Faculty of Agricultural, Environmental and Food Sciences

Free University of Bozen-Bolzano Universitätsplatz 5 I-39100 Bozen-Bolzano Tel: +39 0471 017648 <tel:+390471017648> http://hschuler.people.unibz.it Schuler Hannes <Hannes.Schuler@unibz.it>

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Bristol UK Two BioinformaticsEvoDevo

We are seeking and experienced, creative and energetic postdoc to work on our Wellcome Trust Discovery Grant Developmental control of neural cell number and type'

THE ROLE

This project exploits the extreme levels of neurodiversity of Heliconiini butterflies to develop a unique model system of neurodevelopmental regulation. We previously identified major shifts in the cell population forming the mushroom bodies (insect learning and memory centres) in this tribe, with the number of intrinsic neural cells (Kenyon cells) varying 8-fold between closely related species (Couto et al., Nat Comms 2023). The expanded cell population is produced by a pool of derived intermediate progenitors and affects Kenyon cell sub-types differentially. This provides a novel insect system in which to explore the regulation of cell fate decisions. We will use this system to understand the mechanisms governing expanded neural populations, altered production of cell types, their impacts on wider brain circuits, and their behavioural significance. This will advance our understanding of the fundamental principles and developmental pathways governing neurodevelopment.

WHAT WILL YOU BE DOING?

This role will lead the bioinformatics objectives, including analysing single cell/nuclei datasets across development and species, and integrating different -omics datasets (e.g Cicconardi et al., Nat Comms 2023), while working together with other team members with expertise in development, neuroanatomy and behaviour. You will have responsibility for designing and executing comparative studies of cell type and proliferation using sequencing methods, and will work closely with team members to integrate this data in a cell/developmental framework to advance our understanding of this systems' biology. Ultimately, your work will aim to use sequencing data to reconstruct cell types and cell lineages, and to infer the molecular basis of changes in cell proliferation.

YOU SHOULD APPLY IF

You have experience in handling large genomic/transcriptomic datasets, genome assembly, annotation and phylogenetic analyses, and/or single cell/spatial transcriptomics. You should be able to excel in a team, have excellent data handling and organizational skills, and a strong commitment to open science and inclusive research culture. We encourage under-represented groups to apply, and we are happy to discuss the research culture in our research group and Department. Please get in touch if you have any questions!

FULL DETAILS: https://www.bristol.ac.uk/jobs/find/details/?nPostingId=193234&nPostingTargetId76619&id=Q50FK026203F3VBQBV7V77V83&LG=UK&languageSelect=UK&mask=newuobext LAB WEBSITE: www.shmontgomery@bristol.ac.uk Thanks! Steve

Dr Stephen Montgomery He/him

Associate Professor in Evolutionary Neurobiology and Behaviour School of Biological Sciences University of Bristol

Email: s.montgomery@bristol.ac.uk Tel: +44 117 455 2591 Twitter: @EBaBlab www.shmontgomery.co.uk For outreach and Widening Participation please contact: lsb-biologyoutreach@bristol.ac.uk

I am a friend of the BAME and LGBQT communities because I believe in equality for everyone

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We are seeking and experienced, creative and energetic postdoc to work on our Wellcome Trust Discovery Grant 'Developmental control of neural cell number and type'

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WHAT WILL YOU BE DOING?

This role will lead the cell developmental biology, and embryology, objectives of this project, working together with other team members with expertise in bioinformatics, neuroanatomy and behaviour. You will have responsibility for designing and executing comparative developmental studies of the brain from the embryo through juvenile development,

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CornellU MolecularBiomonitoring

POSTDOC OPPORTUNITY: MOLECULAR MONITORING OF AQUATIC ECOSYSTEMS CORNELL UNIVERSITY

OVERVIEW: The laboratory of Nina Overgaard Therkildsen at Cornell University is seeking a highly motivated postdoctoral to lead a project exploring the use of DNA-based methods to monitor lower food web dynamics. Quantifying zooplankton diversity and abundance is vital for monitoring ecosystem health, but traditional methods based on microscopy are labor-intensive and often provide limited taxonomic resolution. Metabarcoding offers promise of faster, cheaper, more accurate, and higher-resolution characterization of zooplankton biodiversity. However, these methods can be limited by primer biases, incomplete reference databases, and challenges in accurately reflecting organismal biomass. Shotgun metagenomics - sequencing all DNA present in a sample without the need for targeted amplification - may provide a more comprehensive and unbiased view of community composition. This approach has the potential to offer a more accurate estimate of relative abundance, but its performance and practicality for application on complex real-world tissue mixtures has not yet been validated. Accordingly, both metabarcoding and metagenomic approaches will need careful context-specific evaluation and benchmarking against traditional approaches prior to any large-scale implementation in monitoring programs. This position offers the exciting opportunity to assess the performance of these emerging techniques in a real-world monitoring program and help shape the future of aquatic ecosystem assessment.

KEY RESPONSIBILITIES: The project will generate side-by-side comparisons of results from metabarcoding, metagenomics, and traditional microscopy on samples collected by the Hudson River Lower Food Web Monitoring Program. The postdoc is expected to lead efforts in the following five areas: - Design and refine experimental and laboratory protocols for DNA extraction and library preparation from bulk tissue and water samples - Analyze high-throughput sequencing data and optimize bioinformatic pipelines for both metabarcoding and metagenomic workflows - Build and curate taxonomic reference databases from public repositories and de novo sequencing - Collaborate with partners and regional stakeholders and co-organize annual workshops to promote knowledge exchange - Prepare peer-reviewed publications and presentations for both scientific and broader audiences

DESIRED QUALIFICATIONS: - A Ph.D. in molecular ecology, bioinformatics, evolutionary biology, environmental genomics, or a related field - Demonstrated experience with metabarcoding, metagenomics, or other environmental DNA applications - Proficiency in programming and bioinformatics tools for high- throughput sequence analysis - Excellent organizational skills, attention to detail, and ability to work both independently and collaboratively in a team environment. - Strong written and verbal communication skills - Commitment to fostering an inclusive and supportive research environment

TERMS OF APPOINTMENT: This is a full-time position starting in late summer 2025 (or as soon as possible thereafter). The initial appointment is for 12 months, with the potential for renewal based on performance and available funding. The position will be based in Ithaca, NY, in the Department of Natural Resources and the Environment at Cornell University. While on-site work is preferred, we offer some flexibility. Salary will be commensurate with experience and competitive. Our lab and Cornell University are committed to fostering a diverse, equitable, and inclusive environment. We strongly encourage applications from individuals of underrepresented and marginalized backgrounds.

TIMELINE AND APPLICATION PROCESS: To apply, please send a cover letter with a description of your motivation and interest in the position, along with your CV and contact information for three references to Nina Overgaard Therkildsen at nt246@cornell.edu. Review of applications will begin on June 27, and continue until the position is filled. Feel free to reach out with questions prior to applying.

You'll join a vibrant community of researchers dedicated to solving pressing ecological challenges through innovation and collaboration. Our lab (https://www.therkildsenlab.com/) is part of the larger campus-wide Cornell Center for Comparative and Population Genomics (http://3cpg.cornell.edu) whose mission includes fostering research, education, and outreach in comparative and population genetics, and which brings together a vibrant and interactive group of over 350 faculty, postdocs, graduate students and staff who share a commitment to comparative and evolutionary genomic approach to the study of living systems.

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nt246@cornell.edu

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KarlstadU Sweden FlyComparativeMethods

I have openings for a postdoc to work on questions related to the evolution of sexual dimorphism either using flies or comparative methods.

Postdoc add: https://kau.varbi.com/en/what:job/-jobID:828768/iframeEmbedded:0/where:4 Deadline is June 15 Email stephen.de.lisle@kau.se for more information or questions. All the application materials have to be submitted on the online portal varbi

N?r du skickar e-post till Karlstads universitet behandlar vi dina personuppgifter < https://www.kau.se/gdpr >.

When you send an e-mail to Karlstad University, we will process your personal data < https://www.kau.se/-en/gdpr >.

Stephen De Lisle <stephen.de.lisle@kau.se>

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KewRoyalBotanicGardens UK GeneticDiversity

Hi,

I'm Alicia Mastretta-Yanes. I'm starting a new position as Senior Research Leader of the Nature-based solutions (NbS) team at Kew Royal Botanic Gardens, UK, and I'm open for enthusiastic people who would like to become part of the team.

I'm happy to support early career scientists willing to pursue their own interests that fit within the umbrella described below. While I don't have a predefined, funded project, I'm enthusiastic about mentoring applicants for fellowships such as Marie Curie Postdoctoral Fellows < https://marie-sklodowska-curie-actions.ec.europa.eu/actions/postdoctoral-fellowships >, Newton Fellowships < https://royalsociety.org/-grants/newton-international/ >, UK Future Leaders Fellowships < https://www.ukri.org/opportunity/-future-leaders-fellowships-round-10/ >, or similar funding to come to Kew, to be based either at Kew Gardens < https://www.kew.org/kew-gardens > (London) or at Wakehurst < https://www.kew.org/wakehurst > (countryside, 1 hr from London).

Our team focuses on how genetic and epigenetic diversity can be incorporated into Nature-based Solutions to build more resilient landscapes and the human communities that depend on them. A key goal is to couple genetics and *omics research with participatory approaches that involve local communities and land managers in evaluating the ecological effectiveness of our methods. We bring together expertise in population genomics, participatory methods, and seedling ecology, and we collaborate with social scientists to understand and integrate the social benefits of these approaches.

Our work addresses questions such as how the genetic diversity of habitat-forming plant species can support ecosystem management in human-impacted areas, and how effective population size (Ne) influences trait variability that aids adaptation to environmental change. We also support efforts by Parties to monitor genetic diversity under the Global Biodiversity Framework, contributing to the development of indicators that can be estimated with or without DNA-based data.

My own work focuses on conifer trees and crop wild relatives, but proposals involving any plants or fungi are welcome. Research on any ecosystem is encouraged, though I'm particularly interested in work based in biodiversity hotspots, where research and conservation efforts are urgently needed.

We value diverse perspectives and strongly encourage applications from individuals of all nationalities, identities, and life paths. As a woman and Mexican scientist living in the UK, I'm happy to share my experience navigating international challenges. I'm especially keen to encourage applicants from Latin America but I'm equally excited to collaborate with researchers from around the world.

Kew's Science strategy (2020-2025) < https://-www.kew.org/science/our-science/publications-and-reports/science-reports/kew-science-strategy > is currently under revision in preparation for the next five years, but it's still a good reference for understanding Kew's mission, priorities, and direction. I also recommend having a look at the Kew Manifesto for Change (https://www.kew.org/about-us/our-mission-and-priorities). If these ideas and values resonate with you, there's a good chance we'll work well together.

