
E v o l D i r

July 31, 2026

M o n t h i n R e v i e w

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 mail to evoldir@evoldir.net.

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

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Great Lakes Annual Meeting of Evolutionary Genomics (GLAM-EvoGen) 2026

Dear All,

The deadline for abstract submission for the 2026 Great Lakes Annual Meeting of Evolutionary Genomics (GLAM-EvoGen) is approaching: JULY 24. Please encourage your trainees to submit abstracts - it is an awesome event: small, friendly, but very high level.

GLAM will take place on Saturday, August 15, 2026 at the University at Buffalo, Center for the Arts. More information is available on our website: <https://go.kcumenlab.org/glam2026/> Registration and abstract submission are free: <https://forms.gle/84MRmLtMJgbTpY6DA> Again, the abstract submission deadline is July 24; registration will remain open until August 10. The participation is capped at 100 people.

As always, all presenters are trainees, and we warmly encourage you to support your students and postdocs in attending and presenting. Presentations include posters, flash talks, and 12-minute talks.

Please also circulate this announcement broadly within your departments and social media. A flyer is attached.

We look forward to hosting you all in Buffalo!

Cheers, Omer and Luane – Charikleia (Clio) Karageorgiou, Ph.D. Postdoctoral Researcher Buffalo Evolutionary and Anthropological Genomics Lab (BEAGL) Department of Biological Sciences University at Buffalo,

SUNY

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KrakowPoland The Code of Life Beyond the Genome to Multilayer Biology 14-16October2026

We would like to invite applications and abstract submissions for the FEBS-IUBMB-ENABLE conference

The Code of Life: Beyond the Genome to Multilayer Biology,

which will take place in Krakow, Poland, on 14-16 October 2026.

We think this meeting will be of interest to evolutionary biologists because the field is especially aware of how we need to think beyond the idea of a single "genome" toward questions that integrate variation across many genomes with regulation, epigenetics, development, cell states, and phenotype.

The keynote program includes speakers whose work spans multiple biological scales relevant to evolutionary thinking: Mzia Kutateladze (bacteriophages, antimicrobial resistance, host-pathogen systems), Tanja Cirkovic Velickovic (proteomics, food biochemistry, environmental effects on molecular phenotype), Krzysztof Szade (stem-cell heterogeneity and epigenetic memory), Syed Haider (computational analysis of bulk and single-cell multi-modal datasets), Aleksandra Kolodziejczyk

(single-cell genomics, microbiota-host interactions), Daniela Ungureanu (single-cell approaches to signaling and drug response), Alexandre Bonvin (computational structural biology and biomolecular interactions), and Guido Sanguinetti (splicing dynamics, RNA biology, Bayesian and machine-learning methods).

We particularly welcome early-career researchers in population genetics, evolutionary genomics, regulatory evolution, epigenetics, evo-devo, host-microbe interactions, genotype-to-phenotype mapping, and single-cell or spatial approaches with evolutionary relevance. More information and registration can be found here: <https://febs-iubmb-enableconference.org/> Kind regards,

On behalf of the Conference Local Organizing Committee Agata Kalita, PhD Laboratory of Bioinformatics and Genome Biology, Faculty of Biochemistry, Biophysics and Biotechnology Jagiellonian University

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New York American Society of Naturalists Jan 8 12 2027

The American Society of Naturalists will hold its biennial stand-alone meeting from January 8-12, 2027 at The Mansion at Glen Cove on Long Island, New York.

For the last several iterations, this meeting has been held in Pacific Grove, CA and has been referred to as the Asilomar Meeting. We're shifting to the east coast this time to make the meeting easier for the other side of the country. Registration will remain open until the meeting reaches capacity: amnat2027.org

This is a small meeting, limited to 200 attendees, that allows many opportunities for networking, collaboration, and discussion of science, including meals and evening activities. Research presented at the meeting typically includes a broad range of topics in ecology, evolution, and behavior. The meeting kicks off at dinner on Friday evening (Jan 8) and concludes with breakfast on Tuesday morning (Jan 12). Half of each day is devoted to selected symposia with the other half devoted to contributed talks. Evening activities include a poster session, a presidential debate, and many opportunities for conversations. This year's symposia are focused on three topics: (1) Coevolutionary processes in the Geologic Era: Integrating mechanisms & ecological inter-

actions (2) What we lose when we limit participation in science (3) The Synthetic Naturalist: ecological and evolutionary theory in an age of engineered organisms

The registration cost for the meeting is all-inclusive and includes lodging, meals, and conference costs. You might experience some sticker shock at the price, but remember that this includes everything except for travel, so it's actually comparable to other conferences. Travel grants are also available for students, see the website for details. In order to register, you'll need to also submit your title and abstract if you plan to present a talk or poster. Abstracts will be used to group talks into sessions but will not be published. If you plan to share a double room, you and your roommate will need to submit each other's names during registration.

If you have any questions, please feel free to email one of the organizers: Kate Eisen (katherine.eisen@lmu.edu) Lily Khadempour (lily.khadempour@rutgers.edu) Casey terHorst (casey.terhorst@csun.edu)

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Online Animal Behaviour Live 2026 Nov 12

Dear Colleagues,

We are delighted to announce that the seventh Animal Behaviour Live annual online conference will take place on 12 November 2026! This one-day conference is themed around 'Studying Animal Behaviour in a Changing World'. The theme encompasses a range of topics, including behavioural responses to anthropogenic change, the development of more ethical and less intrusive research methods, and the use of emerging technologies (including AI) in animal behaviour research.

This FREE, fully online event provides an accessible platform for animal behaviour researchers worldwide to connect, share their work, and contribute to a more inclusive and sustainable research community.

Register here to attend: <https://ablaoc.sciencesconf.org/>

Submit your abstract (deadline: 6 September 2026): <https://ablaoc.sciencesconf.org/>

The conference is organised by a small team of early-career researchers on a voluntary basis. Its success re-

lies on the enthusiasm and support of the community – you! If you know colleagues or collaborators who may be interested, please help us spread the word.

You can:

- Forward this email
- Share our conference flyer: https://drive.google.com/drive/folders/1AQDEBXEKbz6SmZASCS8fxK13u-vrXI_Y?usp=drive_link - Follow and share our updates on social media: <https://linktr.ee/animalbehaviourlive> Thank you for your support – we hope to see you at Animal Behaviour Live 2026!

Kind regards, The Animal Behaviour Live Organising Committee

Share this message and flyer with your research network

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Online ESEB PolyAdaptSTN July30

You are cordially invited to attend the upcoming ONLINE seminar of the Special Topic Network Polygenic Adaptation (STN-PolyAdapt) funded by the European Society for Evolutionary Biology which will take place on 30th July, 2026, 4 pm CET.

Our speaker for this seminar is Dr. Samuel Yeaman from University of Calgary, Canada.

Title: What can we learn by studying the repeatability of adaptation?

Abstract: Genotypic redundancy is a basic parameter of fundamental importance in evolutionary biology, yet we know very little about its magnitude. If the mapping from genotype to phenotype to fitness involves considerable redundancy, then there are many different ways that species can adapt to a given environment, and evolution is highly flexible. On the other hand, if this mapping involves minimal redundancy, evolution is highly constrained as only certain genes can contribute to adaptation. We may naively expect that traits that integrate across many developmental or molecular pathway or tissue types may involve more redundancy, but we have very limited understanding of this parameter in nature. Studying the repeatability of adaptation provides an indirect way to quantify redundancy, as high repeatability should only happen when redundancy is

minimal (and vice versa). This presentation will explore we can study and interpret observations about the repeatability of adaptation, starting with a brief review of theoretical models of adaptation and some recent results. I will then discuss projects studying the genomic basis of local and global adaptation to climate in plants, which show some significant signals of repeated adaptation, but also imply considerable flexibility. Interestingly, genes that contribute to local vs. global adaptation tend to have different characteristics, consistent with theoretical predictions. Much remains to be learned about the genetic basis of adaptation before we can understand the extent to which evolution is flexible vs. constrained, but data is rapidly accumulating that will help answer this question.

Meeting details: Date: July 30, 2026 Time: 4 PM CET
Zoom link to join the seminar: <https://eu02web.zoom-x.de/j/63438967177?pwd=uA12uZ01cEc3BcdXdgd3aNaHsBLgaj.1> Meeting ID: 634 3896 7177 Passcode: 762007

If you would like to get on our mailing list and take part in our upcoming events, please visit our website (<https://polygenic-adaptation-network.org/>) for more information.

Sincerely, Neda Barghi on behalf of the Special Topic Network Polygenic Adaptation (STN-PolyAdapt) organizing committee

ESEB-funded Special Topic Network " Polygenic Adaptation" <https://polygenic-adaptation-network.org/https://eseb.org/prizes-funding/special-topic-networks/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

SEPEEG2026-Auburn University Oct23-25 Registration Now Open

Please join us for the 53rd annual Southeastern Population Ecology and Evolutionary Genetics (SEPEEG) meeting, hosted by Auburn University at the Alabama 4-H Center in Columbiana, Alabama (<https://alabama4hcenter.org/>). First organized in 1973 as SEEAG (the Southeastern Ecological Genetics Group), SEPEEG is a single-session meeting that brings together students, postdocs, and faculty from across the Southeast for formal and informal discussion of research on ecology, population biology, evolution, and genetics.

Venue: Alabama 4-H Center, Columbiana, AL
 Dates: October 23-25, 2026 Cost: 225 for standard dormhousing (includes meals)
 Website: SEPEEG2026website

Registration is now open via the Auburn University TouchNet portal (link on website). There are also a limited number of on-site hotel accommodations, but they may fill quickly – we encourage early registration if a hotel room is a priority.

Talk and poster abstract submission deadline: August 1, 2026. The submission form is linked on the conference website. This deadline may be extended until we reach capacity.

Student travel awards are in development; trainees should indicate their interest in travel awards when registering for a research presentation. We will contact registered participants individually to let them know if they have been selected! Priority will be given to trainees who register early and who plan to present their research at the conference.

Registration deadline: September 1, 2026.

Please forward this message to potentially interested colleagues, students, and lab groups. Questions can be directed to the Laurie Stevison (lss0021@auburn.edu).

See y'all in Alabama!

Best, Laurie and the SEPEEG '26 Team

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bringing together theoreticians and empiricists working on diverse organisms”

Keynote Speaker Rasmus Nielsen, U California, Berkeley
 Invited Speakers Rachael Bay, UC Davis
 Graham Coop, UC Davis
 Jeff Good, University of Montana
 Thomas Juenger, University of Texas
 Joanna Kelley, UC Santa Cruz
 John Kelly, University of Kansas
 Sarah Kocher, UC Berkeley
 Julia Kreiner, University of Chicago
 Katie Lotterhos, Northeastern University
 Bret Payseur, University of Wisconsin
 Dmitri Petrov, Stanford University
 Paul Schmidt, University of Pennsylvania
 Molly Schumer, Stanford University
 Guy Sella, Columbia University
 Jenny Tung, Max Planck Institute Leipzig
 Trisha Wittkopp, University of Michigan
 Samuel Yeaman, University of Calgary
 Jianzhi Zhang, University of Michigan
 AGA Symposia are small, friendly meetings that provide excellent opportunities for relaxed interaction with speakers and attendees. All attendees must be AGA members - join us now! <https://www.theaga.org/members>
 The event runs from mid-day October 4th to the evening of October 6th. Checkout is on the 7th. All events take place at Granlibakken Lodge in Tahoe City, California. Bookings are made through Granlibakken, click the link for details - <https://www.theaga.org/agatwentytwentysix>
 Your reservation through Granlibakken includes all room, board, conference fees, and registration fees (400 individual/200 student) to the event. Please contact theaga@theaga.org with questions.

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TahoeCity CA AGA2026 Oct4-7 Presidential Symposium–Polygenic Adaptation in a Changing World

Conference: Tahoe City, California AGA2026 Presidential Symposium – Polygenic Adaptation in a Changing World October 4-7 2026

The American Genetic Association is happy to announce our 2026 Symposium: "Polygenic Adaptation in a Changing World" hosted by AGA President Michael Nachman. "We now have good examples of the genetic basis of adaptation for many simple traits. However, most evolutionary change involves complex traits, and our understanding of their evolution remains rudimentary. This symposium will promote a broad, synthetic discussion of adaptive evolution for complex traits,

ZJU Hangzhou China 5th Young Talent Symposium EvolBiol

The 5th Young Talent's Symposium of Evolutionary Biology Date: September 29, 2026 Location: Zhejiang University, Hangzhou, China Host: Center for Evolutionary & Organismal Biology

About the Forum Dedicated to supporting early-career scholars, this forum offers a premier platform to foster academic exchange, connect with peers, and explore career advancement in evolutionary biology. Since 2022, we have welcomed scholars from across the globe (including China, the US, UK, Germany, and France) to discuss cutting-edge topics ranging from molecules to ecosystems—including phylogenetics, computational biology, comparative genomics, ancient DNA, and more.

Remarkably, many of our past participants have successfully secured faculty positions at institutions across China following the forum.

Call for Speakers We invite postdoctoral researchers and senior PhD candidates worldwide working at the frontiers of evolutionary biology to share their research works. Candidates who are interested at working in China in future are preferred, and selected candidates will receive support for travel and accommodation. - **Format:** 30-minute presentation followed by a Q&A discussion. - **Audience:** Peers and distinguished senior professors/experts from across China.

How to Register We warmly encourage all scholars passionate about evolutionary biology to join us! - **Option 1:** Visit the link (<https://forms.gle/qrpgr7K6J3MTccqP7>) to apply. - **Option 2:** Send your CV or questions directly to evolution@zju.edu.cn. (We will contact you shortly with further details.)

Review Panel Members: Luonan Chen (Shanghai Jiao Tong University) Xionglei He (Sun Yat-sen University) Jianquan Liu (Lanzhou University) Bing Su (Kunming Institute of Zoology)

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Bialowieza Poland MRI PAS PhDposition

PhD position at the Mammal Research Institute Polish Academy of Sciences in Bialowieza within the project funded by National Science Centre in Poland

We are looking for a motivated PhD candidate to work in a project „Changes in the range, genetic diversity and habitats of occurrence of two roe deer species in Europe from the last glaciation to modern times”.

Project description

The goal of our project is to study the history and changing distribution of two roe deer species – European roe deer (*Capreolus capreolus*) and Siberian roe deer (*C. pygargus*) – in Europe over the last 50,000 years. We aim to determine when these species started interbreeding, how their ranges shifted over time, and how they responded to climate change and human-induced landscape modifications. These two species differ in morphology, behaviour, genetics, and habitat preferences, which makes them an interesting subject for studying their ecological and evolutionary history. Our main research question focuses on how the ranges of these two species shifted in response to climate changes, particularly during the last glacial period and after it. We hypothesise that both *C. capreolus* and *C. pygargus*

experienced dynamic range shifts, adapting to climatic changes and landscape transformations, such as the expansion of agricultural land. Furthermore, our research aims to determine when the ranges of these two species overlapped and how extensively interbreeding occurred, especially before and after the Last Glacial Maximum. Although the European roe deer is a common species in Europe, its ecological and demographic history is still largely unknown. Furthermore, historical data on the distribution changes of roe deer over thousands of years are difficult to establish, as distinguishing between the two species based solely on morphological features has often been challenging. In our study we will use modern genetic methods to more accurately assign subfossil remains to the one of species and to detect their potential hybrids. These techniques will allow us to better track changes in the distribution of these animals and investigate how environmental changes, such as climate warming during the Holocene or the development of agriculture, influenced their ranges.

Methods

Our project brings together expertise from various fields, including genetics, palaeontology, and biogeography. We will analyse genetic material from both contemporary and subfossil roe deer samples using advanced DNA sequencing methods. Additionally, by analysing carbon and nitrogen isotopes in bones, we will assess ecological differences between the two species and their feeding habitats. Radiocarbon dating will also be used to determine the chronological and geographical shifts in their distribution.

Working environment

The Mammal Research Institute of the Polish Academy of Sciences (MRI PAS) founded in 1952, conducts research in the field of ecology, ethology, morphology, population genetics as well as population management and conservation of mammals and other terrestrial vertebrates. The mission of the Institute is to acquire, advance, and disseminate knowledge of natural patterns and processes in order to improve the scientific basis for effective nature conservation activities and sustainable development. We focus mainly on Bialowieza Primeval Forest (UNESCO Biosphere Reserve and World Heritage Site) as a study area, but also on other regions of Poland and Europe. The Institute employs ca. 60 people, including researchers, PhD students, and qualified technical and office staff. The institute is based in the village of Bialowieza in the middle of Bialowieza Forest, Poland. This is a remote place (ca. 1500 inhabitants) close to the Polish- Belarus border, ca. 20 km from the nearest city. This project is conducted in the Biogeography Group at the MRI PAS as part of a consortium

with dr habil. Mateusz Baca from the Centre of New Technologies at the University of Warsaw, and dr habil. Maciej Krajcarz of the Institute of Geological Sciences, Polish Academy of Sciences, Warsaw, and in collaboration with zooarchaeology and palaeontology specialists from Poland and other European countries.

We provide

- Work in a friendly research team with support and supervision of competent colleagues;
- Possibility to work and live in a nice place: a village (i.e., Bialowieza) located in the middle of Bialowieza Primeval Forest - one of the most important biodiversity hotspot in Europe;
- The possibility of effective scientific development through cooperation with the best world research institutes;
- Participation in an interesting scientific project with travelling opportunities;
- Possibility to attend courses, workshops and conferences organized by MRI PAS and BioPlanet doctoral school.
- The possibility to apply for inexpensive accommodation in MRI PAS flats.

PhD student tasks and duties within the project

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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>

BielefeldU TheoreticalEcologyEvolution

Dear evoldir community,

The Theoretical Biology group in Bielefeld is looking for a new PhD student! We build mathematical models and computer simulations to study questions at the interface between ecology and evolution. We are particularly interested in the biology of small populations and the causes and consequences of diversity, especially of intraspecific genetic and phenotypic diversity.