If you're motivated and have a bold idea go for it. I'd love to hear from you. *Contact me at **A.MastrettaYanes@kew.org*

Cheers,

Alicia Mastretta-Yanes

Senior Research Leader

Ecosystem Stewardship

Kew RBG

PS: By "early-career scientist," I mean anyone who has finished their PhD a few years ago, has done a postdoc, hasn't done a postdoc (for any number of reasons), or is still finishing their PhD but thinking ahead. Life paths are non-linear and diverse don't worry too much about labels. If you think you might be eligible for one or another funding scheme in the up-coming 2 years feel free to reach out.

Alicia Mastretta <ticatla@gmail.com>

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LundU Sweden HybridGeneExpression

Post doc/researcher position focussed on understanding the evolution of gene expression in hybrids at Lund University, Sweden

https://lu.varbi.com/en/what:job/jobID:833332/ The position is part of the ERC project HybridExpress and focussed on addressing the role of gene expression in how novel variation can arise from hybridization. The specific questions that will be addressed will be developed in discussion with the recruited candidate and the team. There is already a data set of three independent lineages of Italian sparrow Passer italiae and their parental species. The researcher will work in a collaborative HybridExpress team consisting of a lab manager, a PhD-student and a post doc. The project is led by Associate Professor Anna Runemark, and set within the SPeciation, Adaptation and Co-Evolution lab in the Biodiversity and Evolution division. The position is for one year but possibilities for extension can be discussed with the PI.

The department of biology at Lund University is a highly international environment with weekly seminars with invited international speakers. The Department also organizes a lot of social activities, including regular joint division breakfasts, a well visited Friday pub, floor hockey, board game nights etc.

Please email anna.runemark@biol.lu.se if you have any questions!

Anna Runemark <anna.runemark@biol.lu.se>

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Montpellier SolutionsAndEvolution

Announcement for a post-doc (2.5 yrs) in Montpellier (France)

Intraspecific diversity and evolutionary processes: how, when and why taking them into consideration in translocation-based programs supporting Nature-based Solutions? - Knowlegde Hub EVOLUTION

- Context and host structures

The Knowledge-Hub (KH) EVOLUTION is part of a large French Priority Exploratory Research Program entitled SOLU-BIOD (Biodiversity and Nature-based Solutions) emanating from France 2030. SOLU-BIOD is managed by the CNRS and INRAE, and structured around several programs. One of these programs is devoted to KHs (including EVOLUTION), managed by the University of Montpellier over the 2025-2029 period with KHs being hosted at FRB-CESAB. As part of the partnership with SOLU-BIOD, the post-doctoral researcher is recruited by the FRB and housed at the FRB-Cesab in Montpellier.

The Foundation for research on biodiversity (FRB) gathers public research institutions, environmental NGOs, land and genetic resources managers and the private sector. It provides a forum where science meets society in order to address the current challenges related to biodiversity research.

The Centre for Synthesis and Analysis of Biodiversity (CESAB) is FRB's main program and a leading research organization in Europe, with an international reputation. Its aim is to implement the innovative work of synthesis and analysis of existing data in the field of biodiversity. Advancing knowledge, developing culture and collaboration, facilitating links between scientific disciplines and with the stakeholders, are the main objectives of FRB-CESAB, which welcomes every year a large number of researchers from all continents.

- Project context and topics

Nature-based Solutions (NbS) are cost-effective solutions supported by Nature, tackling different societal challenges, such as climate change, while providing environmental, social and economic benefits and helping to build resilience. Diversity within species remains little considered in NbS approaches, therefore disregarding the evolutionary dimension of complex socio-ecosystems and their adaptive potential in response to rapid environmental changes. In order to fill this gap, a knowledge basis should be built, including all processes impacting intraspecific diversity and the evolutionary potential (InDEP) of the involved species.

In this context, the current project will focus on "translocation" broadly defined as the transfer of organisms (genes), from point A to point B, with the NbS being implemented in B. Translocation includes both non-intentional processes and all forms of assisted migration and gene flow enhancement. "Translocation" leads to series of questions with regard to NbS success, such as the type, source and fate of translocated intraspecific diversity (possibly including manipulated variation), the conditions of translocations, the impact on recipient socio-ecosystems, or how this diversity can be handled by managers.

The work will draw widely from the corpus of knowledge and methods build up in basic and applied evolutionary biology, including from the conceptual framework and procedures from conservation and restoration biology (considering or not InDEP). A general interdisciplinary approach will be developed, based on the idea of operationalizing intraspecific diversity in NbS. This means developing relevant indicators, procedures and modus operandi. The basis of the work will be a review of the literature, in order to build a systematic map and to retrieve relevant variables or indicators for a subsequent meta-analysis. This will contribute to building a general framework of the role and use of InDEP in NbS, serving to guide research priorities on a scientific basis, but also to identify new research avenues.

- Modus operandi and work to be done

The work will be carried out within the framework of the EVOLUTION Knowledge Hub (KH) - a KH is a working group similar to those in scientific synthesis centers (here FRB-CESAB). EVOLUTION is made up of 15 scientists from several countries with diverse backgrounds and expertise who will work for three years on the above topics, coordinated by the post-doctoral researcher (post-doc) recruited. The post-doc will work more closely with a core group of four to five people. The entire KH will meet in person 4 to 5 times (twice a year) for 3 to 4 days at CESAB, and regular remote meetings will also be organized.

In close collaboration with the KH members, the post-doc is expected to:

* Conduct research along the axes defined above; * Coordinate progress and work of the KH members, and organize (scientifically) the KH meetings at FRB-CESAB as well as any other (virtual) meetings required; * Conduct resource searches (websites, existing databases, etc.) to determine the extent of available resources; * Conduct a systematic literature review and/or meta-analysis to

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Prague DeepSeaEvolutionVision

PostDoc position on evolution of (deep-sea) fish vision in Prague

[LAST CALL!!]

We are looking for a passionate and skilled postdoctoral researcher to join our team focused on evolution of fish vision. Fishes have evolved remarkable visual adaptations to thrive in diverse and often extreme environments, including the deep sea. We take a comparative approach, investigating lineages with striking visual specializations such as multibank rod-only retinas, multiple rhodopsin duplications, or - on the contrary - complete loss of rod cells. Our core methodologies center on genomics and transcriptomics, with the ultimate goal of linking molecular patterns to functional adaptations.

Start date: 1st January 2026

Application deadline - *14th of July 2025* (the candidate has to be selected by 1st of August)

Duration: up to 2 years (with possibility for extension)

Location: Department of Zoology, Charles University, Prague, Czech Republic, EU

Further info: https://www.fishevo.com/open-postdoctoral-position-function-of-fish-vision/ We specifically look for someone with hands-on *expertise in histological techniques such as immunohistochemistry and FISH * to address evolutionary questions related to rod cell diversity, differenciation, or loss in several species with unique vision. The successful candidate will have the opportunity to work independently while also contributing to collaborative, interdisciplinary projects. Prior experience in the field of evolutionary biology, or with experiments on vertebrate retina is a plus, it is not a requirement. This position offers an exciting opportunity to work at the intersection of molecular evolution, sensory biology, and comparative functional genomics.

The successful candidate will join the Fish Evolution research group of Zuzana Musilova at Charles University in Prague and will be part of the *ERC project "SensingDEEP: deep-sea fish vision pushing limits of the vertebrate eye"*.

We offer:

- an international research group with the ERC funding located in an inspiring historical city
- a competitive salary way-exceeding the average for the Prague city
- possibility to participate at international conferences and our collaborations

We seek:

- a candidate with motivation and enthusiasm for biology, nature and science willing to perform research on various groups of fishes
- a candidate with experience with histological techniques such as immunohistochemistry and FISH, and with ability to conduct experiments independently
- a candidate with a PhD degree in biology or related fields (or to be finished before starting the position - to be consulted individually)

The application (CV + motivation letter) should be sent to Zuzana Musilova (zuzmus[AT]gmail.com and/or zuzana.musilova[AT]natur.cuni.cz). The (pre-)selected candidate will additionally apply (with my guidance) for the Charles University Junior Fond programme to be eligible for a more competitive salary. The candidate has to be pre-selected by 1st of August and then proceed with the formal application (everything will be coordinated with me).

THANK YOU FOR YOUR INTEREST!

Zuzana Musilova, PhD. (zuzmus@gmail.com)

Department of Zoology Charles University Vinicna 7, CZ-128 44 Prague Czech Republic - Europe

zuzmus <zuzmus@gmail.com>

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SMNS Stuttgart MolecularBiogeography

Postdoc (m/f/d) at the State Museum of Natural History Stuttgart (SMNS, www.naturkundemuseum-bw.de)

At the earliest possible date, we want to hire a Postdoc (m/f/d; 100 %, limited until 30 September 2026) with a research focus on molecular biogeography, conservation genetics, analysis of faunal change, evolutionary morphology or ecology. Special emphasis will be given to innovative questions that can be answered, for example, using molecular methods. The Postdoc can collaborate in ongoing SMNS projects (see below) or contribute his/her own research projects. These must allow a close taxonomic and methodological link to existing programmes in the Department of Zoology (https://www.naturkundemuseum-bw.de/en/research/zoology).

Collaboration is possible on the following projects for which data already exist: Conservation genetics of freshwater mussels and groundwater snails using NGS data; Feeding ecology and admixture of Malagasy rainforest birds using metabarcoding from faecal samples and stable isotope analysis of feathers, Evolutionary morphology of the genitalia or olfactory system of amphibians (Gymnophiona) using ÂμCT analyses; Morphological and genetic evidence of hybridisation in two Foudia species (weaver birds) at a Madagascan rainforest edge

Requirements: Completeddoctorate in biology or a related subject; knowledge and experience in at least one of the research areas biogeography, ecologyor conservation/population genetics proven through publications; excellentcommand of written and spoken English; basic knowledge of German is a plus. In addition, one or more of the following skills are desirable: Molecular genetic/genomic methods incl. bioinformatic analysis in the field of biogeographical or ecological research(e.g. metabarcoding); statistical analyses, e.g. of genetic and/or ecological data; stable isotope analysis

Your task: Publication of research results in renowned scientific journals

What we offer: Full-time position, remunerated according to TV-L E 13 German salary scheme (limited until 30 September 2026); basic research funding and support for conference travel; cooperation and integration into already established research projects; attractive workplace in the centre of Stuttgart in an internationally renowned research museum; links to the research projects of the University of Hohenheim (e.g. KomBioTa); research in an international and multidisciplinary environment; well-equipped molecular laboratories; support in acquiring German language skills if necessary; monthly public transport allowance of 25 euro (JobTicket BW)

Please send your electronic application - in a single PDF file, max. 10 MB - with cover letter/resume with a description of your motivation, names/addresses of three references, copies of relevant certificates, list of publications, list of acquired third-party funding, outlook (max. one page) for a specific project at the museum within the above-mentioned research programmes. We accept applications in German and English. Please send your application to postdoc-zoologie@smns-bw.de by 30/06/2025 at the latest. Interviews are scheduled for 11/07/2025.

For further information, please contact PD Dr Stefan Merker (Tel.: +49-711/8936-246, Email: stefan.merker@smns-bw.de). You can also contact other scientists of theDepartment of Zoology directly.