The exact research topic for the PhD position is still flexible. Potential topic include: - consequences of individual differences within a species for population dynamics, e.g., establishment of species in new locations, extinction processes and survival - consequences of individual differences for eco-evolutionary dynamics of interacting species in a changing environment - models for evolution of genetic and phenotypic variance - effects of

fluctuating selection on genome-wide genetic diversity
See https://jobs.uni-bielefeld.de/job/view/5077/research-position-phd-candidate?page_lang=en for details and how to apply.

The application deadline is August 14.

If you have questions, please get in touch!

Best wishes, Meike Wittmann

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Germany BayreuthU ManagingMicrobesWithCare

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

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

*** The Challenge *** Animals continuously interact with a vast diversity of harmful and beneficial microbes, and natural selection has favored sophisticated strategies for managing these interactions. However, we still know little about how social behaviors contribute to microbial management. Burying beetles provide an ideal system for addressing this question because they exhibit elaborate parental care and intimately interact with both beneficial symbionts and harmful environmental microbes during family life. In this project, we will examine how parental care (i) influences the effects of symbiotic and environmental microbes on beetle fitness, (ii) shapes interactions among key microbial taxa, and (iii) enables beetles to control complex microbial communities while transforming carrion into an edible nursery for their offspring. The project will integrate standard microbiological approaches with experimental manipulations of host-associated microbial communities and gnotobiotic insect experiments.

*** Your Profile **** We are looking for a highly motivated candidate with: - A Master's degree (or equivalent) in microbiology, evolutionary ecology, microbiome

science, or a related field. - A strong interest in animal-microbe interactions and social evolution. - Prior experience with microbiology and insect experiments (desired but not required). - Proficiency in biostatistics (R) or a strong motivation to develop quantitative and bioinformatic skills. - The ability to work both independently and collaboratively in a team. - Good written and spoken English skills.

*** What We Offer *** - A fully funded 3-year PhD position within an ERC-funded project. Remuneration is based on the German TV-L E13 pay scale (65- A cutting-edge interdisciplinary research ecosystem at the University of Bayreuth, which has recently been ranked in the top 5 percent of young universities worldwide. - A vibrant, supportive, and collaborative research environment in a newly established team, hosted at a department with extensive experience in insect rearing, behavioral experiments, and molecular analyses. - Access to state-of-the-art facilities and equipment for behavioral and microbiological research. - Funding for conference participation and professional training as well as opportunities for national and international collaboration. - Living in Bayreuth, a small but bustling university town with a rich history nestled in scenic Upper Franconia, featuring numerous opportunities for outdoor activities and cultural exploration.

*** How to Apply *** Applications should include: - A cover letter (1-2 pages) describing your research interests, motivation, and relevant work experience. - A detailed CV, including your methodological skillset, B.Sc. and M.Sc. grades, and publications (if any). - A summary of your Master's thesis (max. 500 words). - Names and email addresses of 2-3 academic referees who can provide references upon request.

Please submit your application by August 17th, 2026 as a single PDF to jos.kramer@uni-bayreuth.de with the subject: "PhD Application - Parental Care & Microbes". The anticipated starting date is February 2027.

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

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

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QM London Aigenomics

Domain adaptation to map gene expression across species in economically important crop pests

Start date: By 30th September 2026 Application deadline: 30th July 2026 Open to applicants with home fee status only [British or settled EU nationals]

Apply here <https://www.qmul.ac.uk/deri/ukriaidd-doctoral-training-programme/projects/>
Background

We are looking for an enthusiastic data scientist, with a passion for biological research, to pursue a 4-year fully funded PhD studentship aimed at developing deep learning models for transcriptomic data in crop pests. Specifically, you will develop, apply and evaluate foundation models and domain adaptation techniques to predict the expression profiles of targeted pests across life stages and cell types. This PhD offers a unique opportunity to develop a research career in applied AI, among like-minded people with expertise in genomics, deep learning and bioinformatics.

This entirely computer-based project will be based in Dr Matteo Fumagalli's lab within the Centre for Evolutionary and Functional Genomics at Queen Mary University of London (QMUL), with extensive support from the Digital Environment Research Institute at QMUL and Syngenta UK. The project will build on the Fumagalli lab's prior work on machine learning in genomics, and leverage Syngenta's world leading expertise in the molecular biology of fungal pathogens. Data for the project is already available in the public domain, and in proprietary Syngenta datasets.

Eligibility

We are seeking a highly motivated individual with a proven track record of success in both data science and biology, preferably in genomics. The ideal candidate will have a solid understanding of molecular biology, a high-grade MSc/MRes degree in a subject such as bioinformatics, data science or applied AI, and some data-driven research experience (e.g. a relevant MSc research project).

Applicants must be available to start their PhD by 30th September 2026.

Due to funding terms and availability, this project is open to applicants eligible for home fee status only.

Supervisors

Dr Matteo Fumagalli - Senior Lecturer & Head of Department, QMUL
Dr Oscar Charles - Computational Biologist, Syngenta
Dr Chris O'Grady - Computational Biologist, Syngenta

Informal Queries

For more details of the project, or to discuss your eligibility, feel free to contact Dr Matteo Fumagalli (m.fumagalli@qmul.ac.uk).

About QMUL/DERI

At Queen Mary University of London, we believe that a diversity of ideas helps us achieve the previously unthinkable. Throughout our history, we've fostered social justice and improved lives through academic excellence. And we continue to live and breathe this spirit today, not because it's simply 'the right thing to do' but for what it helps us achieve and the intellectual brilliance it delivers. We continue to embrace diversity of thought and opinion in everything we do, in the belief that when views collide, disciplines interact, and perspectives intersect, truly original thought takes form.

The Digital Environment Research Institute (DERI) is Queen Mary's flagship University Research Institute dedicated to ground-breaking multi-disciplinary research in digital and data science, including artificial intelligence (AI). DERI offers an outstanding research environment including a dedicated physical space along with recently purchased high performance computing infrastructure to enable scientific breakthroughs. Further, DERI leads the University's participation in The Alan Turing Institute, the UK national institute for data science and AI.

About Syngenta

Syngenta Crop Protection is a leader in agricultural innovation, bringing breakthrough technologies and solutions that enable farmers to grow productively and sustainably. We offer a leading portfolio of crop protection solutions for plant and soil health, as well as digital solutions that transform the decision-making capabilities of farmers.

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TrinityCollege Dublin MSc Stability of European freshwater fish communities under multiple environmental changes

TrinityCollege Dublin MSc Stability of European freshwater fish communities under multiple environmental changes Category: Jobs Content:

MSc by Research studentship available on: "Stability of European freshwater fish communities under multiple environmental changes"

We are seeking a highly motivated candidate for a fully funded 2-year MSc by Research project. The student will be supervised by Dr. Conor Waldock and Prof. Ian Donohue at the School of Natural Sciences. This studentship is funded via the School of Natural Sciences MSc to PhD Pathway fund. It is expected that the student will be open to and seeking to find a route or pathway to complete a PhD.

Funds are only available to cover EU citizens.

We are dedicated to foster a diverse and inclusive research environment and strongly encourage applicants from all backgrounds to apply.

Project Background and Description

Global environmental change is increasingly uncertain and unpredictable, with multiple changes acting at once. The response of biodiversity to novel mixtures of anthropogenic impacts remains an urgent knowledge gap. Freshwater ecosystems harbour imperilled fish fauna facing a combination of climate change, pollution, invasive species, physical modification and habitat fragmentation. This project will use fish biodiversity as a model system to explore how natural ecosystems vary in their inherent capacity to remain stable and productive under unpredictable multi-dimensional environmental change.

Ecological communities are made up of sets of species that often have different responses to environmental change because they have evolved specialisations into ecological niches. Quantifying species' different responses gives a community's "response diversity", a property expected to predict the stability of a community under environmental change.

This project will investigate spatial patterns, drivers,

and consequences of response diversity of European fish. It will combine a large-scale pattern-based macroecological investigation with empirical tests of ecological stability theory. The overarching question is: how does response diversity contribute to stability of natural freshwater ecosystems under multiple environmental changes?

The core aims of the project are: 1. Investigate spatial patterns and environmental drivers of response diversity in fish communities across Europe. 2. Examine the empirical relationships between response diversity and stability of community biomass and species' composition.

Candidate Profile The candidate must meet the Trinity postgraduate entry requirements and be eligible for EU student fees (<https://www.tcd.ie/study/apply/admission-requirements/postgraduate/>) and hold at least an upper second class (2.1) Honours Bachelor degree, preferably in Biology, Ecology or Environmental Science or another related discipline.

We hope the candidate will fulfil the below requirements: - Be actively interested in global environmental change and its impact on biological diversity. - Have demonstrated ability to handle and analyse data in R. - Have keen interest in developing skills in advanced data processing and statistical analysis pipelines in R. - Be keen to develop knowledge on freshwater ecology and obtain field experience beyond the theoretical concepts of the MSc. - Have the ability to develop hypothesis-driven questions to advance global biodiversity change modelling. - Contribute positively to team dynamics and atmosphere and have capacity to work well independently.

Funding This is a 2-year MSc by Research project funded by the School of Natural Sciences and covers an annual tax-free stipend of EUR25,000, and EU student fees.

As part of the award, it is expected that the candidate and PI will identify and apply to other funding mechanisms as to meet the terms of the MSc to PhD Pathway fund.

Application procedure Please send a CV and a 1-page personal statement, and any enquiries, to Dr. Conor Waldock (waldockc@tcd.ie) by 24th July.

Your CV should include the name and contact details of two references.

In your personal statement, please explain: - Why you are interested to undertake an MSc. - Why you are interested in this MSc project specifically. - How you fit some of the elements in the above candidate profile.

Interviews will take place (online) in early August with a Project start date September 2026 or March 2027.

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ULaTrobe Australia Evolutionary Ecology of Stingless Bees

PhD Opportunity – Evolutionary Biology / Ecology of Stingless Bees La Trobe University (Melbourne, Australia)

We are seeking an enthusiastic PhD candidate to join a collaborative research project investigating the mechanisms that determine species' geographic range limits. The position will be based at La Trobe University and co-supervised by Dr Vanessa Kellermann (La Trobe University) and Dr Ros Gloag (University of Sydney), with collaboration across a multidisciplinary research team.

Project overview

Understanding which mechanisms shape insect distributions is central to predicting biodiversity responses to climate change, managing pollinators and pests, and safeguarding ecosystem resilience. This project will use native Australian stingless bees (*Tetragonula* spp.) as a tractable field system to test competing predictions about range limits, with a focus on adaptive constraints on cold tolerance. The work will combine field ecology, experimental transplants, thermal physiology, and quantitative/genomic to test range limit theories. The project will generate new insights into species' responses to environmental gradients and contribute knowledge relevant to Australia's pollination systems and emerging stingless-bee industries.

Candidates

Applicants should have: - A background in evolutionary biology, ecology, or a related discipline - Strong motivation for field- and lab-based research - A valid driver's licence (required for fieldwork) - Ability to commence mid-year (2026) - Eligibility to enrol in a PhD program at La Trobe University Experience with one or more of the following in quantitative genetics, entomology, physiology, or genomics is desirable but not essential.

What we offer

- Training across evolutionary ecology, physiology, and genomics - Fieldwork in unique Australian systems -

A collaborative supervisory team spanning institutions - Melbourne is consistently ranked among the world's most liveable cities, known for its multicultural vibe, cafe culture, and vibrant arts and sports scene - La Trobe University is a well-regarded research university with a strong reputation in offering a spacious main campus in Bundoora.

How to apply?

Students are encouraged to reach out with questions before applying to v.kellermann@latrobe.edu.au and ros.gloag@sydney.edu.au.

Applicants should send a copy of their CV, academic transcript and a brief cover letter outlining their interests and motivations for applying

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UMississippi Evolution Phylogeography Biodiversity

The Garrick Lab in the Department of Biology at the University of Mississippi is recruiting M.S. and Ph.D. students interested in evolutionary biology, phylogeography, and biodiversity science.

Research in the lab focuses on understanding processes that shaped patterns of genetic diversity, endemism, and species distributions in the Southern Appalachian Mountains and the Interior Highlands (Ozark and Ouachita Mountains). Prospective students can develop projects centered on one or more of the following themes:

- Comparative phylogeographic testing of abiotic and biotic influences on responses to past environmental change;
- Hotspot / endemism mapping and prediction of centers of diversity, stability, and in situ persistence;
- Methods development for lineage fusion inference, using simulation-based approaches to detect persistent geogenetic signatures of past fusion events in contemporary populations.

Our research integrates field sampling, molecular genetics and genomics, spatial analyses, and computational modeling to address broad questions in evolution, biogeography, and conservation. Current study systems focus primarily on deadwood-associated (saproxylic) forest arthropods, although students with compatible interests in other taxa are encouraged to inquire.

Prospective applicants are encouraged to contact Ryan Garrick (rgarrick[at]olemiss.edu) to discuss potential research projects and funding opportunities.

Information about the University of Mississippi Biology graduate program and application procedures is available at: https://olemiss.edu/biology/graduate_programs For students intending to begin Fall 2027, applications are due January 15, 2027.

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UNCG mammal trait-based response

The McLean Lab (<https://sites.google.com/view/mclean-lab/lab>) at the University of North Carolina Greensboro (<https://biology.uncg.edu/>) is recruiting a PhD level student to investigate phenotypic and life history responses of western North American mammals to environmental change. Our lab combines museum specimens, digitized trait datasets, genomic data, and targeted field resurveys to understand how energetically important traits (e.g., body size, morphology, and reproduction) vary across landscapes and through time. We value applications from prospective lab members interested in mammalogy, specimen-based research, biodiversity informatics, and quantitative biology. Prior experience in mammal-related fieldwork, 2D/3D morphometrics, and/or linear modeling experience in R is strongly preferred.

Research in the lab bridges mammalian evolution and ecology and relies on an integrative toolkit including fieldwork and specimen collection, biodiversity informatics, machine learning, phylogenomics and landscape genomics, and trait evolution. Accepted students will lead projects leveraging data from hundreds of thousands of newly digitized specimen-level traits, the NEON Biorepository, and the lab's recent work in sky islands of the Great Basin to pinpoint phenotypic and life history responses to environmental change across space and time.

To inquire about positions, please email Bryan McLean (b_mclean@uncg.edu) and describe: 1) the broad research questions you are passionate about in ecology and evolution, 2) how these fit with previous research in the McLean Lab, and 3) an updated CV containing a summary of your academic and research experiences,

Students accepted into the UNCG Biology PhD program will compete for a tuition waiver and competitive graduate assistantship stipend. Additional competitive fellowships are available through separate applications.

For more information about the UNCG Graduate Program in Biology, please visit: <https://biology.uncg.edu/graduate/> For more information about the high quality of life and low cost of living in Greensboro, please visit: <https://www.greensboro-nc.gov/> <https://realestate.usnews.com/places/north-carolina/greensboro> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UniFreiburg Germany EvolutionaryTheory

We are seeking a doctoral student to join the group of Jonathan Henshaw at the University of Freiburg in Germany (<https://www.henshaw-lab.com/>). We are a primarily theoretical lab working on a broad set of topics in evolutionary biology, with a particular focus on the evolution of animal behaviour. We develop both individual-based simulations and mathematical models (e.g. using evolutionary game theory, adaptive dynamics and quantitative genetics). We put a strong emphasis on a supportive and inclusive working environment. As a doctoral student in our lab, you would have considerable freedom to shape the direction of your projects within these broad areas of interest.

****Duration, start date, salary****

The initial contract is for 3 years but with the possibility of extension. The start date is flexible. Salary is at the TV-L E13 65

****Role****

As a doctoral student, you will develop simulations or mathematical models to understand the evolution of animal behaviour, with the precise research questions to be decided on in collaboration with Jonathan. You will publish your work in peer-reviewed journals and present it at international conferences. This position comes with a teaching requirement of 2.5 face-to-face hours per week during the semester.

****Requirements****

Applicants must have: - A Master's degree in biology, mathematics, or another relevant discipline - Experi-

ence programming (e.g., in R, Python, Julia or Mathematica) and/or constructing mathematical models - Proficient spoken and written English

Previous publications in peer-reviewed journals will be seen favourably, but are not required.

****How to apply****

Applicants should send an email to Jonathan Henshaw (jonathan.henshaw@biologie.uni-freiburg.de) with the following: - Brief cover letter (max. 1 page) outlining your reasons for wanting to join the lab, your educational background and relevant skills, and (optionally) which topics you would most like to work on - CV (max. 2 pages) - Transcripts of Master's and Bachelor's degrees - Contact details for two referees (it is not necessary to send reference letters)

The deadline for applications is 7 September 2026.

We are committed to building an inclusive workplace and welcome applications from people of all backgrounds, regardless of gender, sexual orientation, race, ethnicity, national origin, religion or belief, disability, age, or family status.

Please feel free to contact me if you have questions about the position or the application process. I look forward to hearing from you.

Jonathan Henshaw

Professor of Theoretical Biology Faculty of Biology University of Freiburg Hauptstrasse 1 79104 Freiburg i. Br. Germany

Email: jonathan.henshaw@biologie.uni-freiburg.de Phone: + 49 761 203 2567

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UNorthCarolina PhD and MSposition SensoryEcology

MS and PhD Positions in Sensory Ecology

There are two open graduate student positions in the Schweikert Lab at the Department of Biology and Marine Biology at the University of North Carolina Wilmington (UNCW). Applicants with experience in neurophysiological or behavioral approaches are preferred, though not required. 1. MSc in Marine Biology: Behavioral Ecology of Dynamic Color Change in Reef Fishes

(starting Spring or Summer 2027)

2. PhD in Integrative, Comparative, and Marine Biology: Neuroethology of Adaptive Camouflage in Flatfishes (starting Fall 2027) Prior to applying to the UNCW graduate program, interested students should email Dr. Lorian Schweikert (schweikertl@uncw.edu) with the following: . Statement of career goals and research interests (1 page max) . Resume or CV . Unofficial transcripts . Contact information for three references

Interviews for both positions will begin in early fall, though interest emails will be accepted until the positions are filled. The UNCW application deadline for the MSc position is October 15th, 2026 and for the PhD position is February 15th, 2027.