The SMNS promotes equal opportunities for its employees and therefore welcomes applications from all people regardless of gender, cultural and social background, age, religion, ideology, disability or sexual identity. We are particularly committed to promoting equality between women and men and therefore expressly encourage qualified women to apply. Severely disabled applicants will be given preference if equally qualified. A pdf of this advertisement and more information for applicants, e.g. on data protection, can be found on our homepage under 'Jobs'.

PD Dr. Stefan Merker Abteilungsleitung Zoologie | Kurator für Mammalogie, Head of the Department of Zoology | Curator of Mammalogy

Naturkundemuseum Stuttgart | Natural History Museum Stuttgart

Rosenstein 1, 70191 Stuttgart, Germany

+49 711 8936-246

stefan.merker@smns-bw.de

www.naturkundemuseum-bw.de "Merker, Stefan" <stefan.merker@smns-bw.de>

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StockholmU ComparativePopGenomicsLepEU

LepEU postdoc: comparative population genomics of European scale adaptation in butterflies

A two-year, full-time post-doctoral stipend position is available in Prof. Chris Wheat's group at the Department of Zoology, Stockholm University.

The aim of this proposal is to place population genomic insights into a comparative framework to gain fundamental insights into the determinants of evolutionary outcomes. The project will work within LepEU, the European Lepidopteran Population Genomics Consortium (https://lepeu.github.io/). LepEU provides access to field samples from European populations of diverse species. Chromosome-scale reference genomes are provided by Project Psyche (https://www.projectpsyche.org/). Networking during the postdoc will be facilitated by participation in the 10kLepGenomes COST Action (https://10klepgenomes.eu/). Existing datasets await analysis, while additional samples need DNA extraction and submission for sequencing. Functional validation capability (CRISPR/Cas9 gene manipulations) is also available to test emergent hypotheses of allele-to-phenotype impacts. Personal research interests of the postdoc will be important to determine the exact project, as the project has a generous sequencing budget.

The successful applicant should have a PhD (obtained within 6 years of the application deadline) in a suitable subject area, such as evolutionary biology or population genomics. A strong interest in population genomics, local adaptation, comparative analyses, and experience working with genomic-scale data is essential. The candidate must have a documented publication record demonstrating relevant skills. Experience working with bioinformatic pipelines (e.g., Snakemake), or working with butterflies is welcome but not essential. The net salary is 28,000 SEK/month (~2,430 Euro, not subject to Swedish income tax) and comes directly from the Carl-Trygger Foundation stipend, which is paid out directly to the postdoc. Only PhD candidates acquired outside of the host department can apply. Currently, the lab of Prof. Wheat consists of 3 postdoctoral researchers, while the Dept. of Zoology provides a vibrant and excellent research environment of active, dynamic researchers.

Applications should include: i) a succinct description of research interests and experience, detailing your contribution to any relevant publications (max 1 page), ii) why you are the ideal candidate for this position in the lab (max 1 page); iii) a CV including a list of publications, and iv) the name and contact information of two personal references.

Start date: 1 October, but flexibility in the starting date can be provided for a suitable candidate. Deadline to apply: applications will be reviewed on a rolling basis with a deadline of 23 August 2025. More information: https://drive.google.com/file/d/-1iBRTWJp8VJhjfsEcfIL5T4y-_6TIfHhf/view Contact Prof. Wheat for additional information. Email: chris.wheat@zoologi.su.se

Christopher Wheat <chris.wheat@zoologi.su.se>

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UBern EvolutionDogViromics

Viromics of free-roaming dogs

PostDoc position, 3 years

University of Bern, Institute of Ecology and Evolution, PI: Gerald Heckel

A PostDoc position is available for research on the diversity, evolution and ecology of virus populations in free-roaming dogs in Africa and Asia. This position is part of an interdisciplinary project funded by the Swiss National Science Foundation (SNSF) determining the role of free-roaming dogs in the spread and persistence of infectious disease. The project combines experts from veterinary and social sciences, epidemiology, mathematical modelling and population genetics to test effects of landscape, infrastructure and human-dog relationships for disease transmission. A PhD student focuses on the population genomics of dogs, and doctoral and postdoctoral researchers from the other disciplines will collaborate. The overarching goal of the project is to formulate effective and socially accepted control strategies to reduce infection and disease burden in dogs and humans.

A very skilled, reliable and highly-motivated researcher is needed who is able to work with a diverse team of local and international collaborators and independently. You must have a solid background in evolutionary biology, and practical experience with the assessment of virome diversity based on NGS, bioinformatics, population genetics and/or evolutionary genomics. A PhD in a relevant field is required. Experience with laboratory work for viromics (RNA/DNA genomics, metabarcoding, shotgun, targeted enrichment) is essential. Participation in fieldwork in Uganda, Chad and Indonesia is not required. Most of your time will be devoted to the production and analysis of genomic datasets, and the preparation of presentations and manuscripts. A key role in the publication of manuscripts in leading scientific journals is expected.

The position is funded for up to three years with an earliest starting date in December 2025. The group is part of the Institute of Ecology and Evolution with a stimulating, multi-national research community and excellent infrastructure. English is the working language. Some knowledge of German or French is beneficial for living in Switzerland but it is not necessary for the project. Informal inquiries can be addressed to Prof. Dr. Gerald Heckel gerald.heckel@unibe.ch

To be considered, your application must be sent as a single (!!!) pdf file to Jolanda Paganoni jolanda.paganoni4@unibe.ch

The pdf must include a description of your motivation for this project and which particular skills and research experience make you a great candidate (maximum 2 pages), a CV with publication list and contact details of 2-3 reference persons. Review of applications will start in July 2025.

Prof. Dr. Gerald Heckel Institute of Ecology and Evolution University of Bern Baltzerstrasse 6 CH-3012 Bern, Switzerland Tel: +41 31 684 30 29 Email: gerald.heckel@unibe.ch

http://www.cmpg.iee.unibe.ch "gerald.heckel@unibe.ch" <gerald.heckel@unibe.ch>

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UEastAnglia RedFoxPopulationGenomics

A 4-year postdoc position on red fox population genomics is available at the University of East Anglia, Norwich, UK

You will be part of Dr Anders Bergström's research group (https://research-portal.uea.ac.uk/en/persons/-anders-bergstr%C3%B6m), and work on a new project aiming to understand the diversity and evolution of red foxes across the United Kingdom, with a particular focus on contrasting foxes living in urban and rural environments. Cities are expanding worldwide, with major implications for wildlife and biodiversity, but the red fox is an iconic example of a species that actually manages to thrive in these new environments. The project will apply whole-genome sequencing to many hundreds of foxes from urban and rural locations across the UK, to study the impact that urban environments have on genetic diversity and adaptation.

You will have a postgraduate level research degree, equivalent qualification or experience in a relevant research area and be able to work in a collaborative and dynamic research environment. This will be a computational post, in which you will be responsible for processing genomic sequencing data from large numbers of fox samples, and lead analyses of population structure, gene flow, kinship, inbreeding and natural selection.

You should have experience working with genomics data and bioinformatics analyses, handling large amounts of data in command line and high-performance computing environments. Expertise in read mapping, genotype calling, genotype imputation, statistical genetics and genome-wide association testing would be particularly beneficial. You should have a strong interest in evolutionary biology and population genetics. The role can be entirely computational, but can also involve some amount of lab work if this would be of interest.

This full-time post is available from 1 December 2025 (or as soon as possible thereafter) on a fixed term basis until 30 November 2029.

Starting salary from 38,249 per annum, dependent on skills and experience, with an annual increment up to 45,413 per annum.

For informal inquiries, contact Anders Bergström at: a.bergstrom@uea.ac.uk

Advert link: https://vacancies.uea.ac.uk/vacancies/-1593/senior-research-associate-in-population-genomics-ra2327.html “Anders Bergstrom (BIO - Staff)” <A.Bergstrom@uea.ac.uk>

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UMainz AntsGenomicsCellBiology

2-Year Postdoc Position: Evolution and Organization of Ant Olfactory Systems at the Johannes Gutenberg University Mainz, Germany

We are seeking a highly motivated postdoctoral researcher to join an interdisciplinary team focused on investigating the evolution and organization of the olfactory system in ants. The team includes Carlotta Martelli (neurobiology and computational biology), Hugo Darras (evolution and genomics), and Susanne Foitzik (behavior and evolution), along with two PhD students.

The project will explore the organizational structure of the olfactory system in ants, from genes to neurons to behavior. The long-term goal is to identify evolutionary signatures of non-canonical organizations of the olfactory system and to understand the computational consequences of different architectures for odor coding and behavior. This innovative, interdisciplinary project combines neurobiological and behavioral experiments, molecular genetic analysis, genomics, transcriptomics, and theory. This position will focus on bioinformatics as applied to genomic, (single-cell) transcriptomic, and neurobiological data, and will be co-supervised by H. Darras and C. Martelli, in collaboration with S. Foitzik. The ideal candidate should have a strong background in bioinformatics, ideally with practical or theoretical experience in single-cell transcriptomics or comparative genomics. A keen interest in neurobiology is essential. Additional skills in evolutionary biology, insect handling, and programming (preferably in Python) would be advantageous, but are not mandatory.

Start Date: Available immediately Duration: 2 years Contract: TVL-E13

Application Process:

If you are interested in joining our team, please send in a combined pdf to cmartell@uni-mainz.de: 1. A letter of motivation 2. Your CV 3. Contact information for two referees

Applications will be reviewed on a rolling basis, and candidates will be considered in the order they are received. For additional information, please contact us!

Carlotta Martelli cmartell@uni-mainz.de, https://-mrtlllab.uni-mainz.de/ Hugo Darras hdarras@uni-mainz.de https://www.blogs.uni-mainz.de/fb10-

evolutionary-biology/darras-hugo/ "Darras, Dr. Hugo" <hdarras@uni-mainz.de>

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UMainz EvolutionInCommunity

Position Details Start Date: September 1, 2025, or earlier, depending on the candidate's availability.

Duration: Initial funding for three years, with the possibility of extension.

Project Focus: Organisms interact in nature and form multitrophic communities. How do species evolve in a complex community? How does the evolutionary process affect community functions? In this ERC funded project, the successful candidate, together with a collaborative team, will deploy cutting-edge multi-omics approaches to address these two fundamental questions by studying real-time evolution of the duckweed and its interacting organisms in a natural community.

Key Requirements

We seek a highly motivated researcher with a doctoral degree (or equivalent) in one of the following fields: biology, evolutionary genetics, bioinformatics, or computer science. The ideal candidate will:

Demonstrate the ability to design, execute, and manage research projects independently. Have a strong background in bioinformatics, evolutionary genetics/genomics, or community ecology. Possess experience in statistics and genomics; expertise in computational modelling is advantageous. Be proficient in both spoken and written English.