Program Synopsis: Dynamic color change allows animals such as certain marine fishes to rapidly change the color and pattern of their skin, yet knowledge is lacking about how these animals gather and process the visual information needed to make color change decisions. Recent discoveries suggest that many color-changing animals can detect light with their skin, a process known as dermal photoreception, which may work alongside the eyes to regulate color change. Our lab investigates how dermal photoreception contributes to color change in fishes and whether the skin acts as a sensory system for monitoring the environment or the animal's own coloration. By uncovering the principles underlying distributed light sensing and adaptive camouflage, the project may inform future technologies related to bioinspired sensing and material science.

Additional Resources: For more information on the Schweikert Lab, please visit: <https://www.schweikertlab.com/> For more information on the Biology/Marine Biology Department at UNCW, visit: <https://uncw.edu/bio/> For more information on UNCW's Center for Marine Science, please visit: <https://uncw.edu/cms/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UOstrava Czech Republic Virus Evolution and Host Interactions

Have you ever wondered how many viruses exist out there? Which species they can infect - and why some, but not others? And how do the viruses evolve to adapt to new host species?

We do. And we're looking for people to help us find out.

At my group "virus evolution and host interactions" at University of Ostrava (Czech Republic), we take an interdisciplinary approach – spanning bioinformatics and molecular biology – to answer these questions at scale, through international collaborations.

PhD position: VP1- Ph.D. student in the Biology doctoral program - University of Ostrava, Faculty of Science, Ostrava, Czechia Link to the original post on research gate: https://www.researchgate.net/job/1038089_VP1-PhD_student_in_the_Biology_doctoral_program Start date: 1st October 2026 (or later by agreement)

Job Description:

- This position is being filled in accordance with the terms of the Life Environment Research Center Ostrava (LERCO, reg. no. CZ.10.03.01/00/22_03/0000003) *project, Research Program 1 : Molecular Biology and Genomics – Ph.D. student in a newly established research group : Virusevolution&hostinteraction Group led by dr. Pascal Mutz()* - The program will last for 4 years - EU research level: R1 - First stage

Responsibilities: - Conduct research in the field of virus evolution and virus-host interactions. - Analyze virus genomics datasets using bioinformatic and computational approaches. - Combine bioinformatic approaches with molecular biology experiments. - Contribute to the development of research and publications in high impact journals. - Present research findings at meetings and conferences. - Collaborate with members of an interdisciplinary research team. Qualifications and other requirements:

Required: - Master's degree in Bioinformatics, Computational Biology, Computer Science, Data Science, Infectious diseases, Evolutionary Biology, Biology or a related field. - Strong interest in virology, primarily eukaryotic RNA viruses. - Either good skills in programming/scripting languages such as Python or R OR experience in molecular biology ('wet-lab') and to learn the complementary skill. At least basic understanding of bioinformatics and molecular biology required. - Excellent communication and scientific writing skills. - Strong written and spoken English (B2 level)

Desirable: - Prior experience in comparative genomics and phylogenetic analysis. - Prior experience using high-performance computing (HPC) or computational clusters. - Prior experience in molecular virology techniques and studying virus-host interactions. - Record of peer-reviewed publications

Deadline for submitting applications: 15th August 2026

List of Documents Required from the Applicant (in English) - Signed Consent to the processing of personal data for the purposes of the selection procedure - Letter of intent - Curriculum vitae

Applications for the selection procedure with all the documents required should be sent electronically to the following address: personalni.prf@osu.cz.

To ask further questions about the position and the research project contact the Pi: pascal.mutz@gmx.de (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

UTasmania Linking genes social behaviour and population dynamics

PhD Position in Family Life in the Wild: Linking Genes, Social Behaviour, and Population Dynamics - University of Tasmania, Australia The Behavioural and Evolutionary Ecology Research Group at the University of Tasmania is seeking a second motivated PhD student to join an Australian Research Council Discovery Award

datasets. - Strong quantitative skills, including experience using R. - Excellent written and verbal communication skills. - An interest in behavioural ecology, evolutionary biology, genomics, or bioinformatics. - Field or laboratory experience with vertebrate systems. The successful applicant will receive a competitive PhD scholarship, opportunities for conference travel and international collaboration, and interdisciplinary training spanning behavioural ecology, molecular biology, bioinformatics, and evolutionary genomics. To apply, please send: - a brief expression of interest outlining your research experience and motivation, - your curriculum vitae, and - the contact details of two academic referees To: Associate Professor Geoff While, Behavioural and Evolutionary Ecology Research Group, University of Tasmania, Email: gwhile@utas.edu.au Expressions of interest should be received by the 1st of September 2026. Shortlisted applicants will be invited to discuss the project before being supported through the formal University of Tasmania PhD application process. Please see the UTAS PhD Project page (<https://www.utas.edu.au/research/degrees/available-projects>) or the Behavioural and Evolutionary Ecology Research Group page (<https://beergrouputas.wordpress.com/2026/06/27/two-phd-opportunities-exploring-the-evolution-of-family-life/>) for more information.

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UToronto PopGen of outbreaking species

PhD Position in Population Genetics and Outbreak Dynamics — University of Toronto

The James Lab (www.jameslab.ca) at the Institute of Forestry and Conservation, University of Toronto, is seeking a motivated, independent, and quantitatively inclined PhD student to investigate the population genetic dynamics of cyclic forest insect outbreaks. Population outbreaks are among the most striking phenomena in ecology, yet many questions remain regarding how fluctuations in abundance, dispersal, connectivity, and synchrony influence patterns of genetic diversity through space and time. The successful candidate will investigate these relationships using one of the largest spatial and temporal genomic datasets available for a forest insect, comprising more than 6,000 spruce budworm (*Choristoneura fumiferana*) individuals collected across eastern Canada over a 16-year period. The project will examine how genetic diversity, connectivity, and population structure change throughout the course of the current outbreak.

The project will also involve developing and applying complementary demo-genetic simulation models to investigate how population processes such as dispersal, population growth, bottlenecks, outbreak synchrony, and local extinction are expected to influence genetic variation under alternative outbreak scenarios. This project sits at the intersection of population ecology, population genetics, and simulation, and is well suited to students interested in combining large genomic datasets with computational approaches to better understand ecological and evolutionary processes.

The student will join a collaborative research team that includes university researchers, federal and provincial government scientists, postdoctoral fellows, and graduate students working on questions related to forest ecology, population genetics, insect outbreaks, and quantitative ecology.

Applicants should possess: - An MSc degree in ecology, evolutionary biology, forestry, genetics, bioinformatics, statistics, computer science, or a related discipline - Strong quantitative and analytical skills - Well developed programming and statistical skills (R, Python) - Excellent written and oral communication skills - A demonstrated interest in population genetics, evolutionary ecology, spatial ecology, or forest disturbances

The following qualifications would be considered assets: - Experience with genomic or population genetic data (e.g., RADseq, SNP datasets, landscape genetics) - Familiarity with Linux, high-performance computing, or bioinformatics workflows - Experience with multivariate statistics, simulation modelling, or spatial analysis (GIS)

Funding is available for four years and includes support for conference travel, professional development, and

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AppalachianStateU AssistantProfessor IntegrativeBiology

The Department of Biology at Appalachian State University is excited to announce a cluster hiring to enhance our research and teaching in the Integrative Biology concentration. We invite applications for two tenure-track positions at the rank of Assistant Professor to begin in Fall 2027.

We seek applicants who take an integrative approach to investigating interactions between organisms and their changing environments in the following areas:

Research that employs integrative techniques to address evolutionary or ecological questions related to host-pathogen/symbiont interactions, disease ecology, quantifying the impact of climate change on species interactions, or quantifying differing responses to change across organismal lineages. We intend to hire one applicant who addresses one or more of these questions in plants and one in animals. We are particularly interested in candidates who complement the current departmental strengths. Teaching responsibilities could include: Evolution, Ecology, Global Change Ecology,

Plant Physiology, and rotate into the first-year biology sequence. The successful candidates will have the opportunity to develop integrative courses in their area of specialty.

Minimum Qualifications: A PhD in Biology or related field with postdoctoral experience. The Department of Biology at Appalachian State University is a community of 44 faculty who are active in teaching and research, along with a support staff of 6 technicians and 3 administrators. We strive to maintain a faculty with diverse research interests, ranging from molecules to organisms to landscapes. The department currently has approximately 950 Biology majors and 70 graduate students. We provide instruction in biology through classroom and laboratory interactions, undergraduate and graduate laboratory research experiences, seminars, professional development programs, and career advising through courses and faculty interactions. Faculty typically teach 3 courses per semester (mixture of lectures and labs). Departmental and university service includes, but is not limited to, undergraduate advising, curriculum development, and assessment.

The Department of Biology manages and provides access to a research greenhouse, a 67 acre nature preserve on campus, an off campus 250 acre field site, I.W. Carpenter Jr. Herbarium (<https://herbarium.appstate.edu/>), and App State Zoological Collections (<https://biology.appstate.edu/facilities/zoological->

collections). The institution and department have facilities to support the use of cutting-edge molecular techniques, including instrumentation for flow cytometry, gel imaging, cell culture, and Illumina sequencing. The Rankin Science Building is home to the William and Ruth Dewel Microscopy Facility, which provides infrastructure for epifluorescence, confocal, scanning electron, and transmission electron microscopy, as well as sample preparation. The department and university support new faculty through a comprehensive Faculty Mentoring Program and Center for Excellence in Teaching, Learning, and Student Success. The mechanisms include peer writing circles, pedagogical workshops, and faculty mentoring.

Appalachian State University, in North Carolina's Blue Ridge Mountains, prepares students to lead purposeful lives as global citizens who understand and engage their responsibilities in creating a sustainable future for all. The transformational Appalachian experience promotes a spirit of inclusion that brings people together in inspiring ways to acquire and create knowledge, to grow holistically, to act with passion and determination, and embrace diversity and difference. As one of 17 campuses in the University of North Carolina system, Appalachian State enrolls over 21,000 students, and offers more than 150 undergraduate and 80 graduate majors.

Applicant Documents: Applications must include (a) a cover letter that includes information on how the applicant's research and teaching interests will complement and/or synergize with current departmental offerings (2 pages max), (b) a curriculum vitae, (c) a research statement that highlights short-term and long-term goals and the involvement of undergraduate and master's student researchers (3 pages max), (d) a teaching statement that includes philosophy, specific interests and experience, strategies for managing a 3-3 teaching load, and mentorship strategies (3 pages max), and (e) the contact information for 3 references (name, address, telephone, email). - Submit applications at App-State People Admin - Review of applications begins on August 31, 2026

Inquiries about the position should be directed to the co-chairs of the search Committee: Dr. Clare Scott Chialvo (chialvoch@appstate.edu) and Dr. Lynn Siefferman (sieffermanlm@appstate.edu).

— / —

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>

Cardiff UK National Museum Head of Botany

Amgueddfa Cymru - Museum Wales seeks a new Head of Botany to lead an experienced curatorial team driving forward innovative research and public engagement programmes. This strategic leadership role offers the opportunity to shape how Wales' national museum addresses global biodiversity and environmental challenges through world-class collections and cutting-edge research.

You will lead a team of curators and researchers, securing funding from bodies such as UKRI and the Royal Society while ensuring our Botany collections remain relevant and accessible. As Project Lead on high-impact research projects, you'll champion interdisciplinary collaboration across sciences, arts, and humanities, directly supporting our Strategy 2030 vision.

Key responsibilities include collection development, managing research budgets, publishing academic outputs, and fostering partnerships with higher education institutions. You'll deputise for the Head of Department as required, mentor staff and promote inclusive practices that reflect our diverse audiences.

We seek a PhD (or equivalent) qualified botanist with proven experience in museum collections management, team leadership, and successful grant applications.

Join us in mobilising scientific knowledge to engage audiences with environmental challenges while advancing Wales' position as a leader in biodiversity research and conservation.

Applications must be received by 29 July 2026 for consideration.

Please contact the Head of Natural Sciences and Research, Jenny Geroni (Jenny.Geroni@museumwales.ac.uk) or the Head of Zoology, Jeff Streicher (Jeffrey.Streicher@museumwales.ac.uk) with any questions.

<https://nmw.ciphir-irecruit.com/Applicants/vacancy/2682/Head-of-Botany-National-Museum-Cardiff?m=0> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Galapagos Field assistants needed Sea Lion Project

Field assistant needed! Sea Lion Project Galapagos

We are looking for two field assistants to join the upcoming field season of the Sea Lion Project Galapagos, a long-term research project on Galapagos sea lions (*Zalophus wollebaeki*) conducted by the research group of Prof. Oliver Kruger at the Department of Animal Behaviour, Bielefeld University, Germany. <https://www.uni-bielefeld.de/fakultaeten/biologie/forschung/arbeitsgruppen/behaviour/research/galapagos-sea-lion/>

Fieldwork will take place from end of October to middle of December 2026 on Caamano, a small islet (300m diameter) near Puerto Ayora on Santa Cruz Island, Galapagos. The project has studied the Caamano population since 2003, with most animals individually marked. The field season will contribute to long-term research on population dynamics, life history, social behaviour, personality, and foraging strategies. Work includes daily census rounds, behavioural observations, behavioural response tests, captures and handling of sea lions for tagging and growth assessment, biologging deployments and recoveries, and sample collection. Fieldwork is physically and mentally demanding and requires walking and climbing over difficult volcanic terrain, working in strong sun and close to the ocean, handling wild animals, and collecting high-quality data under challenging conditions.

Caamano is isolated and has no facilities. The field team will live on the island for 6-7 weeks in tents, share all camp duties, and work under truly primitive conditions. There are no sanitary facilities, fresh water is limited to drinking and cooking, and food is simple. Visits to other islands during the field season is not possible. Applicants must be physically fit, mentally resilient, reliable, and able to work closely in a small team of four colleagues continuously for weeks.

The positions are suitable for students or early-career researchers with a background in biology, animal behaviour, behavioural ecology, population ecology, evolutionary biology, marine biology, or related fields. Previous experience with sea lions is not required, but experience with fieldwork, camping, behavioural observations, biologging, or handling wild animals is a strong advantage.

Good spoken and written English is required; Spanish skills are highly desirable.

The positions are unpaid, but project-related expenses during the field season will be covered, including travel to the Galapagos Islands, accommodation while in town before and after the field season, and food while on Caamano. Field assistants are responsible for their own personal field clothes, equipment, and private expenses.

We also welcome applications from candidates interested in developing a future PhD project within the Sea Lion Project Galapagos. PhD funding cannot be guaranteed at this stage. However, suitable and interested candidates who successfully complete the field season will receive support in developing a PhD proposal and applying for funding. Applicants interested only in the field assistant position are equally welcome.

To apply, please send a single PDF including (I) a short letter of motivation, (II) your CV including relevant fieldwork or animal-handling experience, and (III) contact details of one or two referees.

Please send applications or informal inquiries to: Dr. Jonas Schwarz jonasschwarz@uni-bielefeld.de

Review of applications will begin on 13th of July until positions are filled. We particularly encourage applications from Ecuadorian nationals and from candidates with strong field experience, motivation, and the ability to work responsibly under remote and challenging conditions.

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Hangzhou China ZhejiangU AssistantProfessorandPostdoc Evolution

Job Description

The Center for Evolutionary & Organismal Biology at Zhejiang University in Hangzhou, China, invites applications from evolutionary scientists for all ranks, Assistant or Associate, Full-Professor. Applications from both Chinese and non-Chinese nationals are all welcomed and will be evaluated on experience and qualifications on an equal opportunity basis. Each faculty member will receive an internationally competitive salary and start-up package that includes long-term and sufficient research funds, ample laboratory space, ex-

cellent equipment, and research support. The center already hosts several PIs in the fields of evolutionary genomics, computational biology, and evolutionary developmental biology.

Qualifications: 1. A very good doctorate (Ph.D/M.D) in the relevant research areas; 2. A visible publication track record reflecting your scientific excellence and research focus; 3. A convincing research concept and plan; 4. A team player mentality, good communication skills, and the ability to successfully lead diverse international teams.

Responsibilities: 1. Building an innovative team; 2. Personal advancement skills to secure external funding; 3. Enthusiasm in teaching and nursing the next generation of evolutionary biologists; 4. Engagement in the academic self-administration of the center; 5. Establishing cross-disciplinary research programs in collaboration with researchers from other fields.

We Offer 1. State-of-the-art research space; 2. A workplace that values diversity and promotes junior researchers; 3. A young and internationally recognized, vibrant, and collaborative research environment; 4. Highly-motivated student pool; 5. The cutting-edge genomic and molecular biology facilities; 6. International collaboration network.

Application Instructions 1. Letter of motivation with a clear statement of why the center as a research location is interesting for you & where your career should take you; 2. Curriculum vitae; List of publications; Copies of the certificates; 3. Research concept including graphical abstract (max. 2 pages); 4. References (max. 3).

Please send your application to Yunqiu He: heyunqiu@zju.edu.cn

Other Postdoc positions are available at <https://evolution.zju.edu.cn/en/contacts.html>, and the detailed information about the evolution center in Zhejiang University, China can be found at <https://evolution.zju.edu.cn/en/index.html>

Best Wishes –

Prof. Dr. Qi Zhou Center for Evolutionary & Organismal Biology Zhejiang University 866 Yuhangtang Road Hangzhou 310058, China Lab: <http://qizhoulab.org/> Twitter: @zhouqi1982

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Houston Technician

Laboratory Technician Position in the Department of Biology & Biochemistry at the University of Houston

A laboratory technician position is available in the Department of Biology and Biochemistry, University of Houston, TX, USA in the laboratory of Dr. Richard Meisel, PhD.

The Meisel lab uses genetic and genomic approaches to study evolutionary processes in a diversity of fly models. The laboratory technician will maintain fly strains; perform experiments with flies; carry out molecular biology experiments; oversee laboratory supplies and purchasing; and train lab members in laboratory protocols. Interested applicants should email Richard Meisel (rpmeisel@uh.edu) a resume; cover letter describing experience and goals; and contact information for at least one references. Applications will be reviewed as they are received and continue until the position is filled.

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IFF Wilmington DE USA Associate Researcher BioActives

Associate Researcher (BioActives)

IFF Wilmington, DE https://www.linkedin.com/company/iff?trk=public_jobs_topcard-org-name
Job Summary

Are you passionate about applying molecular biology to build innovative bio-based solutions that make a real-world impact?

IFF is a global leader in taste, scent, and nutrition, offering customers a broad range of natural solutions while accelerating our growth strategy. We apply science and creativity to push beyond traditional boundaries, driving innovation for a more sustainable future.

IFF Health & Biosciences (H&B) applies expert science to advance market-driven, healthy, and sustainable solutions for the food, beverage, dietary supplement, and pharmaceutical industries. Using cutting-edge biotech-

nology, we help customers turn complex challenges into high-value business opportunities.

This role is based in Wilmington, DE and follows an Anchor work model. You will join an innovative, customer-focused, and diverse team supporting host construction, strain improvement, and product development initiatives.

Where You'll Make a Difference

- Contribute to project workstreams focused on understanding the performance of microbial cell factories and their products in industrial applications - Support strain construction initiatives using modern molecular and cell biology techniques - Assist with optimization, analysis, and improvement of cell factories based on project data and direction - Collaborate effectively with cross-functional project teams to deliver defined project goals - Execute laboratory and project tasks as directed by the project leader - Explore and implement new methods and technologies in collaboration with the project team - Generate, analyze, and clearly communicate experimental data - Prepare technical reports, data summaries, presentations, protocols, and technical documentation

What Makes You The Right Fit

- Bachelor's degree in Biology, Microbiology, Molecular Biology, Biochemistry, or a related field with 0-2 years of relevant experience, or a Master's degree with no prior professional experience required - Strong foundational knowledge of molecular biology, biochemistry, or microbial physiology - Demonstrated ability to work as part of a multi-functional project team - Hands-on approach with a strong affinity for laboratory-based work - Willingness and ability to learn new skills, techniques, and methodologies - Adaptability to change and the ability to manage multiple workstreams in parallel - Strong problem-solving skills and collaborative mindset - Goal-oriented approach with the ability to deliver task-based outcomes - Excellent organizational skills and strong attention to detail

How Would You Stand Out?

- Experience working in an industrial or applied Research & Development biotechnology environment - Familiarity with microbial strain engineering or cell factory optimization - Experience contributing to projects in fast-paced, innovation-driven settings

Why Choose Us?

- Opportunity to work at the forefront of biotechnology innovation - Collaborative and inclusive research environment - Exposure to industry-leading technologies and scientific expertise - Professional development

and continuous learning opportunities - The chance to contribute to sustainable solutions that impact everyday lives

We are a global leader in taste, scent, and nutrition, offering our customers a broader range of natural solutions and accelerating our growth strategy. At IFF, we believe that your uniqueness unleashes our potential. We value the diverse mosaic of the ethnicity, national origin, race, age, sex, or veteran status. We strive for an inclusive workplace that allows each of our colleagues to bring their authentic self to work regardless of their religion, gender identity & expression, sexual orientation, or disability.

Visit [IFF.com/careers/workplace-diversity-and-inclusion](https://www.iff.com/careers/workplace-diversity-and-inclusion) to learn more

<https://www.linkedin.com/jobs/view/4422785546/?trk=mcm> This communication contains information of International Flavors & Fragrances (IFF) and/or its affiliates that may be confidential, proprietary, copyrighted and/or legally privileged, and is intended only for the addressee. Any copying, dissemination or other use of this information by anyone other than the intended recipient is prohibited. If you have received this communication in error, please contact the sender and delete it from your system. For details of how IFF handles personal data of individual representatives of its customers, prospects, suppliers, service providers and other business partners, please refer to the IFF's Customer and Vendor Privacy Notice (<https://www.iff.com/privacy/customer-and-vendor-privacy-notice/>).

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IFF Wilmington DE USA Research Associate Molecular Biology

Research Associate IFF Wilmington, DE (https://www.linkedin.com/company/iff?trk=public_jobs_topcard-org-name)

Job Summary

Are you ready to apply cutting-edge molecular biology to engineer innovative bio-based solutions that make a

real impact?

At IFF, we go beyond traditional boundaries, combining science and creativity to build a more sustainable future. Together, we act as catalysts for positive change.

IFF is a global leader in biotechnology, delivering sustainable innovations across food, beverage, health, and biosciences. Our Health & Biosciences business applies expert science to develop bio-based solutions that support a growing global population while protecting our environment.

This role is based in Wilmington, DE, USA (on-site). You will join an experienced, collaborative, and innovation-driven team focused on host engineering, strain development, and molecular biology-driven product innovation.

Where You'll Make a Difference

- Design and execute laboratory experiments using advanced molecular biology techniques
- Engineer and construct microbial cell factories to support product innovation
- Contribute to strain development and optimization using modern genetic and cellular engineering tools
- Analyze and interpret biological data to improve performance in industrial applications
- Act as a key interface between Research & Development (R&D) and Quality Assurance / Quality Control (QA/QC) teams
- Collaborate cross-functionally to translate research insights into scalable solutions
- Maintain high standards of scientific rigor, reproducibility, and data integrity
- Document and communicate experimental findings through reports and presentations

What Makes You The Right Fit

- Bachelor's or Master's degree in Molecular Biology, Microbiology, Biochemistry, or related field
- Strong foundation in molecular biology and microbial physiology
- Hands-on laboratory experience with genetic manipulation and strain engineering
- Ability to work effectively across interdisciplinary teams, including R&D, Quality Analytics, and Quality Control
- Strong analytical and problem-solving skills
- Excellent communication skills, with the ability to translate scientific insights clearly
- Ability to manage multiple priorities in a dynamic R&D environment
- High attention to detail and commitment to high-quality data generation
- Curiosity and passion for scientific innovation

How Would You Stand Out?

- Experience in industrial biotechnology or applied microbiology environments
- Familiarity with scaling microbial processes or product development pipelines
- Exposure to quality systems, regulatory environments, or QA/QC collaboration

Why Choose Us?

- Work at the forefront of biotechnology innovation
- Be part of a global, inclusive, and purpose-driven organization
- Access opportunities for continuous learning and career growth
- Contribute to products that make a real impact in everyday life
- Collaborate with a highly experienced and supportive scientific team
- Competitive compensation and comprehensive benefits

We are a global leader in taste, scent, and nutrition, offering our customers a broader range of natural solutions and accelerating our growth strategy. At IFF, we believe that your uniqueness unleashes our potential. We value the diverse mosaic of the ethnicity, national origin, race, age, sex, or veteran status. We strive for an inclusive workplace that allows each of our colleagues to bring their authentic self to work regardless of their religion, gender identity & expression, sexual orientation, or disability.

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Morris Arboretum
University of Pennsylvania Endowed
Plant Molecular Ecologist

Position Title: John Otto Haas Molecular Ecologist Institution: Morris Arboretum & Gardens of the University of Pennsylvania Location: Philadelphia, PA Position Type: Full-Time, Permanent Link to Application: <https://wd1.myworkdaysite.com/en-US/recruiti>

[ng/upenn/careers-at-penn/job/Morris-Arboretum/John-Otto-Haas-Molecular-Ecologist--Morris-Arboretum---Gardens_JR00123059](https://upenn/careers-at-penn/job/Morris-Arboretum/John-Otto-Haas-Molecular-Ecologist--Morris-Arboretum---Gardens_JR00123059) Review of Applications begins September 1, 2026 and will continue until the position is filled.

The newly endowed John Otto Haas Molecular Ecologist will conduct research at Morris Arboretum & Gardens with a focus on techniques that integrate fieldwork and herbarium collections with resources from the Plant Science Laboratory. The successful candidate will use molecular tools to investigate evolutionary patterns (e.g., conservation genetics, functional genomics), spatial dynamics (e.g., landscape genetics, phylogeography), and/or community-scale processes or community composition, such as plant-animal interactions, relationships within the plant microbiome, and/or metagenomics/eDNA. Will disseminate research through publications and presentations. Must be able to provide expertise and departmental support in bioinformatics and analytical computing, preferably with an active enthusiasm for departmental collaborations. Will actively pursue independent funding through grant proposals and strategic partnerships. Will engage with diverse audiences to educate students and the public by teaching courses at University of Pennsylvania, at Morris, and through the mentorship of students, apprentices, interns, and volunteers. Will engage with professional colleagues and members of the public and work closely with staff in the Plant Science Department and other departments at Morris.

Responsibilities: - Conduct research in Plant Molecular Ecology that incorporates fieldwork, herbarium and living collections, and resources in our new Plant Science Laboratory.

- Lead the development of research projects including, but not limited to: planning, scheduling, fieldwork, and laboratory work.
- Disseminate research findings in peer-reviewed scientific literature and other professional and popular journals.
- Present and share research findings at conferences, through seminars, and other professional and general audience events.
- Provide assistance and expertise to departmental colleagues in support of bioinformatics and analytical computing research needs.
- Seek independent funding for research projects.
- Teach courses at Penn and Morris Arboretum and Gardens.
- Engage in other opportunities for outreach through

professional societies, collaborative networks and partnerships.

- Mentor and supervise students, interns, volunteers, and apprentices.
- Engage with professional colleagues and the general public.
- Work with staff at Morris to advance our institutional mission.

Qualifications: - A Ph.D. in Botany, Ecology, Biology, or equivalent doctoral degree.

- 1 to 2 years of related experience, including but not limited to postdoctoral research or other professional work experience.
- Experience in planning and conducting research, as demonstrated through a strong record of publishing and successful acquisition of grant funding.
- Strong analytical skills are required, including experience with bioinformatics and applied statistics.
- Excellent written, verbal, and interpersonal communication skills and be able to collaborate effectively with colleagues on analyses, research, outreach, and teaching projects.
- A demonstrated ability to mentor/supervise interns/students is desired as well as demonstrated teaching experience.
- Some travel may be required.
- A PA Driver's License is required.

To Apply: Applicants should apply online through the link below at Workday and in addition to the application requirements, they must submit (1) a Cover Letter; (2) updated curriculum vitae; and (3) a Research Statement (up to three pages). Link to Application: https://wd1.myworkdaysite.com/en-US/recruiting/upenn/careers-at-penn/job/Morris-Arboretum/John-Otto-Haas-Molecular-Ecologist--Morris-Arboretum---Gardens_JR00123059 (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Smithsonian NMNH CuratorsX3
Ornithology Herpetology
Ichthyology

Research Zoologist (Curator of Vertebrates)

The Smithsonian's National Museum of Natural History currently has openings for three early-career Research Curators in Vertebrate Zoology, one each from the disciplines of ornithology, herpetology and ichthyology. The Department of Vertebrate Zoology seeks candidates with demonstrated expertise in, and a commitment to, collections-based research centered on systematics and evolution of birds, reptiles, amphibians, and fishes. This includes the ability to pursue an original approach to systematics and comparative analyses using, for example, morphology, development, and/or molecular data, and showing evidence of broader impacts or applications in evolutionary biology and/or collections-based ecology, as demonstrated by a record of peer-reviewed publications.

Candidates must have demonstrated the ability to establish an externally funded research program and to contribute to the growth and curation of the collections. Research in the Department is supported by the Museum's shared laboratories, including the Laboratories of Analytic Biology and the Scientific Imaging facility, among others. The Department's scientific collections are the largest in the world for fishes, amphibians, and reptiles, and the third largest for birds. More about the Department and its collections is available on our website (<https://naturalhistory.si.edu/research/vertebrate-zoology>).

The position in ichthyology is separate and distinct from the one advertised in May. These federal positions will be filled at the GS-12 level, with a starting salary of 102,415 and excellent benefits. The positions are permanent and include a one-year probationary period. The Smithsonian is not able to accommodate spouses at this time. These federal positions are open to U.S. Citizens and permanent residents.

The official announcement is posted on USAJOBS and is open for applications through at least July 20th, where applications must be submitted.

<https://www.usajobs.gov/job/873849000> Please be sure to read the announcement and instructions carefully, as the process of applying via USAJOBS is stringent and differs from applying for an academic position. This website offers helpful advice: <https://serc.si.edu/careers/tips-applying-federal-jobs> Please contact the Search Committee Chair, Michael McGowen (mcgowenm@si.edu) or the Department Chair, Helen James (jamesh@si.edu) with any questions.

The Smithsonian Institution is an Equal Opportunity Employer. To review the Smithsonian's EEO program information, please click the following: <https://www.si.edu/oeo>. (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net

Trinity College Dublin MSc Stability of European freshwater fish communities under multiple environmental changes

MSc by Research studentship available on: "Stability of European freshwater fish communities under multiple environmental changes"

We are seeking a highly motivated candidate for a fully funded 2-year MSc by Research project. The student will be supervised by Dr. Conor Waldock and Prof. Ian Donohue at the School of Natural Sciences. This studentship is funded via the School of Natural Sciences MSc to PhD Pathway fund. It is expected that the student will be open to and seeking to find a route or pathway to complete a PhD.

Funds are only available to cover EU citizens.

We are dedicated to foster a diverse and inclusive research environment and strongly encourage applicants from all backgrounds to apply.

Project Background and Description

Global environmental change is increasingly uncertain and unpredictable, with multiple changes acting at once. The response of biodiversity to novel mixtures of anthropogenic impacts remains an urgent knowledge gap. Freshwater ecosystems harbour imperilled fish fauna facing a combination of climate change, pollution, invasive species, physical modification and habitat fragmentation. This project will use fish biodiversity as a model system to explore how natural ecosystems vary in their inherent capacity to remain stable and productive under unpredictable multi-dimensional environmental change.

Ecological communities are made up of sets of species that often have different responses to environmental change because they have evolved specialisations into ecological niches. Quantifying species' different responses gives a community's "response diversity", a property expected to predict the stability of a community under environmental change.

This project will investigate spatial patterns, drivers, and consequences of response diversity of European fish. It will combine a large-scale pattern-based macroecological investigation with empirical tests of ecological stability theory. The overarching question is: how

does response diversity contribute to stability of natural freshwater ecosystems under multiple environmental changes?

The core aims of the project are: 1. Investigate spatial patterns and environmental drivers of response diversity in fish communities across Europe. 2. Examine the empirical relationships between response diversity and stability of community biomass and species' composition.

Candidate Profile The candidate must meet the Trinity postgraduate entry requirements and be eligible for EU student fees (<https://www.tcd.ie/study/apply/admission-requirements/postgraduate/>) and hold at least an upper second class (2.1) Honours Bachelor degree, preferably in Biology, Ecology or Environmental Science or another related discipline.

We hope the candidate will fulfil the below requirements: - Be actively interested in global environmental change and its impact on biological diversity. - Have demonstrated ability to handle and analyse data in R. - Have keen interest in developing skills in advanced data processing and statistical analysis pipelines in R. - Be keen to develop knowledge on freshwater ecology and obtain field experience beyond the theoretical concepts of the MSc. - Have the ability to develop hypothesis-driven questions to advance global biodiversity change modelling. - Contribute positively to team dynamics and atmosphere and have capacity to work well independently.

Funding This is a 2-year MSc by Research project funded by the School of Natural Sciences and covers an annual tax-free stipend of EUR25,000, and EU student fees.

As part of the award, it is expected that the candidate and PI will identify and apply to other funding mechanisms as to meet the terms of the MSc to PhD Pathway fund.

Application procedure Please send a CV and a 1-page personal statement, and any enquiries, to Dr. Conor Waldock (waldockc@tcd.ie) by 24th July.

Your CV should include the name and contact details of two references.

In your personal statement, please explain: - Why you are interested to undertake an MSc. - Why you are interested in this MSc project specifically. - How you fit some of the elements in the above candidate profile.

Interviews will take place (online) in early August with a Project start date September 2026 or March 2027.

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UCambridge Postdoc in Bat Immunity

Postdoctoral Research Associate in Bat Antiviral Immunity Location: Cambridge, UK Salary: GBP37,694-GBP46,049 Contract: Fixed-term for 18 months in the first instance Start date: 1 September 2026, or as soon as possible thereafter Closing date: 29 July 2026 Reference: PP50380 The Department of Veterinary Medicine at the University of Cambridge invites applications for a BBSRC-funded Postdoctoral Research Associate position in the laboratory of Professor Clare Bryant. The project aims to elucidate the molecular mechanisms underlying antiviral immunity and immune regulation in bats. The main focus will be the functional characterisation of ancestral and lineage-specific variants of the innate immune genes NLRP3, MyD88 and STING. Collaborating research groups have reconstructed ancestral versions of these genes and identified lineage-specific amino-acid substitutions of particular interest. The successful candidate will investigate the functional consequences of these variants in human and bat cell systems. Gene variants will be introduced using plasmid transfection, lentiviral transduction or CRISPR-mediated genome modification, followed by functional analysis of innate immune signalling. Applicants should have, or be close to completing, a PhD in cell biology, biochemistry, evolutionary biology or a related discipline. Experience in cell culture and molecular cloning is essential. A good understanding of innate immunity and knowledge of evolutionary bioinformatics would be advantageous. Experience with lentiviral transduction, CRISPR-mediated genome modification or functional immune assays would also be beneficial. The successful candidate will join a collaborative and interdisciplinary research environment and should value teamwork and cooperation. Good organisational, administrative, interpersonal and presentation skills are also required. The appointment is fixed-term for 18 months in the first instance and is available from 1 September 2026, or as soon as possible thereafter. Full details and online application: <https://www.cam.ac.uk/jobs/research-associate-fixed-term-pp50380> Informal enquiries about the position may be directed to Julie Ingham at ji217@cam.ac.uk. Applicants should submit a completed CHRIS/6 form, a curriculum vitae, a covering letter outlining their suitability for the role, and contact details for two referees. Applications must be

submitted through the University of Cambridge online recruitment system. Please quote reference PP50380 in your application and in any correspondence concerning the vacancy. Interviews are expected to be held during the week commencing 24 August 2026. Enquiries about the application process may be directed to hr.enquiries@vet.cam.ac.uk. The University of Cambridge actively supports equality, diversity and inclusion and encourages applications from all sections of society. The University is committed to promoting an inclusive culture and valuing diversity. The University has a responsibility to ensure that all employees are eligible to live and work in the United Kingdom.