Why Join Us

Supported by a collaborative research team (https://plant-x.uni-mainz.de/), this project will provide the candidate with opportunities to enhance his/her scientific skills, gain independence in project planning and management, and develop leadership abilities. The candidate may also supervise PhD and Master's students, with the potential to establish their own research group. The University of Mainz is home to numerous outstanding scientific institutions (http://www.uni-mainz.de/eng/) and fosters a vibrant academic environment. Mainz is a historic city located on the Rhine River, offering a rich social and cultural life, and is home to a dynamic student population.

Application Requirements

- Applications must be written in English and include the following documents: - Motivation Letter: A statement of research interests and how they align with the position, addressing the specified requirements (maximum 2 pages). - Curriculum Vitae: A detailed CV, including academic achievements, research experience, and extracurricular activities. - PhD Abstract: A concise summary of the doctoral thesis. - Referees: Contact details for at least two references.

Compile all documents into a single PDF file and send the application to Prof. Shuqing Xu via email at shuqing.xu@uni-mainz.de with the subject line: " Evol-Community Postdoc Position - [Your Name]".

Application Deadline The review of applications will begin on July 31, 2025. The position will remain open until filled.

Prof. Dr. Shuqing Xu Institute of Organismic and Molecular Evolution (IomE) Johannes Gutenberg University Mainz Biozentrum I Hanns-Dieter-Hüsch-Weg 15 D-55128 Mainz Germany Phone: +49 6131 39 26907 E-mail: shuqing.xu@uni-mainz.de

Shuqing Xu <shuqing.xu@uni-mainz.de>

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UMontana Claremont Two FloralEvolGenomics

The Fishman Lab at the University of Montana (with the Finseth Lab at Scripps College) is seeking a postdoctoral associate to join our NSF-funded research programs in plant evolutionary genomics. The focal project investigates the roles of satellite DNA, centromeric proteins, and linked genes in selfish chromosomal drive through female meiosis. The postdoctoral associate's key responsibility will be analyses of satellite DNA diversification across functionally distinct centromeres, using new chromosome-scale genome assemblies of yellow monkeyflowers. Monkeyflowers are a uniquely powerful system for investigating how selfish centromeres violate Mendelian rules, while˜40 new genome assemblies from across the genus also provide excellent opportunities for exploring the evolution of plant genome architecture more broadly. Therefore, we particularly encourage applicants interested in developing their own long-term research program on chromosomal evolution and/or genetic conflict.

The postdoctoral associate's primary activities will include:

ï¿½Using genomic and epigenomic (e.g., CenH3 Cut&Tag) analyses to understand satellite DNA diversification and its relationship to centromere functional variation

ï¿½Contributing to training and mentoring of graduate and undergraduate students

ï¿½Disseminating project results through publications (i.e., writing papers) and presentations

ï¿½Participating in outreach and training/teaching activities, including a bioinformatics SURE and CURE

The postdoc would ideally also contribute to other aspects of the centromere drive project (e.g., field work, genetic mapping, transcriptomics, functional assays), develop related research questions, and engage with other collaborative projects on selfish evolution, adaptation, and/or speciation in monkeyflowers.

The postdoc will be co-mentored by Dr. Lila Fishman (University of Montana, Missoula, MT;http://www.fishmanlab.org) and Dr. Findley Finseth (Scripps College, Claremont, CA;https://www.findleyfinseth.com/). The postdoc may choose to work and live in either location (but not a third remote location), with support available for cross-institution travel.Both Missoula and Claremont offer awesome quality of life and strong intellectual communities. Missoula is a welcoming mountain town with abundant outdoor recreational opportunities nearby, and the five highly-interactive evolutionary genomics labs at UM share a new research space and dedicated wetlab/bioinformatics support staff. Claremont is a liveable suburb of Los Angeles and the Claremont Colleges provide the perfect training context for those interested in a research-active PUI career.

Qualifications: Candidates must have a Ph.D. in Evolutionary Biology, Genetics, Genomics, Bioinformatics, Plant Biology, or a related discipline, as well as experience generating, analyzing, and interpreting large (epi)genomic datasets. The successful candidate is also expected to have a solid background in biostatistics, a strong work ethic, and excellent logical problem-solving and communication skills. A track record of research activity resulting in publications and evidence of a commitment to mentoring undergraduate students is also expected. Prior experience with the population genetics of conflict/selfish evolution, plant cytogenetics or epigenetics, and/or genomic analysis of repetitive DNA elements in any system would be particularly valuable but is not required.

Salary and appointment term: ~$65,000-70,000 per year (depending on prior experience) with full benefits. The initial appointment will be for one year, with up to 2 additional years possible pending satisfactory performance and no changes to current funding. The start date is flexible, but ideally in Fall 2025. The University of Montana (hiring institution) is an Equal Opportunity and ADA/EOE/Veteran's Preference Employer.

Applications are due by July 30, 2025 for full consideration. Potential applicants are welcome to email Lila (lila.fishman AT umontana.edu and Findley (ffinseth AT natsci.claremont.edu) directly with any questions about the project or work/life in either location. However, applications can only be considered if submitted through the UMJobs page for the position, following the directions there:https://apply.interfolio.com/169143 . Lila Fishman, PhD (she/her) Professor and Director,Ecology &Evolution Graduate Program Division of BiologicalSciences University of Montana, Missoula MT 59812

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The Fishman Lab (www.fishmanlab.org) is seeking a highly-motivated postdoctoral researcher to join our research program in plant evolutionary genomics at the University of Montana. The NSF-funded focal project

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UPuertoRico ButterflyGenomics

TWO (2) POST-DOCTORAL position in butterfly wing development single cell genomics

NSF GRANT: Genomic Logic Underlying Adaptive Morphological Divergence

TYPE OF APPOINTMENT: Special Appointment

BASIC SALARY: $50K - $65K annually

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

DATE OF PUBLICATION: From: May 21, 2025- Until June 18, 2025

STARTING DATE: August, 2025

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

JOB DESCRIPTION

This is a unique opportunity to join a large team and international network of scientists to work on a multi-year project that embraces the most important questions in development and evolution utilizing state of the art technologies. We are seeking a highly motivated Post-Doctoral Fellows to join our research team focusing on developmental evolutionary questions. We are recruiting 2 post-doctoral fellows. We use butterflies as a study system and omics, computational biology and AI as tools to determine fundamental molecular rules in the making of life.

Project Team

The team Principal Investigator, Riccardo Papa, is an expert in genomics, evolution, and development. The project is composed by a large team of researchers with diverse skills that will enrich the learning capability of the applicants and future job opportunities. Finally, we have a large network of national (USA) and international collaborators that will participate in the development of this project and will represent an added value for personal growth.

Professional development

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

Project Description:

This project aims to tackle a fundamental problem of developmental biology and evolution, using butterflies as a model system. The project will integrate a diverse set of omics, developmental, computational and artificial intelligence (AI) techniques to illuminate the single cell architecture, diversity and fate of a butterfly wing across development. The project aspires to create a detailed map of molecular processes to interpret the connection between genome and pohenome and use it for broader evolutionary comparisons. The project will address a scientifically important topic: the mechanistic underpinnings that instruct cells to undergo fates and acquire diverse functions to build complex tissues, organs, and traits. The project's ambition is to decode the genomic architecture and molecular logic of the differentiation and function of wing tissue.

Principal Investigator Google Scholar profile

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

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

Responsibilities:

Design and conduct experiments related to development and evolutionary questions in butterflies

Analyze complex omics datasets

Maintain big data repositories

Develop computational pipelines

Develop and apply bioinformatics tools for data analysis

Prepare manuscripts for publication in peer-reviewed journals

Present research findings at conferences and seminars

Mentor graduate and undergraduate students

Assist in grant writing and project management

Qualifications:

Ph.D. in Genetics, Developmental Biology, Genomics, Bioinformatics, Computational Science or a related field

Strong background in computational science and molecular biology techniques

Proficiency in bioinformatics and data analysis (e.g., R, Python, Unix/Linux)

Experience with next-generation sequencing data analysis

Excellent written and verbal communication skills

Ability to work independently and as part of a collaborative team

Publication record in peer-reviewed journals

Preferred Qualifications:

Knowledge in computational science

Genomics data analyses

Familiarity with evolutionary developmental biology concepts

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USouthBohemia AvianEvolEcol

Post-Doc: USouthBohemia.EvolutionaryEcology

Faculty of Science, University of South Bohemia in Ãeské BudÃ, Czech Republic is seeking qualified applicants for the position of

Post-doctoral researcher in Evolutionary Ecology-Bird Migration

Global Life-history, Ornithology & Behavioural Ecology (GLOBE) research group (https://GLOBEresearchgroup.com - new webpages under construction will be launched soon) focuses on ecology, behaviour, life-history strategies and population dynamics of wild animals, particularly birds, including impacts and consequences of recent environmental changes. The GLOBE research group, led by VojtÃKubelka from Department of Zoology and Centre for Polar Ecology at the Faculty of Sciences, University of South Bohemia in the Czech republic, has been recently awarded a prestigious ERC CZ grant: Animal migrations in a changing world - still advantageous strategy or maladaptive behaviour? for five years till 2029.

Animal migrations represent one of the greatest spectacles in nature, providing crucial ecosystem services as well as resources for human communities. Why do animals migrate? It has been thought that animals migrate to reproduce at higher latitudes, taking advantage of lower predation pressure, fewer parasites and seasonally high pulses in food supply. However, it has been highlighted that recent climate change and human pressure impacts can erode such benefits and migratory animals are declining globally with poorly understood underlying mechanisms.

We strive to tackle pressing issues: Are there still latitudinal gradients in predation, parasitism and seasonal food availability, supporting the benefits of migratory behaviour? How are migratory animals able to cope with environmental changes? What are the most important drivers and life stages limiting populations of migratory animals? To achieve this, we are executing comprehensive research of migration profitability, combining experimental, observational and comparative approaches - investigating latitudinal gradients in predation, parasites, food supply and whole life-cycles of tracked shorebirds, a suitable model taxon with intraspecific variability in migratory strategies and exposed ground nests - at 16 study sites from the Arctic to Patagonia.

What would be your main responsibilities - Organize and conduct ornithological field work at selected study sites across Western Palearctic and South America in association with international collaborators - Combine experimental and observational fieldwork with a comparative approach based on extracting relevant information from published literature - Coordinate data collection and analyses, working with large datasets in relational databases - Prepare and write manuscripts for publication in peer-reviewed journals - Lead or participate in funding applications for research in collaboration with team members - Supervise students and research assistants - Participate in conservation activities - Present and promote the results at conferences and seminars - Disseminate the project outputs to stakeholders and public, - Carry out other scientific and/or academic activities that are important for the success of the project

What we offer - A two-year position with the possibility of extension based on the performance - Excellent instruments, equipment and multiple research platforms within the Faculty of Sciences, University of South Bohemia in Ãeské BudÃ, Czech Republic - Access to the Czech Arctic research station at Svalbard and fieldwork at study sites along latitudinal gradients from Morocco to Arctic and from tropical South America to Patagonia - Extensive international networking and mentoring opportunities - Full logistical support for own follow-up research funding applications - English speaking, stimulating & friendly international research environment - HR Award certificate, jcu.cz/about-the-university/development/hr-award-hrs4r - Professional administration support and assistance with all personal, economic, legal, project, IT, intellectual property needs, flexible working time - Competitive salary + possible bonuses, 5 weeks of paid vacation per year - Meals allowance, special mobile services, university kindergarten - Work-life balance in a historical middle-sized university city, budejce.cz/en/

Competitive candidates are expected to have - PhD in evolutionary biology, behavioural ecology, zoology, or relevant field of life sciences - A foundation of knowledge in two or more fields: evolutionary ecology, climate change biology, demography and population dynamics, predator- prey interactions and animal migration - Experience in conducting or supervising international research projects - 3+ years hands-on experience in field research, with preference for experience with fieldwork in tropical or Arctic locations

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UtahStateU EvolutionaryGenomics

Job Title: Postdoctoral Fellow II

Overview:

The Gompert Lab at Utah State University (Department of Biology) is recruiting a postdoctoral research scientist in evolutionary genomics to start in fall 2025. The postdoc will work on a NIH-funded project exploring the contribution of structural genetic variation (chromosomal rearrangements) to trait variation and adaptation in three insect systems: Lycaeides butterflies, Timema stick insects and Callosobruchus seed beetles.

Responsibilities:

The postdoctoral researcher will collaborate with Dr. Gompert on evolutionary genomic data analyses, including comparative genome alignments and pangenome graph construction. The goal is to identify structural variants from genome assemblies and conduct downstream analyses that integrate structural variant discovery with population and quantitative genomic data. This research will focus on studying trait variation, adaptation, and hybridization. Depending on the postdoc's skills, interests, and expertise, they may focus exclusively on data analysis or also take on a central role in lab or fieldwork. Applicants interested in working remotely are eligible to apply.

Key responsibilities include: (i) leading data analysis and interpretation, (ii) managing and contributing to individual research projects within the scope of the Gompert lab's program, (iii) collaborating with other research team members, (iv) mentoring undergraduate and graduate students in the lab, (v) writing scientific papers, and (vi) presenting research findings at conferences and participating in regular lab meetings.

Qualifications: Minimum Qualifications:

- Ph.D. in biology, computational biology, data science, or a related discipline - Demonstrated experience working with genomic or population genomic data - Strong understanding of the scientific process, including experimental design and research integrity - Excellent written and verbal communication skills - A record of peer-reviewed publications - Ability to work both independently and collaboratively in a research environment - Genuine enthusiasm for scientific discovery and contributing to the advancement of knowledge

Preferred Qualifications: A subset of the following skills and experiences is desirable, but not required:

- Strong background in evolutionary biology or computational biology - Proficiency or familiarity with programming or scripting in languages such as R, Python, Perl, C, or similar - Experience analyzing and managing data on a high-performance computing cluster, including use of a Unix command-line environment - Experience working with structural genetic variant data or pangenomes - Laboratory skills in molecular biology, particularly techniques relevant to modern genome sequencing - Experience or interest in working with insects in either laboratory or field settings

Link to apply: https://careers-usu.icims.com/jobs/9276/job Jobs | Human Resources < https://careers-usu.icims.com/jobs/9276/job > Learn more about finding a career at Utah State University. Apply for open positions, and learn about the campus community and culture. careers-usu.icims.com

zach.gompert@usu.edu

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VrijeU Belgium Two SexChromosomeEvolution

The Evolutionary Genomics of Sex lab at Vrije Universiteit Brussel (Brussels, Belgium) is hiring 2 postdoctoral researchers to investigate the evolution, genetic mechanism and genomic signatures of sex chromosomes in various frog lineages. Our lab explores how sex chromosomes and sex-determining systems evolve across eukaryotes, and how and why they are stable in some lineages (i.e. mammals, birds) but remarkably labile in others (amphibians, fishes, reptiles, insects and flowering plants). These positions are part of an

ERC-funded project aiming to understand the genomic signatures of both differentiated and undifferentiated sex chromosomes in species with male (XX/XY) and female (ZW/ZZ) heterogamety, using an integrative approach combining comparative and functional genomics, population genetics, molecular evolution and genetics, cytogenetics, and fieldwork.

Position 1: Comparative & Evolutionary Genomics

We are looking for a highly motivated postdoctoral researcher with a PhD in bioinformatics, evolutionary genomics, computational biology or a closely related field. The ideal candidate has strong experience in:

High-throughput sequencing workflows (WGS, RNA-seq, RAD-seq)

Genome assembly and annotation, transcriptomic

Comparative genomics and population genomics analyses Proficient coding in Python, R, Bash, Perl, (or equivalent) Fieldwork experience is a plus.

Responsibilities include curating and maintaining lab codebases, leading genomics projects, mentor Master's, bachelor's and practical-course students. Strong communication skills and a collaborative team spirit are essential. Fieldwork experience is a plus. Teaching opportunities are available if desired.

Position 2: Molecular and Evolutionary Genetics We are seeking a highly motivated candidate with a PhD in evolutionary genetics or molecular evolution, with solid experience with diverse molecular and functional techniques, Responsibilities include:

Leading ongoing research projects Help PI coordinate the molecular lab Mentoring Master's, Bachelor's, and practical-course students Opportunity to develop independent research projects Field experience is a plus. Teaching opportunities are available if desired.

Application instructions: Applicationsshould be emailed to Prof. Wen-Juan Ma (wen-juan.ma@vub.be) and include:

(1) a CV

(2) a cover letter outlining your qualifications, research interests and career goals

(3) Contact details for three references.

Application deadline:

Rolling, until the positions are filled.

Each position is offered as a 2-year contract, with renewal on an annual basis. Support will be provided for applying to independent postdoctoral fellowships. Informal inquiries are welcome (wen-juan.ma@vub.be). The positions are available immediately.

The Ma lab is part of Ecology, Evolution and Genetics (bDIV) research group and funded by a prestigious ERC starting grant. Learn more about our work at the Ma lab page. https://wmalab.com Dr. Wen-Juan Ma

Assistant Professor Biology Department Vrije Universiteit Brussel Pleinlaan 2 1050 Brussels, Belgium Office: 0032 (0)2 629 3416 Lab page: http://www.wmalab.com Twitter: @WenJuanMa84 https://academic.oup.com/jeb/pages/why-publish Wen-Juan Ma <Wen-Juan.Ma@vub.be>

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WSL Switzerland EcologicalGenomicsWhiteOaks

Please find here an announcement for a 2-year post-doc position in ecological genomics (of white oaks) in the framework of the Horizon project OptFORESTS: https://apply.refline.ch/273855/1740/pub/1/index.html Looking for somebody with strong skills in bioinformatics, landscape genomics, forest genomics, GWAS, and population genetic simulations.

Christian Rellstab, Ecological Genetics, WSL Birmensdorf, Switzerland

Christian Rellstab <christian.rellstab@wsl.ch>

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Zurich ConservationGenomics

We are hiring a Postdoc in conservation genomics at Eawag - the Swiss Federal Institute of Aquatic Science and Technology (Switzerland). The position is funded for 3 years (SNSF) and based in the Adaptation & Conservation Genomics group led by Alexandra A.-T. Weber.

The project focuses on the Unio crassus species complex and integrates:

* Whole-genome resequencing * Transcriptomics and epigenomics * Environmental and fitness data with the

goal of understanding mussel decline and resilience in the face of climate change. The postdoc will work in an interdisciplinary team and in close collaboration with partners in Croatia and Poland, with opportunities for fieldwork, student supervision, and developing independent ideas.

Start date: January 2026 Deadline to apply: 22 August 2025 More info & apply here: https://apply.refline.ch/673277/1264/pub/en/index.html We're looking for someone with a PhD in evolutionary or conservation genomics (or related fields), experience with large-scale genomic data and HPC, and a collaborative mindset.

Please share with anyone who might be interested!

Dr. Alexandra A.-T. Weber Group Leader, Department of Aquatic Ecology Eawag, Swiss Federal Institute of Aquatic Science and Technology Ueberlandstrasse 133 8600 DÃÂ¼bendorf, Switzerland

email: Alexandra.weber@eawag.ch

"Weber, Alexandra Anh-Thu" <Alexandra.Weber@eawag.ch>

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WorkshopsCourses

Barcelona ESEB GenomicsCoevol Aug20 Reminder

REMINDER: Call for Poster Submissions - ESEB 2025 Satellite Symposium: Ecological Genomics of Coevolution

We are pleased to announce the ESEB 2025 Satellite Symposium "Ecological Genomics of Coevolution", taking place on 20th August 20, 2025 at the International Convention Centre of Barcelona (CCIB) Venue:Google Maps link.

This one-day event will bring together researchers at the interface of ecology, evolution, and genomics to explore coevolutionary processes across diverse systems.

Program: - 2:00 - 2:10 PM - Welcome & Opening Remarks - 2:10 - 2:40 PM - Ellen Leffler (University of Utah) - Talk + Q&A - 2:40 - 3:25 PM - Young Researcher Talks 1-3 - 3:25 - 3:40 PM - Coffee Break - 3:40 - 4:10 PM - Joy Bergelson (New York University) - Talk + Q&A - 4:10 - 4:40 PM - Young Researcher Talks 4-5 - 4:40 - 5:40 PM - Poster Session & Networking

Poster Submissions Are Now Open!

We warmly invite early-career researchers to present their work during the poster session & networking hour.Submit your abstract here:https://forms.gle/3JXDCeBDvA1Cyabu7 Notes: *This submission is separate from the main ESEB 2025 abstract call and deadline, as this is a satellite workshop. This is entirely normal for satellite events. *Oral presentation slots have already been allocated by invitation and are not part of this call. *People must have registered at the ESEB conference 2025 to apply for a poster here.

Please feel free to circulate this opportunity to colleagues or students who may be interested. We look forward to your contributions!

The Organizing Committee

Amandine Cornille, Ph.D. She/Her/Hers

Associate Professor of Biology, NYU Abu Dhabi

Saadiyat Island campus

P.O. Box 129188 Abu Dhabi, United Arab Emirates

Twitter:@CornilleAmand or

@PommierVerger Bluesky: @CornilleAmand.bsky.social Google Scholar profile

Group page (new to be announced soon)

To schedule a brief meeting with me, please use my appointment calendar.

Any message I send outside regular working hours does not require an immediate response.

Amandine Cornille <amandine.cornille@nyu.edu>

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Belgium BehaviourEvolution Sep26-27

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External email.

External email.

Dear Brian,

I hope this email finds you well. Could you please share the below call for abstracts for a workshop on comparative behavioral biology with members of the “Evolution Directory”?

Thank you in advance for your kind attention to this matter.