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UC Berkeley Director University and Jepson Herbaria

We are pleased to share that the search for the next Director of the University and Jepson Herbaria is now underway. The Director is critical to advancing the Herbaria's mission as a leading center for botanical research, biodiversity science, and public engagement. The position will be held by a tenured faculty member in UC Berkeley's Department of Integrative Biology. They will work closely with our dedicated staff, faculty curators, students, and supporters. We appreciate your help in sharing this opportunity as we seek an outstanding leader for the next chapter of the University and Jepson Herbaria! Position announcement: Associate or Full Professor in the Department of Integrative Biology (Plant Ecology, Evolution, and Systematics) & Director of the University and Jepson Herbaria UC Berkeley invites applications for a tenured Associate or Full Professor in Plant Ecology, Evolution, and Systematics, who will also serve as Director of the University and Jepson Herbaria. We seek an internationally recognized scientist with a distinguished research program and a vision for leading one of the world's premier university herbaria. For the complete position description, qualifications, and application instructions, please visit: <https://aprecruit.berkeley.edu/JPF05405> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UF Assistant Professor Genetics

Assistant Professor of Genetics

Department of Molecular Genetics and Microbiology, University of Florida

The Department of Molecular Genetics and Microbiology at the University of Florida (UF) College of Medicine invites applications for a tenure-track position at the rank of Assistant Professor of Genetics. The Department has begun a major expansion of the faculty as part of a 5-year strategic plan. We seek outstanding creative investigators in any area of genetics (using any genetic systems), including but not limited to gene expression and regulation, functional genomics and systems biology, developmental genetics, immunogenetics, molecular mechanisms of disease, evolutionary genetics, and other related fields.

The Department has active research programs in mammalian (human, mouse), *Drosophila*, viral, bacterial, cancer, and comparative genetics, together with expertise in gene discovery, genome editing, transcriptional and co/post-transcriptional regulation, Developmental biology (including evo-devo), RNA biochemistry, disease mechanisms, structural biology, protein biochemistry, multi-omics, and computational biology. The Department offers a highly collegial and collaborative environment and interactions with numerous Colleges (Agriculture, Engineering, Liberal Arts and Sciences, Medicine, Public Health and Health Professions), Institutes (Emerging Pathogens, Genetics, McKnight Brain) and Centers (Cancer, CDC Southeastern Center of Excellence in Vector Borne Diseases, Inflammation & Mucosal Immunology, NeuroGenetics, NIH Southeast Center for Integrated Metabolomics) that foster interdisciplinary research at UF. Further information about the Department can be found at <https://mgm.ufl.edu>. All applicants MUST apply online through Careers at UF. <https://explore.jobs.ufl.edu/en-us/job/539676/assistant-professor-genetics-mammalian-genetics> In order to be considered, you must upload references, cover letter, CV, Research Statement, and Teaching Statement. Applications received by August 31, 2026 will receive full consideration.

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University of Goettingen Germany Research Engineer- Image Analysis Plant Disease Ecology

The Division of Plant Diseases and Crop Protection at the University of Goettingen, Germany, is advertising a position for an

Research engineer for AI-based image analysis and optical sensing in plant disease ecology. Starting date: as soon as possible. Initial duration: two years, with the possibility to convert the position to a permanent contract after a successful evaluation. Application deadline: 31 July 2026.

The position supports research on plant diseases through the development and application of AI-based image analysis workflows and optical sensing approaches. The successful candidate will work at the interface of scientific programming, machine learning, image analysis, optical sensing technologies and plant disease experiments. This position is ideal for a candidate with strong AI/image analysis skills who also has experience with experimentation on plants and a genuine interest in plant disease ecology and evolution.

We are looking for a highly motivated and technically skilled engineer with at least a Bachelor's degree in computer science, data science or a related field, and strong experience in scientific programming, AI-based image analysis, machine learning and data management. Experience with large image datasets, image analysis pipelines, and training, testing and validating machine-learning or deep-learning models is expected. Experience with RGB, multispectral, hyperspectral, thermal infrared or 3D/LiDAR-based image data acquisition applied to biological systems (ideally plants or plant diseases) would be an advantage.

Main tasks include: - developing, testing and documenting workflows for image annotation, preprocessing, quality control, model training, validation and structured storage of results from plant disease experiments; - applying image analysis, machine learning and deep learning to RGB, multispectral, hyperspectral, thermal infrared and 3D/LiDAR-based image data; - supporting optical sensing experiments under controlled conditions, including sensor setup, calibration and data quality control; - supporting field-based sensing campaigns using ground-based robotic platforms and UAV-based systems; - training and supporting MSc students, doc-

toral researchers, postdocs and other members of the division in image analysis, annotation tools, data management and model validation.

The position offers an interdisciplinary working environment at the interface of plant pathology, optical sensing, artificial intelligence and data science, within a growing research division developing modern quantitative approaches for studying plant diseases.

More details here <https://obp.uni-goettingen.de/en-US/Stellen/StellenDruck/76465>. Applications should be uploaded as a single PDF file via the University of Goettingen application portal:

<http://obp.uni-goettingen.de/de-de/0BF/Index/76465>. For further information, please contact:

Professor Alexey Mikaberidze, Division of Plant Diseases and Crop Protection, University of Goettingen.
Email: alexey.mikaberidze@uni-goettingen.de

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UNacionalAutonomaDeMexico Systematic Botany

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

https://www.ib.unam.mx/ibunam/Convocatoria_Inv_Botanica_Jun26.pdf. The Universidad Nacional Autonoma de Mexico (UNAM, www.unam.mx) is the pre-eminent 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 de Tiempo Completo) in the field of Systematic Botany, in the Department of Botany.

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

REQUIREMENTS - Doctorate or Ph.D. degree in botany, systematics or evolution. - Preferably with postdoctoral experience. - Knowledge and professional experience of at least 3 years in research in phylogenetic systematics and evolution of a group of angiosperms. - Field work experience. - Experience in the use or development of biological collections. - Ability to teach and supervise undergraduate and graduate students from UNAM's Schools of Science and Graduate Programs, as well as to participate in outreach and institutional activities. - Develop their own line of independent research, including procurement of funds for research and interaction and collaboration with other research groups. - Non-native speakers must be fluent in the Spanish language.

Applications from early- and mid-career scientists are encouraged.

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. 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 a long-term research plan, centered on the systematics and evolution of a group of angiosperms, 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). 6. Shortlisted candidates should provide academic recommendation letters from three persons.

Applications, accompanied by supporting documents, will be received from June 22nd, 2026 until the close

of this call, on August 31st, 2026 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

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U Vienna Assistant Professor Rapid Marine Adaptation

The University of Vienna invites applications for a Tenure Track Professorship in the field of Rapid Marine Adaptation. We seek a scientist with an outstanding record in marine evolutionary genomics who investigates rapid evolutionary responses—such as evolutionary rescue—through field studies and/or experimental evolution in the laboratory. Preferred model systems should be eukaryotic marine organisms that have vital roles in oceanic or coastal ecosystems. The successful candidate will cooperate with physiologists, ecologists, biochemists, systems biologists and evolutionary biologists in Vienna to link genomic targets of selection to organismal phenotypes and local environmental conditions. This integrative work will advance mechanistic understanding and predictive modeling of rapid adaptation to climate change in marine environments and inform effective marine conservation strategies across Europe. For more information see: <https://jobs.univie.ac.at/job/Tenure-Track-Professorship-in-Rapid-Marine-Adaptation/1417563233/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

VanderbiltU ResearchAssistant ExperimentalEvolution

The Behringer Lab is looking for a research assistant to help oversee long-term culture of various anaerobic and

aerobic bacteria, including Lactobacilli and Escherichia coli. The major research focus of this position is understanding how oxygen exposure shapes microbial evolution, which aligns with the global lab interests of how microbes evolve in stressful environments.

This position would be a wonderful opportunity for recent graduates looking for an interim position to gain valuable research experience prior to pursuing a graduate degree. Applicants with microbiology experience or experience with experimental evolution are strongly encouraged to apply.

For more information visit: https://ecsr.fa.us2.oracledcloud.com/hcmUI/CandidateExperience/en/sites/CX_1/job/10008521 (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

WashingtonStateU VertebrateEvolutionaryGenomics

Position Details: The School of Biological Sciences at Washington State University invites applications for a permanent, full-time, 9-month, tenure-track Assistant Professor position in Pullman, WA, with a specialty in Vertebrate Evolutionary Genomics. We seek to hire a creative and engaging scholar whose research leverages modern genomic tools to gain fundamental or applied insights into evolutionary processes. We seek candidates working on functional and/or evolutionary genomics in vertebrate systems, broadly defined. We are especially interested in candidates who link variation in genome organization and function to evolutionary outcomes by studying themes that include but are not limited to mutation, recombination, gene duplication and loss, structural variation (e.g., inversions, translocations, copy number variation), transposable elements, gene expression and regulatory evolution, and epigenetic modification.

Ideal candidates will apply integrative and innovative analytical approaches to inform the relationship between genome and phenome, other aspects of genome architecture, or between genomic variation and evolutionary processes such as hybridization, adaptation, introgression, or speciation. The successful candidate will contribute to training the next generation of biology students in skills such as bioinformatics, genomics, and the analysis of large datasets.

Additional Information: This is a full-time (100%) position is NOT eligible for overtime. This position works on-site/in-person at the WSU campus in Pullman, WA. 9-Month Academic Salary: 80,000.00 to 95,000.00 — Commensurate with experience and qualifications

In accordance with RCW 49.58.110 (<https://app.leg.wa.gov/RCW/default.aspx?cite=49.58.110>), the above salary reflects the full salary range for this position. Individual placement within the range is based on the candidate's current experience, education, skills, and abilities related to the position. Successful candidates typically begin up to mid-point of the salary range.

Benefits: WSU offers a comprehensive benefits package which includes paid sick and vacation leave; paid holidays; medical, dental, life and disability insurance package for employees and dependents; retirement; deferred compensation, optional supplemental retirement accounts. For additional information, please review the detailed Summary of Benefits offered by WSU for Faculty (<https://hrs.wsu.edu/wp-content/uploads/2025/12/2026-Benefit-Overview-for-Faculty-and-AP.pdf>) and Total Compensation (<https://hrs.wsu.edu/managers/recruitment-toolkit/total-compensation/>).

Required Qualifications: - Earned Ph.D. in biology or related discipline and at least 6 months of postdoctoral research experience prior to the anticipated start date. - Record of research accomplishment in vertebrate evolutionary genomics, as demonstrated by publications and presentations at scientific meetings. - Effective communication skills with both students and colleagues. - Demonstrated record of or potential to engage in productive collaborations. - Demonstrated record of supporting, or potential to support, access and opportunity in research, teaching, and service in alignment with WSU's land grant mission. - Record indicating past teaching effectiveness or evidence of the potential for effective teaching of undergraduate and graduate courses in biology. - Demonstrated record or potential to teach comparative vertebrate anatomy or vertebrate taxon-focused courses, as well as one or more of the following courses: evolutionary biology, genome biology, contemporary genetics, or evolutionary medicine. - Experience with or potential for quality mentoring of undergraduate and graduate students undertaking independent research projects. - Evidence of seeking or being awarded intramural or extramural funding, with levels of activity commensurate with opportunities at the candidate's career stage

Position Sponsorship Eligibility: May be eligible for work visa sponsorship About Department - School of

Biological Sciences [https://sbs.wsu.edu/About the College](https://sbs.wsu.edu/About-the-College) - College of Arts & Sciences <https://cas.wsu.edu/> Location: Pullman, WA

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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>

Wellesley College Assistant Professor of Biological Sciences Vertebrate Biology

Dear colleagues, please see and distribute the job posting below. (Text version in the message, but the link provides the complete link to apply)

Position: R0007818 - Assistant Professor of Biological Sciences External Job Posting Link: Assistant Professor of Biological Sciences - https://wd1.myworkdaysite.com/recruiting/wellesley/wellesley-faculty/job/Wellesley-College-Assistant-Professor-of-Biological-Sciences_R0007818 Job Description The Biological Sciences Department at Wellesley College invites applications for a tenure-track position in vertebrate biology at the rank of Assistant Professor to begin in Fall 2027. We seek to hire a broadly trained vertebrate biologist who is strongly committed to excellence in both teaching and research in an undergraduate liberal arts college environment. The position is open to candidates whose research is at the organismal level and addresses questions of physiology or form and function. A Ph.D. is required at the time of application. Candidates are expected to develop an active and productive research program that involves Wellesley undergraduates. A competitive start-up package will be provided. Candidates will be expected to teach the equivalent of four courses per year within the Biological Sciences curriculum. This will include introductory organismal biology and a course in comparative anatomy and physiology of vertebrates. In addition, the successful candidate will develop and offer an advanced course in their specialty. We welcome candidates with familiarity and/or experience with best practices in inclusive STEM pedagogies to apply.

Applications are due Friday, September 11, 2026 and should be submitted via our application web site (<https://www.wellesley.edu/about-us/working-at-w>

[ellesley](https://www.wellesley.edu/about-us/working-at-wellesley)). Materials must include 1) a cover letter (ca. 1-2 pages), 2) curriculum vitae, 3) a statement of teaching philosophy, experience, and interests, and how those inform your pedagogical practices (ca. 2-3 pages), 4) a statement of research accomplishments and plans for the future including the incorporation of undergraduates (ca. 2-4 pages), and 5) the names/email addresses of three references who will be asked to submit confidential letters of recommendation. Individually, the three letters of recommendation can be from any prior or current component of the candidate's education or experience, but collectively, they should explicitly speak to the candidate's promise for both successful teaching and research.

First-round interviews will be held on Zoom in early to mid-October with campus visits in late October and November. Questions should be directed to the Biological Sciences search co-chairs, John Goss (jgoss@wellesley.edu) and Steven Biller (sbiller@wellesley.edu).

The minimum salary for Assistant Professors is 103,000.00 *annually*.

Company Description: Wellesley's mission is to provide an excellent liberal arts education to women who will make a difference in the world. We advance our mission by working together as a community—faculty, students, staff, and alumnae. Embark on a fulfilling career journey at Wellesley College, where we prioritize your well-being. For those roles that are half-time or greater, we offer a comprehensive array of benefits and resources designed to enhance both your work-life balance and long-term success.

- Exceptional Benefits Package: Access a comprehensive benefits package, including health, dental, vision and pre-tax saving benefits, life insurance, disability coverage (for full-time Faculty), and more to safeguard your health and that of your loved ones.
- Retirement Savings: Plan for the future with our retirement savings plan. Wellesley College contributes up to 10.5-Work/Life and Wellness: Caregiving support through Wellthy, legal plan insurance, pet insurance discount and a variety of other resources including retirement planning, and access to cultural and leisure activities throughout metro-Boston.
- Commuting and Transportation: Enjoy the convenience of free parking on our picturesque campus, easily accessible from major roadways. We are also accessible via the MBTA commuter rail.
- Campus Privileges: Enjoy free use of our state-of-the-art athletic and fitness facilities with onsite fitness classes, Library resources, and seize opportunities to attend diverse campus events that contribute to a vibrant community.

Apply today and take your first step toward a rewarding career with Wellesley College - where your unique strengths and success are celebrated as part of our shared commitment to inclusivity!

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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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Call for papers perennial plants

The American Journal of Botany is publishing a special issue focused on perennial plants, which are understudied despite their importance to many ecosystems. Papers related to the evolution of perenniality, phenotypic plasticity, stress tolerance, aboveground-belowground trait coordination, evolutionary ecology, and any other area of integrative plant biology are potentially good fits for the call. Methods-focused papers targeting Applications in Plant Science are also welcome.

The deadline to propose a paper for the collection is August 31st, 2026. If accepted, the deadline to submit the manuscript will be April 5th, 2027.

Visit this link for more details on the special issue: <https://botany.org/home/publications/ajb/ajb-and-apps-special-issue-call-for-proposals-advancing-restoration-of-natural-and-agricultural-systems.html> Please consider submitting a paper proposal by 8/31!

Very best wishes,

— Maggie R. Wagner, Ph.D. Associate Professor, Department of Ecology and Evolutionary Biology Asso-

ciate Scientist, Kansas Biological Survey & Center for Ecological Research University of Kansas

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EEB Mentor Match

The Diversity Committee of the American Society of Naturalists is once again organizing EEB Mentor Match. eebmentormatch.com

There is a short application window (apps due Aug 17), but the application is only a short form.

Mentees: Get help applying for grad school or fellowships in ecology & evolution (broadly defined to also include animal behavior, marine science, conservation biology, wildlife management, etc.). Learn the hidden curriculum of what works and what not to do from folks who have already trod this path successfully.