Best regards,

Alejandro

—

Call for Abstracts:

“Behavior Across the Tree of Life:

Theoretical and Methodological Challenges”

Interdisciplinary Workshop

Raadzaal, Institute of Philosophy, KU Leuven, Leuven, Belgium

Topic: Comparative Behavioral Biology

Dates: 26-27 September 2025

Organizers: Gianmaria Dani, Alejandro Fábregas-Tejeda, and Grant Ramsey (Institute of Philosophy, KU Leuven)

Deadline: July 14th2025

Notification: July 18th2025

Confirmed Speakers

Kristin Aleklett (Lund University)

Silvia Guerra (University of Padua)

Tobias Starzak (Ruhr University Bochum)

Kirsty Y. Wan (University of Exeter)

Frameworks from animal behavior studies are increasingly being borrowed and adapted to interpret a wealth of empirical findings in creatures outside the animal kingdom, such as plants, fungi, and bacteria. These findings include goal-oriented dynamics, adjustments in growth and development, and signaling. Collectively, they have complicated our understanding of what constitutes organismal activity and stretched the concept of behavior, prompting a reevaluation of how behavior should be understood and how it can be distinguished from related activities, such as growth and development.

Even though cross-kingdom comparisons are increasingly employed to frame and explain the activities of non-animal organisms, the issue of whether these comparisons are epistemologically and methodologically warranted remains under explored.

This workshop will explore the theoretical and methodological foundations of comparative research on behavior across the tree of life and will spell out some of its challenges.It will convene philosophers and scientists working on different groups of (putatively) behaving organisms to assess the status of what could be called 'comparative behavioral biology.' This comparative approach aims to build systematic knowledge of the diversity and evolution of behavior across kingdoms and to complement other branches of comparative biology with much-needed clarifications.

The themes and topics that we will cover include (but are not restricted to):

I. Can the theoretical and methodological frameworks already developed in animal behavior studies be extrapolated to investigate behavior in non-metazoan organisms? II. What concepts and frameworks are useful for laying the groundwork of a genuine inter-kingdom comparative behavioral biology? III. Through which criteria can we individuate behaviors and behavioral characters? How projectible are trait individuation criteria across taxonomic groups? IV. What experimental set-ups and methodological considerations do we need to take into account for sound inter-kingdom comparisons? Do we need one-size-fits-all standards, or can we have different standards depending on the particularities of certain taxa? V. How is comparative behavioral biology situated with respect to research in comparative cognition and comparative psychology? What are some of its overlaps and points of divergence?

We welcome contributions from theoretical and empirical researchers philosophers and scientists alike interested in fostering interdisciplinary dialogues on comparative behavioral biology and its theoretical and methodological foundations.

We invite submissions of abstracts (max. 500 words, excluding references). Abstracts must include personal information (affiliation, contact info). Please send the abstracts to Gianmaria Dani (gianmaria.dani@kuleuven.be) and Alejandro Fábregas-Tejeda (alejandro.fabregastejeda@kuleuven.be). Deadline: July 14th 2025. Notifications of acceptance: July 18th 2025.

For more information, please visit: https://hiw.kuleuven.be/clps/events/agenda/workshop-behavior-across-the-tree-of-life-theoretical-and-methodological-challenges Alejandro Fábregas-Tejeda

Centre for Logic and Philosophy of Science, Institute of Philosophy, KU Leuven Kardinaal Mercierplein 2 - box 3200 BE-3000 Leuven / Belgium Email: alejandro.fabregastejeda@kuleuven.be https://www.alejandrofabregastejeda.com/ Alejandro Fábregas Tejeda <alejandro.fabregastejeda@kuleuven.be>

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Berlin AngiospermDiversification Jul28-Aug8

Dear colleagues,

This is a final invitation to apply for the workshop on floral morphology and angiosperm diversification.

We still have places on this exciting workshop in Berlin from 28 July until 8 August 2025.

This unique and intensive two-week course provides a critical basis for diverse areas of research in botany that is becoming increasingly overlooked in the university curriculum.

Below some comments of former students: “ The course is true to how it is advertised. It, however, exceeded my expectations. It opened up a new world of complexity. I am grateful for having attended.”

“I liked the dynamic of the course, it was great having theory classes and then heading out to collect and see plants. Doing it in a botanical garden is a wonderful idea, it is great to see plants from all over the world and have material to work with. The professors where very attentive to our needs and questions.”

“ Thank you for the immense effort in putting this course together and all the passion and care with which these topics were delivered. It was wonderful to be challenged, overwhelmed and awed in this workshop and to have a chance to meet with such kind people. This workshop has definitely given me new eyes through which to see the world - and a newfound curiosity for its flowers. I don’t think anyone, after taking this course, can walk past a flower without first rummaging through its stamens and frowning into its centre, or dissecting its various parts - much to the confusion of unfortunate onlookers.”

“The style of teaching as well as the amount of input was great! It did not matter if you were familiar with the topic/order/family/.. it was easy to follow, and one could take up as much as desired. Now I have (I would say) a good overview over the phylogeny of angiosperms, which hopefully will help me further to learn new species and recognize orders and families on future adventures.”

Please distribute widely!

Louis Ronse De Craene and Julien Bachelier

==$\frac{3}{4}$rlin Summer Course in Flower Morphology and Angiosperm diversification

28 July - 8 August 2025

This is the third version of a highly successful two-week workshop based at the Biological Institute of the Freie Universität Berlin and the Berlin Botanical Garden. The workshop benefits from extensive facilities, including functional microscopy laboratories and a huge plant collection of more than 20,000 species. The course is set up as lecture-based, laboratory taught, and interactive visits of the living collections.

FORMAT:

2-week workshop, lectures and hands-on practical sessions.

INTENDED AUDIENCE:

Final year undergraduate students, PhD students, postdoctoral and advanced researchers, professionals (but no formal restriction). A basic knowledge of botany is preferred but not essential.

COURSE INSTRUCTORS AND CONTACT:

Dr. Louis Ronse De Craene, Research Associate Royal Botanic Garden Edinburgh (l.ronsedecraene@gmail.com)

Prof. Julien Bachelier, Freie Universität Berlin (julien.bachelier@fu-berlin.de)

REGISTRATION FEE:

euro 800 (euro 600 for Undergraduate and Master students)

(Registration includes coffee breaks, daily lunches with snacks, but does not include travel and accommodation).

HOW TO APPLY, PAY AND SECURE A PLACE:

visit https://www.conftool.net/berlin-summer-course-2025/ For further information please contact Dr. Louis Ronse De Craene (l.ronsedecraene@gmail.com).

PROGRAMME:

Course Description and outline:

This short course will introduce students to the structure and development of flowers, with a focus on floral diversity and evolution and the significance of flowers for systematics. Major plant families will be studied within the framework of the main lineages of seed plants to understand their evolution and diversification. Additionally, students will learn to analyse, describe, and study the structure of inflorescences, flowers, and fruits, and based on their observations, to identify the main evolutionary patterns underlying their tremendous morphological diversity, as well as their potential pollination and dispersal mechanisms.

Course objectives and learning outcomes:

Through this course students will acquire the following skills:

- guidelines to identifying plants using morphological characters in the context of the molecular classification system. - a better understanding of the origin and evolution of floral structures, including their importance for classification, and of the main developmental patterns and evolutionary trends which underlie the tremendous diversity of reproductive structures. - an ability to observe and recognise key characters through the study of live floral material and the building up of floral diagrams.

Contents:

- Introduction to morphology of vegetative structures and flowers, inflorescence and flower structure (floral diagrams and formulas).

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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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CE3C Portugal EvolutionaryBiology

Subject: Portugal-CE3C-AdvancedCourses for 2025/26: offer already available

cE3c Advanced Courses 2025/2026 - List already available

The detailed program of the Advanced Courses organized by cE3c - Centre for Ecology, Evolution and Environmental Changes for the academic year 2025/2026 is already available. Except when said otherwise the courses will be given in person, not online.

These courses are aimed for PhD students enrolled in Doctoral Programmes in Biology or related areas. They can also be attended by professionals and others with basic biology formation (such as BSc in Biology or related areas).

The courses have in general an intensive format, with one week of duration, with 5-6 ECTs recognition for the above mentioned Doctoral Programmes. Some have a shorter format (see details in each course's programme).

We detail below the list of courses of higher interest for Ecology & Evolutionary Biology students and researchers. Other courses and more details (including programmes, fees, procedures and deadlines for applications) can be found at:

https://www.ce3c.pt/training Selected CE3C Advanced Courses 2025/2026 10-14 Nov 2025 - Write and Publish Scientific Works - Luís Catarino, Maria Manuel Romeiras & Lillian Barros

17-21 Nov 2025 - Stable isotopes in Ecology and Environment: a tool to integrate scales and complexity - Cristina Antunes et al.

05-09 Jan 2026 - Bioinformatics Analysis of biological sequences from sequence to structure- Teresa Nogueira (ONLINE)

26-30 Jan 2026 - Remote sensing of the environment: a practical course - Maria Alexandra Oliveira et al.

18-20 Mar 2026 - Data Collection and Analysis in Qualitative and Participatory Methods - Inês Campos, João Limão & Filipe Moreira Alves (NEW!)

23-27 Mar 2026 - Concepts and Applications in Macroecology - Pedro Cardoso et al. (NEW!)

06-10 Apr 2026 - Entomology: Insect diversity and decline - Ana Sofia Reboleira & Roberto Keller (organizers) et al.

13-17 Apr 2026 - Strategies for citizen engagement in Science Communication - Cristina Luís & Patrícia Tiago

11-15 May 2026 - Hands on Functional Diversity: from Ecological Indicators to Ecosystem Services - Alice Nunes et al.

15-19 Jun 2026 - Museum Techniques in the 21st Century - Ricardo Lopes, Judite Alves & Pedro Andrade

24-26 Jun 2026 - Introduction to R programming and biological data analysis - Inês Fragata & Alexandre Blanckaert

19 Jun-03 Jul 2026 - Advanced R for Ecology and Evolutionary Biology - Inês Fragata, Vitor Sousa & & Alexandre Blanckaert

27-31 Jul 2026 - Measuring Biodiversity: how to get data, assess its quality and measure different aspects of diversity - Joaquin Hortal & Ana Margarida Santos

Margarida Matos Executive Committee of the Centre for Ecology, Evolution and Environmental Changes Faculdade de Ciências da Universidade de Lisboa

Margarida Matos <mmmatos@ciencias.ulisboa.pt>

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EvolBiol RecordedCoursesSale

I think a lot of these resources will be useful to many. It?s very general but with some evolutionary courses.

Big Changes Coming to PR Stats Recorded Courses! We're revamping our recorded courses with brand-new features, improved structure, updated content, and exciting new topics. As we work on these upgrades, our recorded courses will beunavailable from July through August. To celebrate the changes, we're offering50% off all recorded coursespurchasedbefore the end of this week-plus, you?ll getextended access until January 1st, 2026. Don't miss out on this opportunity to learn at your own pace and lock in huge savings before the update!