Mentors: We're looking for senior grads, post-docs, or faculty in these fields willing to give advice to those looking to apply for grad school or fellowships. The number of mentors is often the limiting step in this process, but it's rewarding "work".

EEB Mentor Match is organized by the Diversity Committee of The American Society of Naturalists, but forever indebted to Samniqueka Halsey (University of Missouri) and Terry McGlynn (Cal State Dominguez Hills) who made it a success!

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ESEB Call Policy and Evolutionary Biology Funds

Policy and Evolutionary Biology (PEB) Funds *Annual Call for Proposals 2026* The ESEB Policy Committee (PC) is excited to launch the first call for proposals that focus on policy and/or societal impact of evolutionary biology research organised by ESEB members. Such activities can include local meetings on policy, societal impact, and related issues as well as actions to influence policy. The typical amount awarded will be EUR 500 - EUR 2,000 per project, although larger amounts may be considered where justified. **Deadline: Wednesday, 30 September 2026, 23.59 UTC** *Eligibility* The funds are available for ESEB members (most applicants on one proposal must be ESEB members before the call's deadline). You can become a member or check your current membership status at the membership website <https://eseb.org/society/eseb-membership/> Further guidance from the committee is outlined in the criteria: PEB Funds Criteria (<https://eseb.org/wp-content/uploads/2026/05/Criteria-for-PEB-Funds-2026.pdf>) *Application procedure* Please download and fill the application form (<https://eseb.org/wp-content/uploads/2026/05/ESEB-PEB-Grant-2026.docx>) and return it as pdf file by ***Sep 30th, 2026 23.59 UTC*** to Dr. Friedrich at the ESEB Office (office@eseb.org) with the subject "PEB Funds Call 2026". Email attachments should not exceed 10 MB. We will acknowledge receipt of all applications within a week. If you have not received our confirmation by then, please contact the ESEB office again! The applications will be evaluated by the Policy Committee Jon Bridle (chair), Rui Faria, John Pannell, Marjo Saastamainen, and Martijn Schenkel *European Society for Evolutionary Biology | Homepage: eseb.org | Email:* (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Genome Project Declaration Survey

The i5k Genome Project Coordination working group needs your insights on genome project coordination! Specifically, we would like to hear what you think about publicly declaring your intent to sequence a genome.

Please take this short (5-10 minute), anonymous survey to help us gather data on how we coordinate genome sequencing: <https://tinyurl.com/4ktj43nv> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Genome Sequencing Intent survey

Dear Evo Enthusiasts,

The i5k Genome Project Coordination working group needs your insights on genome project coordination! Specifically, we'd like to hear what you think about publicly declaring your intent to sequence a species' genome, e.g.

worry! Please find the recording now published on YouTube - <https://youtu.be/CKP0k0nS9DY> Best, Gautham and Leo

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Responsible AI in Academic Research a policy proposal

Hello colleagues

I'm sharing a new open-access policy document that you may find useful: Responsible AI in Academic Research: A Competency Framework for Research Training - <https://instats.org/publications/responsible-ai-in-academic-research> It came from a deceptively simple question: what does "responsible AI use" actually mean at the level of everyday research practice? This seemed like a priority given the substantial AI research training that Instats has been offering since ChatGPT's launch - <https://instats.org/results?nav=On-Demand&view=Seminars>. Over time, the document grew into a survey of AI policy at 38 top-tier doctoral universities across 15 countries, only six of which currently go beyond research-integrity rules into AI literacy and valid research practice. The piece sets out a five-dimension competency framework and a plain-language maturity grid that any department, graduate school, or research office can use to see where it stands today and what a credible next step looks like. A key takeaway is that plagiarism is not the central issue AI raises for research training. The deeper concern is whether research remains valid, and whether our training equips students with the knowledge and skills to conduct it responsibly.

The policy document is written for the people actually making these calls – supervisors, deans, graduate-school directors, and research-integrity committees – and it's free to read, share, and download. Please feel free to pass it along to anyone wrestling with these questions.

Best wishes

Michael Zyphur Professor and Director Instats — instats.org

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Survey on the taxonomic category and the taxa of the highest rank

Dear colleagues,

We would like to invite you to take part in the LPSN survey on high-level taxonomy, which can be found at:

<https://s.surveylegend.com/s/6aa7> The survey is anonymous and will only take a few minutes.

BACKGROUND

The principal categories 'kingdom' and 'domain', which are above the phylum rank, were recently included in the International Code of Nomenclature of Prokaryotes (ICNP). Similarly, official virus nomenclature was augmented by several principal categories, including 'kingdom' and 'realm'. Apparently, 'realm' and 'domain' represent the same principal rank directly above 'kingdom'. If so, the viral hierarchy is compatible with the ICNP and the botanical code, which goes up to the rank of kingdom, and the zoological code, which does not formally regulate these high ranks but mentions 'kingdom' as the highest rank in its glossary. In brief, the sequence of principal

PostDocs

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Aix Marseille Universite-Paris Introgression octocorals

A postdoctoral or engineer position is offered at Aix-Marseille University in population genomics focusing on the role of adaptive introgression for the persistence of marine and terrestrial biodiversity in a context of coastal pollution by past industrial activities. The project HYAM (for "Hybridization and Adaptation in a Mediterranean coastal city") is funded by the A*Midex foundation and started in 2024. HYAM is led by Alex Baumel (IMBE laboratory) and Didier Aurelle (ISYEB laboratory) and brings together several teams offering rich and enthusiastic collaborations at the frontiers of evolutionary biology, ecology, and conservation of biodiversity. Activities: The selected candidate will be responsible for analysing reduced and whole genome sequencing data, and screening their diversity to detect introgression and selection marks. The data will be acquired, allowing the analyses to start as soon as the contract begins. The contract will be focused on octocoral populations. The project will involve a collaboration with the Calanques National Park.

The candidate will benefit from an initial phase of environmental characterization and assessment of the genetic diversity structure of the studied organisms, and of the supports of high-performance computing clusters of OSU Pytheas and IFB. Requirements for the position: The candidate must have a strong background in bioinformatics and population genomics. Experience in the analysis of whole genome data and evolutionary inferences would be an advantage. The candidate must be fluent in written and spoken English. The candidate must not have completed his last degree at Aix-Marseille University. Contract: The contract is for 12 months. The expected starting date is 4 January 2027. Applications must be sent to alex.baumel@imbe.fr and didier.aurelle@univ-amu.fr with CV, covering letter, list of publications, and the email of two referees, from April 1st and no later than June 1st. The selection of candidates will be carried out by a committee from the HYAM project and based on CVs and interviews by videoconference and possibly in person.

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Debrecen Shorebird behavioural and microbial ecology

POSTDOCTORAL POSITION IN SHOREBIRD BEHAVIOURAL AND MICROBIAL ECOLOGY

University of Debrecen, Hungary

We invite applications for a postdoctoral position investigating the behavioural and microbial ecology of breeding and non-breeding shorebirds. The researcher will combine shorebird fieldwork with microbial sampling to investigate the role of migratory birds in spreading antimicrobial resistance.

The position is part of a HUN-REN-funded collaborative project led by Prof. Tamas Szekely and Prof. Sam Sheppard, University of Oxford.

Main responsibilities: - Conduct field investigations of breeding and non-breeding shorebirds - Collect microbiological samples using established field protocols - Analyse ecological, behavioural and microbial data - Lead scientific publications - Contribute to the supervision of MSc and PhD students

Applicants should have:

- A PhD in evolutionary ecology, behavioural ecology, population ecology, disease ecology, microbiology or a related discipline
- Strong quantitative skills and experience using R
- Substantial fieldwork experience
- A bird-ringing licence and full driving licence
- Excellent written and spoken English
- A publication record appropriate to their career stage

The position is based in the Department of Evolutionary Zoology at the University of Debrecen, Hungary. The research group works internationally on shorebird ecology, behaviour, evolution and conservation and collaborates closely with Hortobagy National Park.

Duration: Available immediately until 31 December 2027

Salary: Up to HUF 800,000 gross per month, approximately EUR 2,200. Employer-paid social and health insurance contributions are provided separately.

APPLICATION

Please send: A cover letter describing your research interests and suitability

A CV including a publication list

Contact details for two referees

Applications should be sent to: Ms Rita Nagy nagy.rita@science.unideb.hu

Informal enquiries: Prof. Tamas Szekely T.Szekely@bath.ac.uk

Further information about the research group: www.szekelylab.com (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Harvard PostdocEvolutionaryNeuroscience

Position description: The Department of Human Evolutionary Biology at Harvard University invites applications for a Postdoctoral Fellow in the Evolutionary Neuroscience Laboratory of Dr. Erin Hecht to contribute to neuroimaging, behavioral, endocrine, and genomic analyses in domestic dog breeds. The project seeks to identify evolved change relating to behavior under artificial selection in working dogs. Experience with neuroimaging data collection and analysis, animal behavior, and/or hormone analysis is preferred. This research is non-invasive.

The project is a collaboration with the Kukekova Lab at the University of Illinois Urbana-Champaign. A partnered postdoctoral position in canine behavioral genomics is also available in the Kukekova Lab, and we anticipate opportunities for cross-training and interdisciplinary collaboration.

This is a one-year position, expected to begin in fall 2026, with possibility of renewal dependent upon adequate funding and satisfactory performance. The postdoctoral position is funded through a 4-year grant from Mae Philanthropies.

Location: The research will take place in the Evolutionary Neuroscience Laboratory directed by Dr. Hecht and located in the Peabody Museum on Harvard University's Cambridge, Massachusetts campus. Broadly, the Evolutionary Neuroscience Laboratory studies how brains change in response to selection pressure on behavior, and how brains acquire heritable adaptations for complex, learned behaviors. The lab's websites are: <http://hechtlab.org/> and <http://caninebrains.org>

There will be opportunities for cross-training and interaction with an interdisciplinary research team including

neuroscientists, primatologists, geneticists, and animal behavior scientists. Additional projects and training opportunities can be tailored to suit the candidate's goals and interests, and may include comparative human/nonhuman primate neuroimaging, neuroimaging and behavior studies with experimentally bred foxes, histological analyses of fixed brain tissue, and/or human neuroimaging, behavior and psychological assessments.

Qualifications: A doctoral degree is required for this position. Desired qualifications include research in neuroscience, psychology, neuroimaging, and/or animal behavior. Please submit a letter of interest, an updated CV, and the names of three references at <https://academicpositions.harvard.edu/postings/16417>. Evaluation will begin at the time the advertisement is placed and will continue until the position is filled.

Contact Information: Professor Erin Hecht, erin_hecht@fas.harvard.edu

Salary Range: 67,600–80,000 Pay offered to the selected candidate is dependent on factors such as years of experience, training or qualification, field of scholarship, and accomplishments in the field

Harvard University is an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, sexual identity, national origin, disability status, protected veteran status, or any other characteristic protected by law.

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Helsinki Finland Ecological Evolutionary Genomics 3positions

Three post-doc positions in salmonid fish ecological and evolutionary genomics and conservation The University of Helsinki is an international scientific community of 40,000 students and researchers. It is one of the leading multidisciplinary research universities and ranks among the top 100 international universities in the world, and 8th in the world in Ecology. We are an equal opportunity employer and offer an attractive and diverse workplace in an inspiring environment with a variety of development opportunities and benefits. The Faculty of Biological and Environmental Sciences is Finland's largest and most high-profile and extensive hub

of research and teaching in the field. The Faculty educates experts to meet the needs of universities, research institutes, government, schools and the business sector. ***The positions*** Up to three post-doctoral positions are available at the University of Helsinki, Finland working in the research groups of Prof. Craig Primmer and Dr. Tutku Aykanat (<http://www.helsinki.fi/evolution-conservation-and-genomics>) as a part of several related research consortia funded by the Research Council of Finland, the Kone Foundation and the ERC, with a focus on using the well studied Teno Atlantic salmon system as a model for adaptive management to assess biological and societal effects of recent anthropogenic changes on the Atlantic salmon metapopulation, alongside a detailed genetic and ecological evaluation of Pink salmon invasion in the river basin and the greater region. Successful applicants will likely have a strong background in research related to at least one of the themes listed below, but the specific combination of expertise is flexible, with the overall composition of the team being most important. ***Effects of management and ecosystem-related changes on salmon life-history phenotype and genotypes*** Evolutionary genomic approaches for assessing the effects of recent fishing management changes and invasive Pink salmon abundance on life-history phenotypes and genotypes. Relevant consortium publications: Erkinaro et al. 2019; Czorlich et al. 2018, 2022 ***Assessing sex-specific natural selection effects at key life-history loci due to anthropogenic and environmental factors*** Use of long-term data on Teno salmon reproductive fitness to assess potential sex-specific effects of recent fishing management changes and invasive Pink salmon abundance selection on Atlantic salmon life-history traits Relevant consortium publications: Czorlich et al. 2018; Mobley et al. 2019, 2020, 2024 ***Pink salmon genetics: determining the genetic basis of successful invasion*** Use of long-term scale material to identify genomic regions and structural variation potentially associated with higher invasion success. Relevant consortium publications: Erkinaro et al. 2026 ***Instructions for applying*** Appointees to the positions shall hold a doctoral degree and have the ability to conduct independent scholarly work. Suitable applicants will likely have a strong background in at least some of the themes and approaches listed above, although the species/system with which they have experience is less important. The ability to work as a part of a larger multidisciplinary research team addressing related questions is also important. Informal inquiries can be directed to Professor Craig Primmer (craig.primmer@helsinki.fi) and Dr. Tutku Aykanat (tutku.aykanat@helsinki.fi).

Formal applications should include as a single pdf file:

- a CV including a list of publications and with names and contact details of at least two referees - an approx. 1 page letter of motivation that includes specification of the theme (or themes) you are most interested in To apply, please submit your application via the University of Helsinki electronic recruitment system https://jobs.helsinki.fi/job/Helsinki-Tthree-post-doc-positions-in-salmonid-fish-e-cological-and-evolutionary-genomics-and-conservation/1365060357/?feedId=350602&utm_source=CareerSite_UniversityOfHelsinki by clicking on the Apply now button. If you need technical support with the recruitment system, please contact recruitment(at)helsinki.fi.

The deadline for applications is 23:59 EEST on 7.8.2026 and remote interviews of short-listed candidates are planned for 17-21.8.2026. The positions are available from 1.9.2026 but start dates up to mid 2027 will be considered (although an earlier start is preferred). Positions are available for up to three years, with continuations dependent on obtaining additional funding. ***Salary***

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Italy InvasiveSpecies eDNA Morphometrics

Dear EvolDir members, a new one-year research position to join my lab at the University of Catania, in sunny Sicily (Italy), has just been officially advertised, funded by the Interreg Italia-Malta project RECLAIM on invasive alien species. The search is broadly defined in terms of ideal background and, while the project itself is on invasive species, there is substantial opportunity to develop research in various directions. The official call (in Italian) is at <https://www.unict.it/ibt/bandi/ricerca/borsa-di-ricerca?k=9917> and a short write-up on the position is available on the lab's website at <https://www.fruciano.org/events/were-hiring-again/> The deadline for applying is August, 3rd 2026. Please note that I cannot accept applications directly via email, as applications are only accepted through the official channels outlined in the call. I am,

however, available for further clarifications in case there are questions not clarified on the write-up on the lab website. Best regards, Carmelo Fruciano

Carmelo Fruciano Department of Biological, Geological and Environmental Sciences University of Catania <https://www.fruciano.org/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

KewGardens London UK ElmGenomics

Hello,

We are seeking a postdoctoral research associate to conduct genomic analyses of elms affected by Dutch elm disease. The project will involve fieldwork, sample preparation, processing large sequence data and statistical analyses using computing clusters.

- PhD or equivalent in a relevant subject area (e.g. evolutionary biology, bioinformatics, genomics, population genetics) - Expertise in de novo genome assembly, analysing RNAseq data and genome annotation, phylogenomic analyses, building pangenome, and use of computing clusters - Experience of coding in a relevant programming language (e.g. Python, R) and of shell/Unix scripting - Experience of publishing research results in peer reviewed scientific journals - Experience of presenting research results to the wider scientific community and stakeholders at conferences or workshops

This role is based at Kew with the option of regular home working, subject to operational requirements. Hours of work: Full time Contract Type: Fixed Term (FTA) Contract start date: Provisionally September 2026 Contract end date: 2 years from start date Salary: GBP39,243 - GBP42,153 per annum [Band D] Location: Kew Gardens, Richmond, Hybrid Closing Date: 26/07/2026

The Royal Botanic Gardens, Kew (RBG Kew) is a leading plant science institute, UNESCO World Heritage Site, and major visitor attraction. Our mission is to understand and protect plants and fungi for the well-being of people and the future of all life on Earth.

To read more and apply from the following link:

<https://careers.kew.org/vacancy/postdoctoral>

[-research-associate-pdra-615109.html](#)

The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, United Kingdom.

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SLU Uppsala Sweden Ash Resistance Pangenomics

Postdoctoral Position: Harnessing the Full Range of Resistance in Ash Through a Pan-European Pangenome

The Yant Lab at the Swedish University of Agricultural Sciences (SLU) in Uppsala, Sweden, is recruiting a postdoctoral researcher to join a new project investigating the genomic basis of resistance in European ash (*Fraxinus excelsior*). The project will build a pan-European pangenome and apply population genomics to identify and understand naturally occurring resistance to ash dieback, with the goal of supporting resilient forest restoration.

Applicants with expertise in evolutionary genomics, population genomics, bioinformatics, plant genetics, forest genetics, or related fields are encouraged to apply.