General Advancing in R (ADVR01)

Introduction to generalised linear models using R and Rstudio (IGLM06)

Introduction To Mixed Models Using R And Rstudio (IMMR07)

Model selection and model simplification (MSMS04)

Data visualization with ggplot2 using R and Rstudio (DVGG04)

Reproducible and collaborative data analysis with R (RACR03)

Time Series Data Analysis (TSDA02)

Time Series Analysis and Forecasting using R and Rstudio (TSAF01)

Introduction to Machine Learning using R and Rstudio (IMLR02)

Machine Learning with R (Intermediate - Advanced) (MLIA01)

Bayesian

Introduction / Fundamentals of Bayesian Data Analysis statistics using R (FBDA01)

Bayesian Approaches To Regression And Mixed Effects Models Using R and brms (BARM01)

Introduction To Stan For Bayesian Data Analysis (ISBD01)

Bayesian Data Analysis (BADA02)

Spatial

Making Beautiful And Effective Maps In R (MAPR04)

Adapting To The Recent Changes In R Spatial Packages (sf, terra, PROJ library) (PROJ02)

Using Google Earth Engine in Ecological Studies (GEEE01)

Remote sensing data analysis and coding in R for ecology (RSDA01)

Movement

Movement Ecology Using R(MOVEPR)

Hidden Markov Models for movement, acceleration and other ecological data - an introduction using moveHMM and momentumHMM in R (HMMMPR)

Miscellaneous

Bioacoustics For Ecologists: Hardware, Survey design And Data analysis (BIAC03)

Multivariate Analysis Of Ecological Communities Using R With The VEGAN package (VGNR06)

Stable Isotope Mixing Models Using SIBER, SIAR, MixSIAR (SIMMPR)

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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

oliverhooker@prstatistics.com

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Online aDNAPopulationGenomics Sep22-26

Dear all,

We are pleased to announce the upcoming Physalia online course: Population Genomics Using Ancient DNA DataDates: 22nd-26th September -Daily sessions: 2-8 PM (Berlin time)

Course website: (https://www.physalia-courses.org/-courses-workshops/adna-popgen/)

This course introduces participants to the unique challenges and opportunities of working with ancient DNA (aDNA) in population genomics. You'll learn how aDNA data is generated, processed, authenticated, and analyzed to answer key evolutionary and demographic questions. Through a mix of lectures and hands-on exercises, attendees wiill gain practical experience with:

Authenticating and processing ancient genomic data

Exploring population structure and relatedness

Applying D and F statistics to assess population affinity and gene flow

Performing demographic inference and simulations

Detecting signatures of natural selection For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/-adna-popgen/)

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/-in/physalia-courses-a64418127/)

"info@physalia-courses.org" <info@physalia-courses.org>

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Online AIforGenomics

Dear colleagues,

We're excited to announce our upcoming online course: AI FOR GENOMICS: FROM CNNS AND LSTMS TO TRANSFORMERS

Dates: 9'11 SeptemberCourse website: (https://-www.physalia-courses.org/courses-workshops/ai-for-genomics/)

This course offers a hands-on introduction to modern AI approaches in genomics, including CNNs, LSTMs, and Transformers. Participants will learn how to apply these powerful tools to sequence classification, functional element prediction, metagenomic source tracking, and more'using practical coding labs and interactive notebooks.

By the end of this course, participants will be able to:

- Understand and implement LSTM and CNN architectures for genomic sequence data - Apply attention mechanisms to improve genomic feature extraction and prediction - Train simple Transformer models for sequence classification or functional element prediction - Use notebooks to run and modify ML & DL workflows for genomics research - Interpret model outputs and assess performance using biological context

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 BiodiversityAnalysis Aug1822

Dear all,

there are still a few seats available for the upcoming Physalia online course: "Analysing Biodiversity Through Time and Space Using R"

Dates: 18-22 August

DAILY SCHEDULE: Lecture/discussion: 15:00 to 18:00 (Berlin-time) Practical: self-paced (~4 hours)

Course website: (https://www.physalia-courses.org/courses-workshops/biodiversity-in-r/)

This course offers a powerful, hands-on approach to analysing biodiversity patterns using both modern and fossil datasets. You'll learn how to build reproducible workflows in R, clean and integrate occurrence data, and quantify biodiversity across spatial and temporal scales.

Participants will explore key biodiversity metrics, tackle challenges related to sampling bias, and gain practical experience in working with major databases like GBIF and the Paleobiology Database. You'll learn to combine palaeontological and neontological data, apply GIS and stratigraphic tools, and model diversification through deep time all while producing insightful visualisations to support your findings.

For the full list of courses and workshop, please have a look (https://www.physalia-courses.org/courses-workshops/biodiversity-in-r/)

Best regards, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 (https://www.linkedin.com/in/physalia-courses-a64418127/)

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Online GeometricMorphometrics Jul28-Aug5

Dear colleagues,

I am excited to announce the 11th edition of the course "Geometric Morphometrics in R" (live online).

Dates: Online live sessions on July 28th, 29th, 30th, 31st, and August 1st, 4th, 5th, 2025.

Daily schedule: from 12:00 to 17:00 (Madrid time zone).

Course webpage: https://www.transmittingscience.com/courses/geometric-morphometrics/geometric-morphometrics-r/ Instructor: Dr. Julien Claude, author of the book "Morphometrics with R [1]" (Institut des Sciences de l'ï¿½volution de Montpellier, France).

Course Overview

Concepts in geometric morphometrics will be taught using a series of original data sets and working in R for solving a series of tasks. The course will start with an introduction to R and will rapidly go into shape analysis with measurements, landmark data and outlines. The participants are welcome to bring their own data and problems so that we may find R solutions.

Geometric morphometrics is important in the study of evolutionary biology because it provides a powerful and precise way to quantify and analyze shape variation among organisms. Unlike traditional morphometric methods, geometric morphometrics retains the spatial relationships among landmarks, allowing researchers to visualize shape changes and compare morphological differences in a statistically rigorous manner. This helps in understanding patterns of evolutionary change, adaptation, and developmental processes, as well as in reconstructing the evolutionary relationships between species based on their morphological traits.

Best wishes

Sole

Transmitting Science's upcoming courses: https://-www.transmittingscience.com/courses/ Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses Bluesky @soledeesteban.bsky.social X @SoleDeEsteban Orcid: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or http://transmittingscience.com/additional-terms. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es . Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction. Disclaimer of liability. - The sending of this communication does not imply any obligation on the part of the sender to control the absence of viruses, worms, Trojan horses and/or any other harmful computer program, and it corresponds to the recipient to have the necessary hardware and software tools to guarantee both the security of its information system and the detection and elimination of harmful computer programs. TRANSMITTING SCIENCE SL shall not be liable.

Links:

[1] http://www.amazon.com/Morphometrics-R-Use-Julien-Claude/dp/038777789X Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

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Online GeometricMorphometricsR Jul28-Aug5

Dear colleagues,

Registration is open for the Transmitting Science online course "Geometric Morphometrics in R". Geometric morphometrics has been shown to be a useful method to quantify shape changes in evolution.

Dates: Online live sessions on July 28th, 29th, 30th, 31st, and August 1st, 4th, 5th, 2025.

Daily schedule: from 12:00 to 17:00 (Madrid time zone).

Course webpage: https://-www.transmittingscience.com/courses/geometric-morphometrics/geometric-morphometrics-r/ Instructor: Dr. Julien Claude, author of the book "Morphometrics with R [1]" (Institut des Sciences de l'ï¿½volution de Montpellier, France).

Course Overview

Concepts in geometric morphometrics will be taught using a series of original data sets and working in R for solving a series of tasks. The course will start with an introduction to R and will rapidly go into shape analysis with measurements, landmark data and outlines. The participants are welcome to bring their own data and problems so that we may find R solutions.

More information and registration:

Best wishes

Sole

Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses Bluesky @soledeesteban.bsky.social X @SoleDeEsteban Orcid: https://orcid.org/0000-0002-2049-0890 Under the provisions of current regulations on the protection of personal data, Regulation (EU) 2016/679 of 27 April 2016 (GDPR), we inform you that personal data and email address, collected from the data subject will be used by TRANSMITTING SCIENCE SL to manage communications through email and properly manage the professional relationship with you. The data are obtained based on a contractual relationship or the legitimate interest of the Responsible, likewise the data will be kept as long as there is a mutual interest for it. The data will not be communicated to third parties, except for legal obligations. We inform you that you can request detailed information on the processing as well as exercise your rights of access, rectification, portability and deletion of your data and those of limitation and opposition to its treatment by contacting Calle Gardenia, 2 Urb. Can Claramunt de Piera CP: 08784 (Barcelona) or sending an email to info@transmittingscience.com or http://transmittingscience.com/additional-terms. If you consider that the processing does not comply with current legislation, you can complain with the supervisory authority at www. aepd.es . Confidentiality. - The content of this communication, as well as that of all the attached documentation, is confidential and is addressed to the addressee. If you are not the recipient, we request that you indicate this to us and do not communicate its contents to third parties, proceeding to its destruction.

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[1] http://www.amazon.com/Morphometrics-R-Use-Julien-Claude/dp/038777789X Soledad De Esteban-Trivigno <soledad.esteban@transmittingscience.com>

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Online InvasionGenomics Sep8-11

Dear all,

We are pleased to announce our upcoming online course:Invasion Genomics in R.

Dates:8th, 10th & 11th September

Course website: https://www.physalia-courses.org/courses-workshops/invasion-genomics/ This three-day course offers a practical introduction to invasion genomics.On Day One, participants will learn a variety of methods for understanding population diversity and differentiation. Day Two will include an introduction to various selection outlier scanning methods. Day Three will focus on the role of environmental variables in determining adaptive outcomes.

Each session includes a pre-recorded lecture (~1-2 hours) and a hands-on R-based tutorial (~3 hours), allowing for flexible participation. Instructors will be available for questions, discussion, and troubleshooting during the course.

For the full list of our courses and workshops, please visit: https://www.physalia-courses.org/courses-workshops/ Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org mobile: +49 17645230846 BlueskyLinkedin

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Online NanoporeGenomeAssembly Sep29-Oct2

Dear all,

Are you working with long-read sequencing data or planning to dive into genome assembly using Oxford Nanopore Technologies? Join us this 29 September-2 October 2025 for the Physalia online course: Assembling Genomes with Oxford Nanopore: A Hands-On Guide to Long-Read Sequencing

Course website: (https://www.physalia-courses.org/courses-workshops/course59/) This course will guide you step-by-step through the process of transforming raw Nanopore data into fully assembled, polished, and quality-checked genomes whether or not you have short-read data or a reference genome. With a mix of theory and hands-on practice, you’ll work with real datasets and apply state-of-the-art tools for basecalling, assembly, polishing, and QC.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/course59/)

Best regards, Carlo

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Onliner AnalysisCommunitiesWithTheVEGANpackage

Multivariate Analysis Of Ecological Communities Using R With The VEGAN package (VGNR08)

Course dates:15-19th September 2025 Location:Live and Online

Instructor:Dr.Antoine Becker-Scarpitta

This course is designed for ecologists and environmental scientists who want to apply multivariate techniques using R's vegan package. You'll gain hands-on experience with the tools used to interpret species-environment relationships and community composition. Taught by expert instructors, you'll learn to:

Understand the principles of multivariate analysis

Apply ordination methods (PCA, NMDS, CCA, RDA)

Work with dissimilarity matrices and ecological distance measures

Analyse species-environment relationships

Use vegan effectively for real-world datasets

Who should attend? Field ecologists, biodiversity researchers, and community ecologists who already have some R experience and want to apply robust multivariate methods to ecological data.

Why join us? Deepen your statistical toolkit, sharpen your interpretation of community data, and gain confidence in your analysis using vegan.

Spaces are limited - reserve your place now.

View full course details and register here Email oliverhooker@prstatitics.com with any questions

–

Oliver Hooker PhD.

PR stats

Oliver Hooker <oliverhooker@prstatistics.com>

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Online SexChromosomeEvolution Oct6-10

Dear all,

registration is open for the Physalia upcoming online course: Sex Chromosome Evolution

Dates: 6-10 October (11:00-16:00 Berlin time)

Course website: (https://www.physalia-courses.org/courses-workshops/sexchr/)

This course will introduce attendees to how genomic and transcriptomic data can be used to detect sex chromosomes and inform the cause and consequences of sex chromosome differentiation. We will guide attendees through study design, genomic/transcriptomic data collection methods, handling of raw genomic/transcriptomic data, and methods to identify sex chromosomes. Then, we will work through a suite of analyses looking at the molecular evolution of sex chromosomes, particularly the timing and patterns of recombination suppression, gene gain/loss, gene expression differentiation, and genome divergence. We will also provide background on different types of sex chromosomes and sex determination systems, and hands-on exercises, running analyses, and interpreting results.

After completing the course, the participants should be able to manipulate, visualize, and interpret genomic data and patterns of sex chromosome evolution.

For the full list of our courses and workshops, please visit: (https://www.physalia-courses.org/courses-workshops/sexchr/)

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 SingleCellTranscriptomics Jun24-26

The Computational Biology Core at the University of Connecticut is hosting virtual bioinformatics workshops this summer! We still have space available in our Single-Cell Transcriptomics Workshop (virtual but live instruction - June 24-26).

This hands-on workshop will guide participants through the full single-cell RNA-seq workflow from raw data to biological insight. You'll learn how to process and quality-check single-cell data, perform clustering and cell type identification, and integrate multiple samples using Jupyter notebooks with Python and R.

A self-guided introduction to Linux, HPC, and R will be provided two weeks before the workshop to ensure participants are ready to dive in.

Learn more & register here: https://bioinformatics.uconn.edu/cbc-workshops/ WHERE: Virtual (Zoom) WHEN: 10:00 AM - 2:00 PM EST COST: $400 (UConn affiliates) $500 (External participants)

Registration is first come, first served.

Questions? E-mail: cbcsupport@helpspotmail.com

"Lambert, Karelyn" <zsc25001@uconn.edu>

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Paris BlackCoralTaxonomy Oct6-17

Object: Free Taxonomic training workshop in Paris on black corals (Antipatharia) - October 6-17, 2025

Dear all,

The Museum of Paris (MNHN) is organizing a 2-weeks Training Course on the Taxonomy of black corals (Antipatharia) from October 6 to 17, 2025. Targeted audience are students, researchers, collection managers, and all professionals involved in the study of these organisms.

The goal of the workshop is to bring together professional taxonomists and students (in the broad sense) around samples recently collected during the Tropical Deep-Sea Benthos Program and deposited in the MNHN collections to transmit taxonomic knowledge while speeding up sorting, identification and digitization of natural collections.

During 10 days, we will sort specimens to the lowest taxonomic level possible and use best practices to taxa identification (macroscopic and microscopic observations, including SEM) and data collection management, preservation, and traceability. In addition, there will be courses on Antipatharia biology, phylogeny,evolutionary genetics, and deep-sea ecology. We will aslo propose to participants to present their work objectives related to Antipatharia.

The workshop will take place at the MNHN, rue Buffon in Paris: https://maps.app.goo.gl/wonYQfwN2fPY3N2c6 Registration is free but mandatory. For registration, send an email with a CV and a motivation letter (explaining the added value of this workshop to your objectives) to: didier.aurelle@mnhn.fr / magalie.castelin@mnhn.fr

Deadline: July 13

Thank you for relaying widely this information within your laboratories.

Maï¿½tre de Confï¿½rences ISYEB / AMU

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UPretoria ConservationGenetics Dec7-14

Population Genomics Data Analysis Course & Workshop

Themes: Conservation Genetics, Population Genomics, and Molecular Ecology. Understanding Population Structure and Environmental Influences on Genomic Variation - using Next Gen Sequencing Data & key computational approaches. Includes RADseq, genome sequencing & assembly, & SNP typing from raw reads to genotypes and many analyses to prepare you for future genomics data analyses. Also includes microsatellite data and concepts because many labs & countries still use microsat markers.

Instructors include experts: Eric Anderson, Ellie Armstrong, Jessica Da Silva, Marty Kardos, Brenna Forester, Paul Grobler, Will Hemstrom, Gordon Luikart, Monica Mwale, Rena Schweizer, Lisette Waits, Robin Waples, and more.

When: December 7 - 14, 2025. First (Overview) Lecture Sunday night the 7th, last lecture Saturday14th

Where: University of Pretoria, South Africa (https://www.up.ac.za/).

Details and registration: see https://www.umt.edu/congen/africa/ Course Objective: To teach conceptual and practical aspects of data analysis to understand the evolutionary and ecological genomics of natural and managed populations. Emphasis is on next-generation sequence data analysis (RADs, whole-genome sequence analyses) and interpretation of output from common and new statistical approaches, software, and bioinformatic pipelines. We teach how work from raw reads to produce quality genotypes and the crucial steps of filtering (Hemstrom et al. 2024). The course teaches the coalescent, Bayesian, and likelihood-based approaches. Special lectures and hands-on exercises are conducted on population structure, detecting selection, effective population size, landscape genomics, inbreeding detection (RoH), genome assembly, and more. Evening sessions allow hands-on analyses of your data with instructors.

Who should apply: Advanced Undergrads, M.S. & Ph.D. students, post-docs, PIs (agency biologists), and faculty who have understanding of population genetics & population ecology, R and Linux (see below).

Credit/certificate: Students can get 3 credits from The U of Montana, and a Certificate of course completion.

What you receive: 3 Lectures a day (video-recorded) by >10 expert instructors with question & answer sessions, copies of lecture PowerPoint slides, and hands-on exercise worksheets with dummy datasets. Training running RStudio and Linux that starts 4 weeks BEFORE the course; Tutorials are given 4 weeks before the course to help you learn Linux & R. Links to video recordings of past ConGen lectures. A field trip to amazing Kruger National Park is the 4 days after the course to learn wildlife and habitat ecology, and local research.

Publication: We will likely publish together a meeting review (e.g., below) to help advance the field and improve your ability to publish. Schweizer et al. 2021: doi.org/10.1093/jhered/esab019; Stahlke et al. 2020: doi.org/10.1093/jhered/esaa001; Hendricks et al. 2018: doi.org/10.1111/eva.12659

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UPretoria PopGeneticsDataAnalysis Dec7-14

Population Genomics Data Analysis Course & Workshop

Themes: Conservation Genetics, Population Genomics, and Molecular Ecology. Understanding Population Structure and Environmental Influences on Genomic Variation - using Next Gen Sequencing Data & key computational approaches. Includes RADseq, genome sequencing & assembly, & SNP typing from raw reads to genotypes and many analyses to prepare you for future genomics data analyses. Also includes microsatellite data and concepts because many labs & countries still use microsat markers.

Instructors include experts: Eric Anderson, Ellie Armstrong, Jessica Da Silva, Marty Kardos, Brenna Forester, Paul Grobler, Will Hemstrom, Gordon Luikart, Monica Mwale, Rena Schweizer, Lisette Waits, Robin Waples, and more.

When: December 7 - 14, 2025. First (Overview) Lecture Sunday night (7th), last lecture Saturday14th

Where: University of Pretoria, South Africa (https://www.up.ac.za/).

Details and registration: see https://www.umt.edu/congen/africa/ Course Objective: To teach conceptual and practical aspects of data analysis to understand the evolutionary and ecological genomics of natural and managed populations. Emphasis is on next-generation sequence data analysis (RADs, whole-genome sequence analyses) and interpretation of output from common and new statistical approaches, software, and bioinformatic pipelines. We teach how work from raw reads to produce quality genotypes and the crucial steps of filtering (Hemstrom et al. 2024). The course teaches the coalescent, Bayesian, and likelihood-based approaches. Special lectures and hands-on exercises are conducted on population structure, detecting selection, effective population size, landscape genomics, inbreeding detection (RoH), genome assembly, and more. Evening sessions allow hands-on analyses of your data with instructors.

Who should apply: Advanced Undergrads, M.S. & Ph.D.

students, post-docs, PIs (agency biologists), and faculty who have understanding of population genetics & population ecology, R and Linux (see below).

Credit/certificate: Students can get 3 credits from The U of Montana, and a Certificate of course completion.

What you receive: 3 Lectures a day (video-recorded) by >10 expert instructors with question & answer sessions, copies of lecture PowerPoint slides, and hands-on exercise worksheets with dummy datasets. Training running RStudio and Linux that starts 4 weeks BEFORE the course; Tutorials are given 4 weeks before the course to help you learn Linux & R. Links to video recordings of past ConGen lectures. A field trip to amazing Kruger National Park is the 4 days after the course to learn wildlife and habitat ecology, and local research.

Publication: We will likely publish together a meeting review (e.g., below) to help advance the field and improve your ability to publish.

Schweizer et al. 2021: doi.org/10.1093/jhered/esab019;

Stahlke et al. 2020: doi.org/10.1093/jhered/esaa001;

Hendricks et al. 2018: doi.org/10.1111/eva.12659

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UTromso Norway FieldCoursePlants Aug11-15

Dear Colleagues, We have some vacant places on ForBio/UiT field course: "Northern Biodiversity Hotspots, Flora of Skibotn and surroundings", 5 ECTS The course will run from 11-15 Aug 2025 at the Skibotn Field station of the University of Tromsï¿½, Storfjord, Troms, North Norway. This course will provide training in the identification of Boreal and Arctic groups of vascular plants. The teaching will take place in Skibotn area with a remarkably high species number for such northern latitudes (68-69 degrees N) challenging the general concept that species richness decreases as latitude increases. Daily excursions to both lowland and mountain habitats will be combined with practical work in the class to identify the collected materials using the identification keys and learn diagnostic characters of plant taxa. Please find more details about the course and a registration link at the ForBio reaserch school webpages: https://www.forbio.uio.no/-events/courses/2025/Skibotn_field_course2025.html The application deadline is 10 June 2025. Contact Galina Gusarova (galina.gusarova@uit.no) for more information

Best regards, Galina

Galina Gusarova Researcher & ForBio Coordinator The Arctic University Museum of Norway, UiT NO-9037 Tromsï¿½, Norway

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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.