Location: Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden

Full advertisement and application details: <https://www.slu.se/en/about-slu/work-at-slu/jobs-and-vacancies/postoc-harnessing-the-full-range-of-resistance-in-ash-through-a-pan-european-pangenome/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Spain AuSpire Postdoctoral Opportunities Application Deadline Monday 7 September 2026

Dear Sir or Madam,

We are pleased to announce the third and final call for applications to the Australia-Spain Network for Innovation and Research Excellence (AuSpire), a postdoctoral network co-funded by the European Union. In the final recruitment call, we are advertising five postdoctoral positions based in Spain related to: Bioinformatics; Biology; Metabolic Diseases; Neurobiology; Immunometabolism; Microbiome and Gut-Brain Axis; Underwater Laser Communications; Optical Systems Engineering; Chemical Engineering; Drinking Water Quality Production; Population and Comparative Genomics. Benefits of joining the AuSpire Program include: - Full-time employment in Spain for 36 months (3 years) with excellent conditions - A competitive salary, including a relocation mobility allowance - Up to 12 months international/intersectoral secondment in Australia or Spain - Participation in an international research environment centred on Planetary Wellbeing - An innovative research training program - Collaboration with industry leaders - A sustainable and collaborative research community - Engagement in projects with significant societal and commercial value - Family allowances to ensure equal opportunities for Postdoctoral Fellows with families We are looking for outstanding researchers from around the world who have not resided or carried out their main activity in Spain for more than 12 months in the past 3 years and who hold a PhD. Successful applicants are expected to start in January 2027. The call for applications is open from 1 July 2026 until 7 September 2026. For more information, please visit the AuSpire website [auspire.eu](https://www.auspire.eu) and connect with us on LinkedIn (<https://www.linkedin.in/company/auspire-program/>), Facebook (<https://www.facebook.com/auspire.eu/>) and Instagram (<https://www.instagram.com/auspire.eu/>). We

encourage you to share this information with your networks. Kind regards, Maela (on behalf of AuSpire Program Management Team).

AuSpire Program Management Team Australia-Spain Network for Innovation and Research Excellence — AuSpire Phone: +34-935 47 77 15 Email: auspire@rmit.edu.au Cornerstone Complex Building A, Floor 1, Eurecat c/Bilbao 72, 08005, Barcelona (Spain) www.auspire.eu (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

StonyBrookU Evolutionary Genomics and Conservation Genetics

Postdoctoral Associate in Evolutionary Genomics and Conservation Genetics

Location: Stony Brook, NY, USA Duration: 2 years initial Salary: 61,000–65,000 (based on experience) Target Start Date: flexible, as soon as September 2026

A two-year postdoctoral position is available in the laboratory of Dr. Sheila Kitchen (<https://www.sheilakitchen.com/>) in the Department of Ecology and Evolution at the Stony Brook University. We seek a postdoctoral candidate at the intersection of molecular ecology, evolutionary genomics, and bioinformatics. The successful candidate will split their time between two core research areas: (1) investigating the evolutionary genomics and symbiosis dynamics of cnidarians, and (2) managing the deployment and development of STAGdb (Standard Tools for Acroporid Genotyping Database). The candidate will also be encouraged to develop and pursue their own areas of research interest. The candidate will conduct original research, write manuscripts for publication, participate in professional meetings, and collaborate with faculty and graduate students at Stony Brook University and the Marine Conservation Group led by Dr. Iliana Baums at the Helmholtz Institute for Functional Marine Biodiversity (<https://baumslab.org/>).

Applicants must hold a Ph.D. in marine biology, genomics, computational biology, evolutionary biology, or a closely related field. They should possess a strong track record of research productivity as evidenced by peer-reviewed publications, alongside proficiency in R and at least one scripting language such as Python. Ad-

ditionally, a proven record of managing and analyzing large-scale genomics or population genetics datasets is required. The ideal candidate will demonstrate both the ability and the willingness to work independently as well as collaboratively, and they must be comfortable working in both laboratory and field environments. Finally, excellent written and oral English communication skills are essential for this role.

Additionally, applicants with a strong background in evolutionary genetics/genomics, specifically using genomic approaches to analyze introgression, clonal diversity, and/or host-symbiont associations. Experience developing, scaling, or maintaining workflows within the Galaxy platform or similar bioinformatics workflow management systems is highly desirable. It is also beneficial to have experience querying and managing relational databases, including handling SQL queries and database syncing routines will be valuable to these projects. Lastly, familiarity with the biological challenges of cnidarian-algal symbioses such as co-analyzing host and symbiont data is considered an asset but not required. How to Apply: <https://stonybrook.edu/leo.net/careersection/2/jobdetail.ftl?job=2602622> First review date: 27 August 2026 Include 1) a cover letter (2-pg max) that includes your research experience and interests, future research and career goals and your preferred start date, 2) names and contact information of three references, including your current supervisor, and 3) a CV. Applications will be reviewed until the position is filled. Position can begin as early as September 1, 2026, and no later than January 1, 2027. Salary commensurate with the NIH postdoctoral scale with a benefits package. This is a two-year appointment with the potential for extension, contingent upon satisfactory performance.

Inquiries about the job can be made by email to sheila.kitchen@stonybrook.edu

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UCaliforniaLosAngeles ConservationScience

The 2027 UCLA La Kretz Center Postdoctoral Fellowship in California Conservation Science

The UCLA La Kretz Center for California Conservation Science invites applications for its 2027 Postdoctoral Fellowship in California Conservation Science. Each

year, we hire one or more postdoctoral scholars who conduct innovative biological research at the interface of applied and basic science. Our long-term goal is to help fund a cadre of innovative young scientists who will work closely with UCLA faculty, help broaden the mission of conservation science for the campus, and lead to long-term collaborations between our academic scientists and applied conservation practitioners that will direct and lead California conservation efforts.

Candidates may work in any discipline that provides the scientific underpinnings for the preservation, protection, management, or restoration of at-risk species, environments, or ecological communities in California. Current and past La Kretz Postdocs have worked on a wide variety of research topics, ranging from urban biodiversity and evolutionary adaptation, to wildfire management and conservation, to the interface of conservation and animal behavior; we are open to work in any California ecosystem or group of organisms, as long as the research is innovative, creative, and has clear practical significance. An important initiative, the California Conservation Genomics Project (CCGP), is a large, multi-campus initiative led by the La Kretz Center that is delivering genomic resources to California decision-makers to enhance species and habitat management, and candidates may seek to build off of that project in the realm of conservation genomics. For a full description of past fellows and their work, please visit us at <https://www.ioes.ucla.edu/lakretz/>. Fellows must have both an on-campus UCLA mentor, and an off-campus, non-university mentor. The on-campus UCLA mentor must also be a La Kretz Center affiliate. A list of applicable affiliates is available at <https://www.ioes.ucla.edu/lakretz/people/>. The Fellow is expected to work closely with their identified UCLA mentor and one or more off-campus agency partner(s) in developing their project proposal. All applications should include a letter (which may be brief) from each mentor stating their support for the project, what they can contribute to it, and how it fits into their work in conservation biology. Applications that do not include these letters of support will be considered incomplete and ineligible for consideration, and we strongly advise candidates to secure mentor support as early as possible. While we encourage project proponents to identify co-funding, from mentors or other agencies, co-funding is not a requirement. Off-campus mentors may be drawn from any California-focused agency or NGO, including federal and state groups. A partial list of some of our active partners and contact people includes:

The Nature Conservancy: Sophie Parker (climate adaptation and mitigation, nature-based solutions, desert

wetland ecology) Note: TNC has been a particularly active partner and co-funder in recent years, and we encourage applicants interested in working with TNC mentors to consult: <https://tnc.box.com/shared/static/mpnsvure3vmf29xgpnrn00wl3t5me9l.pdf> Natural History Museum of Los Angeles County: Jann Vendetti (mollusk ecology and evolution; species natural history)

US Geological Survey: Robert Fisher (applied conservation; biodiversity; ecology and evolution)

US Geological Survey: Damian Higgins (research manager, western ecological research center)

US Bureau of Land Management: Mike Westphal (applied conservation, climate change)

US Fish and Wildlife Service: Cat Darst (endangered species management)

Natural Communities Coalition: James Sulentic/Danny L. Fry (protection/recovery of sensitive species)

National Park Service: Katy Delaney (amphibian and avian ecology, evolution, and conservation)

National Park Service: Seth Riley (mammalian ecology, evolution, and conservation)

The La Kretz Fellowship is for two years, subject to review after the first year. The target start date is September 2027, but this date is quite flexible. The position offers a competitive salary, full benefits, and a research/travel allowance of 7500. *Candidates who have recently completed their Ph.D. or will have completed their Ph.D. by the start date are eligible.*

To apply, please send applications to lakretz@ioes.ucla.edu as a single PDF file that includes:

- (i) Cover Letter: Briefly introducing yourself and your project
- (ii) CV: Composed of your work and accomplishments.
- (iii) Research and Management Accomplishments Statement (maximum one page)

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UCambridge Postdoc in Bat Immunity

Postdoctoral Research Associate in Bat Antiviral Immunity Location: Cambridge, UK Salary: GBP 37,694 - GBP 46,049 Contract: Fixed-term for 18 months in the first instance Start date: 1 September 2026, or as soon as possible thereafter Closing date: 29 July 2026 Reference: PP50380 The Department of Veterinary Medicine at the University of Cambridge invites applications for a BBSRC-funded Postdoctoral Research Associate position in the laboratory of Professor Clare Bryant. The project aims to elucidate the molecular mechanisms underlying antiviral immunity and immune regulation in bats. The main focus will be the functional characterisation of ancestral and lineage-specific variants of the innate immune genes NLRP3, MyD88 and STING. Collaborating research groups have reconstructed ancestral versions of these genes and identified lineage-specific amino-acid substitutions of particular interest. The successful candidate will investigate the functional consequences of these variants in human and bat cell systems. Gene variants will be introduced using plasmid transfection, lentiviral transduction or CRISPR-mediated genome modification, followed by functional analysis of innate immune signalling. Applicants should have, or be close to completing, a PhD in cell biology, biochemistry, evolutionary biology or a related discipline. Experience in cell culture and molecular cloning is essential. A good understanding of innate immunity and knowledge of evolutionary bioinformatics would be advantageous. Experience with lentiviral transduction, CRISPR-mediated genome modification or functional immune assays would also be beneficial. The successful candidate will join a collaborative and interdisciplinary research environment and should value teamwork and cooperation. Good organisational, administrative, interpersonal and presentation skills are also required. The appointment is fixed-term for 18 months in the first instance and is available from 1 September 2026, or as soon as possible thereafter. Full details and online application: <https://www.cam.ac.uk/jobs/research-associate-fixed-term-pp50380> Informal enquiries about the position may be directed to Julie Ingham at ji217@cam.ac.uk. Applicants should submit a completed CHRIS/6 form, a curriculum vitae, a covering letter outlining their suitability for the role, and contact details for two referees. Applications must be

submitted through the University of Cambridge online recruitment system. Please quote reference PP50380 in your application and in any correspondence concerning the vacancy. Interviews are expected to be held during the week commencing 24 August 2026. Enquiries about the application process may be directed to hr.enquiries@vet.cam.ac.uk. The University of Cambridge actively supports equality, diversity and inclusion and encourages applications from all sections of society. The University is committed to promoting an inclusive culture and valuing diversity. The University has a responsibility to ensure that all employees are eligible to live and work in the United Kingdom.

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UCLA USA Evolutionary Genomics HybridZones

Postdoctoral Researcher at the University of California, Los Angeles

Location: Los Angeles, CA, USA Duration: 2 years initial Salary: 71,491–85,736 (based on experience) Target Start Date: flexible, as soon as October 2026

How to Apply: <https://recruit.apo.ucla.edu/JPF11142> First review date: 8 August 2026

Dr. Stepfanie Aguillon in the Department of Ecology and Evolutionary Biology at UCLA invites applicants for a full-time Postdoctoral Scholar. This position is an in-person two-year appointment, contingent upon satisfactory performance after the first year, with a flexible start date as early as October 2026.

Research in The Aguillon Lab focuses on understanding the speciation process through the use of genomic datasets collected from the field and natural history collections. Ongoing research leverages hybridizing bird systems, which provide natural experiments that test the boundaries between closely related species.

The successful candidate will analyze whole genome sequencing datasets from a North American woodpecker hybrid zone to characterize patterns of introgression and selection, and connect genomic variation to phenotypic and environmental variables. The position involves analyzing existing data, leading publications, writing grants, and potentially collecting new data in the molecular lab and field. In addition to working

with existing sequencing data, the postdoc will have the flexibility to develop independent research projects and collaborate with other lab members: including working with long-read genomic sequencing for the study of genomic structural variation and collecting phenotypic data from museum specimens to study coloration.

The ideal candidate will have an interest in the study of speciation and hybridization. They will have strong bioinformatic coding skills for the study of genomic datasets from birds and/or hybrid zones and molecular lab and/or field experience. Importantly, the ideal candidate will have an interest in joining a new and growing lab community. Potential candidates are encouraged to read more about The Aguillon Lab before applying: www.stephanieaguillon.com Basic qualifications: - PhD in evolutionary biology, ecology, genomics, or a related field by appointment start date - Demonstrated ability to work with genomic datasets - Strong writing skills with a record of peer-reviewed publications - Ability to lead independent projects and work collaboratively as a team

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UF Evolution of Organs and Cell Types

Postdoc Position in Evolutionary and Developmental Genetics

A postdoc position is available in the Hopkins Lab at the University of Florida. The successful candidate will use computational and experimental approaches to study the evolution of organs and cell types.

Our research seeks to understand the genetic mechanisms and evolutionary pathways through which organs originate and diversify through time. We take a comparative approach, using patterns of evolutionary diversification across species to uncover general principles of biological design that shape organ architecture, function, and evolution. Much of our work focuses on *Drosophila*, moving beyond *melanogaster* as a model organism to develop the wider *Drosophilidae* family and its ~4000 morphologically, ecologically, and behaviourally diverse species as a model clade. But we are also starting to branch out into other insect and vertebrate groups. In pursuit of this work, we make use of a wide range of computational and experimental ap-

proaches, including gene regulatory network inference, comparative genomics, genome editing, and single-cell 'omics. Over time, postdocs will be provided with support to develop an independent research program that aligns with the lab's broad interests in evolutionary and developmental genetics.

The Hopkins Lab is based at the University of Florida, which is consistently ranked as one of the top public universities in the US. The lab is housed in UF's Genetics Institute, a cross-departmental institute that brings together a wide variety of researchers with interests in genetics. Our corridor is home to groups working on evolutionary biology, comparative genomics, developmental biology, and functional genetics in both model and non-model animal systems, opening up rich opportunities for interactions and collaboration with like-minded researchers. Our building also houses UF's biotechnology core, complete with state-of-the art imaging suites and sequencing facilities. Gainesville itself is a vibrant college town with a lively nightlife and live music scene, and offers easy access to Florida's diverse natural landscapes—from crystal-clear springs and pine forests to wetlands and the white sandy beaches of the coast.

Start date is flexible. Multi-year funding is available from start-up funds.

If interested, please contact Ben Hopkins (br.hopkins@ufl.edu) with a CV, a statement of research interests and experience, and the names of three references.

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UGoettingenGermany PostdocPermanent

Dear colleagues,

I would like to draw your attention to an exceptional career opportunity offered at the University of Göttingen in Germany. We are currently looking for candidates that have the potential to successfully apply for an ERC grant or the Emmy Noether program. If successful, the applicant will subsequently receive a permanent, 100

The research topic for the proposal must relate to Forest Sciences in a broad sense, which also includes the evolution of forest species (both plants and animals), or even wildlife ecology, management, or genetics/genomics, provided that some link to, or relevance

for, forestry or forest ecosystems can be demonstrated. Please see <https://www.uni-goettingen.de/de/644546.html?details=76508> for more details and note the application deadline of August 15th.

For any general questions related to this position, please contact my colleague Prof. Dr. Alexander Knohl (email: bioklima-job@uni-goettingen.de) with subject "Forst-Talent Fellowships".

If your proposal ideas for this position relate to wildlife, and you would like feedback on these ideas, feel free to contact me.

Kind regards Niko

Niko Balkenhol, Ph.D. Professor of Wildlife Management Dept. of Wildlife Sciences Faculty of Forest Sciences and Forest Ecology University of Goettingen nbalken@gwdg.de

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ULa Rochelle France Cancer Resistance in Wild Mammals

Postdoctoral Position in Cancer Resistance in Wild Mammals The WICANE team (wicane.recherche.univ-lr.fr) is seeking a motivated and innovative postdoctoral researcher to join a project aimed at understanding why some wild mammal species exhibit remarkable resistance to cancer. Cancer remains one of the leading causes of death in modern human societies, with nearly one in two people developing the disease during their lifetime. Despite decades of research and significant investments, cancer continues to pose a major challenge to prevention and treatment, indicating the need for new perspectives in cancer research. One fundamental, but informative track could be the exploration of why some animal species develop very few, or no cancer at all, especially despite their long lifespans and extensive cell numbers, which are expected to exacerbate their risk of malignant transformation? This question offers a unique opportunity to discover new natural mechanisms of cancer resistance. Over millions of years of evolution, nature has repeatedly found effective solutions to suppress cancer. By studying species that appear naturally protected, we can uncover the mechanisms that eliminate abnormal cells or prevent tumor development, and ultimately translate these dis-

coveries into strategies that may improve cancer prevention and treatment in humans. The WICANE team addresses this challenge through two complementary approaches. The first approach involves large-scale comparative studies to explore the variation in cancer prevalence across a broad range of vertebrate species. This includes analyzing phylogenetic patterns to identify evolutionary trends associated with cancer resistance. We combine large scale physiological and life-history databases with comparative genomics and bioinformatic approaches to identify the key traits, genes or pathways that predict cancer resistance. These studies help to uncover macroevolutionary patterns in cancer resistance and generate candidate mechanisms for subsequent functional validation. The second approach focuses on small number of exceptionally resistant species, such as whales, the blackbuck, the Greenland shark, or the Patagonian mara. Using established primary cell cultures and in vitro and in vivo functional assays, we investigate how cells of these remarkable species maintain genome stability with such high efficiency, for example through enhanced protection against DNA damage or more effective DNA repair. The project aims to systematically study the extent of cellular transformation and cellular response to carcinogenic stressors, such as ionizing radiation, radiomimetic compounds, oxidative stress, and other DNA-damaging agents. By comparing these responses to those observed in more cancer-prone organisms, we seek to identify the cellular and molecular mechanisms that limit malignant transformation and preserve tissue integrity throughout life in cancer resistant taxa. We are looking for a postdoctoral researcher with expertise in one of the two complementary approaches described above. The successful candidate may choose to focus primarily on either approach, depending on their background and interests. For the large-scale comparative studies, we seek a candidate with a strong background in evolutionary biology. Experience in biostatistical analyses, including phylogenetic modelling, comparative genomics and bioinformatic analyses, the integration of large-scale databases, and a good understanding of animal physiology and cancer biology would be an advantage. For the functional studies in highly resistant species, we are interested in candidates with experience in maintaining primary cell cultures, in vitro and in vivo functional assays, DNA damage and repair assays. Experience in bioinformatics, transcriptomic, proteomic and epigenomic profiling, as well as comparative analyses of cellular responses to carcinogenic stressors would be an advantage. Experience in both approaches would be a significant advantage, as it would allow the candidate to contribute comprehensively to the project's objectives by bridging evolutionary insights with func-

tional validation. The postdoc will primarily work at LIENSs (Universite de La Rochelle, France), but some experimental work may also be carried out in the laboratory of Mauro Modesti at the CRCM (Marseille), a comprehensive research center focused on cancer. More information about the CRCM can be found here : <https://crcm-marseille.fr/en/> Please also see: <https://crcm-marseille.fr/en/genome-integrity-department/homologous-recombination-nhej-and-genomic-integrity/>

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Umea Sweden EvolutionaryImmunology TheoreticalBiology

Postdoctoral fellowship/scholarship in evolutionary immunology and theoretical biology Umea University, Sweden A 2-year interdisciplinary postdoctoral fellowship/scholarship is available through the IceLab Interdisciplinary Postdoctoral Programme at Umea University, Sweden. Our project, listed as Project C in the joint advertisement, is titled: Adaptive immunity as an evolutionary response to unforeseen stress Why did adaptive immunity evolve despite its enormous biological costs? This project will explore adaptive immunity as an evolutionary strategy for coping with uncertain future pathogenic threats. Adaptive immune systems generate diverse receptor repertoires and immune memory, but require substantial energetic investment, large immune cell populations, and mechanisms to avoid self-reactivity. The project asks under which ecological and evolutionary conditions such complex anticipatory defense systems become advantageous, and why immune systems differ so dramatically across species. The fellowship is suitable for candidates interested in evolutionary biology, theoretical biology, mathematical modeling, computational biology, complex systems, immunology, host-pathogen interactions, stochastic processes, dynamical systems, or control theory. The postdoctoral researcher will have the opportunity to develop mathematical and computational models of adaptive immune evolution, investigate trade-offs between immune protection and biological costs, and work in the

interdisciplinary environment of IceLab at Umea University. The project is a collaboration between: Ryo Morimoto Department of Molecular Biology and Molecular Infection Medicine Sweden (MIMS), Umea University ryo.morimoto@umu.se Eric Libby Department of Mathematics and Mathematical Statistics and IceLab, Umea University eric.libby@umu.se The full advertisement and application information are available here: https://www.umu.se/en/work-with-us/post-doctoral-scholarships/three-multidisciplinary-postdoctoral-scholarships-2-years-_950146/ Application deadline: 17 September 2026 Candidates should apply through the official Umea University advertisement and indicate interest in Project C.

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UmeaU Mathematical Modeling the Evolution of Endosymbioses

Postdoc in Mathematical Modeling the Evolution of Endosymbioses

We are happy to announce a Kempe-funded postdoctoral fellowship available for a start date sometime in late 2026 or early 2027. The position is available for two years and will be based at Umea University's interdisciplinary center IceLab in the research group of Eric Libby and also affiliated with the Department of Mathematics and Mathematical Statistics at Umea University. Candidates should have a quantitative background with an interest in analyzing mathematical models of biological systems. Below we provide descriptions of the postdoc and the required qualifications. Importantly we note that this call is completely open and interested candidates should apply.

Overview:

Endosymbiotic relationships have fueled the evolution of complex life. Indeed, the entire eukaryotic lineage—which includes all animals, plants, and fungi—owes its existence to an endosymbiosis between a bacterium and an archaea. Yet, a wealth of recent scientific studies have shown that endosymbioses are not part of an inexorable path to complexity; rather they are fluid such that relationships can form and dissolve. For many organisms, their evolutionary history is marked by repeated gains and losses of different endosymbionts. The consequences of these repeated ventures into en-

dosymbioses are largely unknown, and there are many substantial open questions, such as what determines whether relationships persist or fall apart? The answers to such questions have important consequences for our understanding of evolution as well as how species adapt to changing environments—since many species, e.g. insects and corals, are dependent on endosymbioses for survival.

Within the project the postdoctoral fellow will have the opportunity to address these questions using mathematical modeling (featuring dynamical systems and metabolic models) under supervision of project leader, Eric Libby at Umea University. The postdoctoral fellow will be based in the interdisciplinary research environment IceLab and will be part of an active research team using mathematical models to study microbial evolution.

The postdoctoral fellow will be hosted by the Department of Mathematics and Mathematical Statistics and will be located at IceLab, a research centre of excellence. The postdoctoral scholarship is financed and administered by the Kempe Foundation (JCSMK261-0049). The tax-free scholarship will be SEK 750,000 for two years, which means SEK 375,000 per year.

Qualifications:

To qualify as a postdoctoral scholarship holder, the postdoctoral fellow is required to have completed a doctoral degree or a foreign degree deemed equivalent to a doctoral degree. This qualification requirement must be fulfilled no later than at the time of the decision about scholarship recipient.

Priority should be given to candidates who completed their doctoral degree, according to what is stipulated in the paragraph above, no later than three years prior. If there are special reasons, candidates who completed their doctoral degree before that may also be eligible. Special reasons include absence due to illness, parental leave, appointments of trust in trade union organisations, military service or similar circumstances, as well as clinical practice or other forms of appointment/assignment relevant to the subject area.

The doctoral degree should be within the field of mathematical biology, evolutionary biology, or applied mathematics, or be deemed to provide equivalent academic competence.

Oral and written skills in English are required. Skills in a numerical programming language such as MATLAB, Python, or Julia are also a requirement.

Experience applying mathematical models such as dynamical systems approaches or metabolic models to bi-

ological systems or questions is desired. Documented knowledge and experience working in the field of endosymbiosis, evolution, microbiology is also a desired qualification. Candidates with successful experience collaborating and working on interdisciplinary research projects are preferred.

Apply:

The application deadline is August 30, 2026. Please apply using the link in the official ad: https://www.umu.se/en/work-with-us/postdoctoral-scholarships/postdoctoral-scholarship-2-years-within-mathematical-modelling-of-endosymbioses_944778/ Questions:

If there are any questions please contact Eric Libby at jeric.libby@umu.se

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UMissouri Postdoc in Animal Behavior

Hiring Department: The Goyes Lab in the Division of Biology in the College of Arts & Science.

Job Description: The Goyes Lab (goyeslab.org) in the Division of Biological Sciences at the University of Missouri is recruiting a postdoctoral researcher to join a dynamic research program focused on the reproductive behavior and ecology of Belostomatidae (water bugs) in Missouri, with an emphasis on parental care behavior.

The successful candidate will contribute to various research themes in the lab, focusing on the evolution of mating systems, sexual selection, parental care, and intersexual communication. They will conduct research on *Belostoma* species that exhibit parental care in Missouri, with opportunities to explore acoustic and vibrational communication, social behavior, and reproductive strategies.

The preferred start date for this position is September 1, 2026. Funding is available for up to two years; the initial appointment is for one year, with the possibility of renewal contingent on satisfactory performance.

This position is mentored by Dr. Johana Goyes Vallejos, whose research investigates how ecological, behavioral, and life-history factors shape the evolution of parental care. The lab integrates animal behavior, bioacoustics,

morphology, and ecology. We are committed to building a curiosity-driven research environment.

Responsibilities:

The postdoctoral researcher will join an active research community with opportunities to lead and collaborate on new research directions, gain mentoring experience, and contribute to grant development. The postdoctoral researcher is expected to contribute to a collaborative lab culture and to engage in outreach and professional development activities.

This position involves extensive fieldwork with wild animals and requires a strong interest in field-based research. Enthusiasm for working outdoors in the Midwestern United States is essential. Fieldwork may involve long hours in wetlands and forested habitats under challenging environmental conditions, including heat, humidity, wading ponds, biting insects, and unpredictable weather. An appreciation for Midwestern ecosystems and comfort working in remote outdoor settings are important for success in this role.

The postdoctoral researcher will also be responsible for establishing and maintaining a laboratory colony of water bugs, designing, and conducting behavioral experiments, collecting, managing, and analyzing data, and disseminating research through peer-reviewed publications.

Research activities are driven by seasonal animal behavior and environmental conditions, and therefore, periods of intensive fieldwork may involve night and weekend work, extended field hours, and flexible scheduling during peak activity periods. Candidates should be comfortable with dynamic and time-sensitive field research.

Candidates must be willing and able to drive to and from field sites; a valid driver's license is required.

Qualifications:

- Ph.D. in biology, organismal biology, ecology, evolution, animal behavior, or a closely related field.
- Demonstrated expertise in behavioral ecology, particularly in collecting and scoring animal behavior data.
- Excellent organizational, analytical, and writing skills, with a strong publication record (appropriate to their career stage) in animal behavior and/or entomology journals, demonstrating the ability to bring projects to completion.
- Quantitative/data analysis skills. (e.g., R or similar).
- Available to work flexibly during hours that will include nights and weekends during the field season.
- Interest in mentoring student researchers and contributing to a collaborative laboratory environment.

Preferred Qualifications:

- Experience with fieldwork, establishing and maintain-

we will reconstruct the evolutionary history and speciation dynamics of this radiation while investigating the roles of polyploidy and hybridisation in adaptation and speciation. The ideal applicant will be a highly motivated and independent bioinformatics researcher interested in understanding the evolutionary dynamics of allopolyploid organisms. Our study system—Labeobarbus fishes from Lake Tana—is allohexaploid, presenting exciting computational and evolutionary challenges. The complexity of this reference genome requires someone with strong bioinformatics expertise, excellent problem-solving skills, and a willingness to develop new analytical approaches. The successful candidate will work closely with me, with responsibilities including: Genome and homoeologue annotation of a high-quality genome assembly. Homoeologue-aware phylogenomic reconstruction of the Lake Tana species flock. Collaborating with two PhD students on population genomics and hybridisation analyses. Requirements Essential - Background in bioinformatics, evolutionary genetics, genomics, or a closely related field. - Extensive experience working in Linux environments and on high-performance computing (HPC) systems. - Strong programming skills in R and/or Python. - Extensive experience analysing large-scale genomic datasets (HiC, PacBio HiFi and IsoSeq, Illumina Novaseq), and using bioinformatics tools. - Demonstrated ability to solve complex bioinformatics challenges through code development and/or methodological innovation. - Good knowledge of orthology inference, phylogenomics, and associated analytical methods. - Ability to work independently while collaborating effectively and respectfully with colleagues from diverse backgrounds. - Excellent written and spoken English. - Strong organisational, communication, and teamwork skills. Desirable - Experience working with allopolyploid genomes. Application Please submit a single PDF file named: `FirstNameSurname_UBern_postdoc2026.pdf` The PDF should contain the following documents in order : 1. Letter of motivation (maximum two pages) describing your research experience, your interest in this position, and how it aligns with the subject line: "Postdoc application Labeobarbus" The application deadline is 31 July 2026 (23:59 GMT+1). Salary Salary will be determined according to the University of Bern salary scheme for post-doctoral researchers. Diversity and Inclusion Diversity, equity, and inclusion are core values of our team. We especially encourage applications from women, people of colour, individuals from the Global South, and others who are underrepresented in bioinformatics and computational biology, particularly those who experience multiple intersecting forms of marginalisation. Further Information For informal inquiries, please contact: Dr. Pooja Singh pooja.singh@unibe.ch More information about my research can be found at: <https://poojasinghevogen.weebly.com> The successful candidate will be based jointly at the Division of Aquatic Ecology & Evolution, University of Bern, and the Department of Fish Ecology & Evolution, Swiss Federal Institute of Aquatic Science and Technology (Eawag).

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UniFreiburg Germany Evolutionary Theory

We are seeking a postdoctoral researcher to join the group of Jonathan Henshaw at the University of Freiburg in Germany (<https://www.henshaw-lab.com/>). We are a primarily theoretical lab working on a broad set of topics in evolutionary biology, with a particular focus on the evolution of animal behaviour. We develop both individual-based simulations and mathematical models (e.g., using evolutionary game theory, adaptive dynamics and quantitative genetics). We put a strong emphasis on a supportive and inclusive working environment. As a postdoc in our lab, you would have considerable freedom to shape the direction of your projects within these broad areas of interest.

****Duration, start date, salary****

The initial contract is for 3 years with the possibility of extension. The start date is flexible. Salary is at the TV-L E13 100

****Role****

As a postdoc, you will develop simulations or mathematical models to understand the evolution of animal behaviour, with the precise research questions to be decided on in collaboration with Jonathan. You will publish your work in peer-reviewed journals and present it at international conferences. This position comes with a teaching requirement of 4 face-to-face hours per week during the semester. Opportunities to supervise Bachelor's and Master's student are available and count partially towards the teaching requirement.

****Requirements****

Applicants must have: - A PhD in biology, mathematics, or another relevant discipline (applicants who will graduate soon are welcome to apply, but should have received their PhD officially before starting the position) - Strong theoretical skills with relevance to evolutionary biology (e.g. in quantitative genetics, game theory, adaptive dynamics) - Strong coding abilities (e.g. in R, Python, Julia or Mathematica) - A record of excellent publications in peer-reviewed journals - Excellent spoken and written English

****How to apply****

Applicants should send an email to Dr. Jonathan Henshaw (jonathan.henshaw@biologie.uni-freiburg.de) with the following: - Brief cover letter (max. 1 page) outlining your reasons for wanting to join the lab, your educational background and relevant skills, and which topics you would most like to work on - CV including a list of publications (max. 2 pages) - Contact details for two referees (it is not necessary to send reference letters)

The deadline for applications is 7 September 2026.

We are committed to building an inclusive workplace and welcome applications from people of all backgrounds, regardless of gender, sexual orientation, race, ethnicity, national origin, religion or belief, disability, age, or family status.

Please feel free to contact me if you have questions about the position or the application process. I look forward to hearing from you.

Jonathan Henshaw

Professor of Theoretical Biology Faculty of Biology University of Freiburg Hauptstrasse 1 79104 Freiburg i. Br. Germany

Email: jonathan.henshaw@biologie.uni-freiburg.de Phone: + 49 761 203 2567

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University of Illinois
PostdocBehavioralGenomics

Position Description: The Kukekova Lab at the University of Illinois at Urbana-Champaign invites applications for a postdoctoral position in Canine Behavior Genetics. We seek a highly motivated and collaborative individual with strong background in bioinformatics to join a project focused on the genetic analysis of evolved neuroanatomical and behavioral phenotypes in populations of selectively-bred working dogs. The position provides opportunities for interdisciplinary training in genomics, neurobiology, and animal behavior through collaborations with the Carl R. Woese Institute for Genomic Biology and external partners.

The project is a collaboration with the Hecht Lab at Harvard University. A partnered postdoctoral position in canine evolutionary neuroscience is also available in the Hecht Lab, and we anticipate opportunities for cross-training and interdisciplinary collaboration.

This is a one-year position, expected to begin in fall 2026, with possibility of renewal dependent upon adequate funding and satisfactory performance. The postdoctoral position will be funded through a 4-year grant from

Mae Philanthropies.

Basic Qualifications: A doctoral degree is required for this position. Desired qualifications include experience in mammalian genomics, coding, the whole genome sequencing data analysis, and genome wide association studies.

Location: Urbana, IL. Department of Animal Sciences, College of Agricultural, Consumer and Environmental Sciences (ACES), University of Illinois at Urbana-Champaign.

Special Instructions: Please submit a letter of interest, an updated CV, and the names of three references. These letters should be from people who are familiar with your research and can assess your potential as a postdoctoral researcher. Evaluation will begin at the time the advertisement is placed and will continue until the position is filled.

Contact Information: Professor Anna Kukekova

Contact Email: avk@illinois.edu

Salary Range: 62,000–65,000; *Pay offered to the selected candidate is dependent on factors such as years of experience, training or*
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University Virginia Disease Evolution Ecology

The Gibson lab is hiring a postdoc on the evolution of dispersal as a parasite avoidance mechanism. Apply here: https://uva.wd1.myworkdayjobs.com/UVAJobs/job/Charlottesville-VA/Research-Associate-in-Biology_R0084866 Application review will begin at the end of August. The ad: The Department of Biology at the University of Virginia invites applicants for a post-doctoral Research Associate position in the lab of Professor Amanda Gibson as part of an NSF-funded project. The Gibson lab is broadly interested in the evolution of avoidance versus resistance as modes of parasite defense. This project specifically tests the idea that host dispersal evolves as an escape in space from parasites, and it evaluates the downstream consequences of dispersal for the evolution of host resistance. The work makes use of the experimental tools and resources available for the model nematode *C. elegans* and its natural parasites. Associated projects entail evolve-and-resequencing, quantitative trait mapping, and field sampling with spatial analyses. The selected candidate will also mentor undergraduate students in independent research projects through a summer program for incoming transfer students. Find out more about the lab at <https://coevolving.org>. REQUIRED QUALIFICATIONS: - A PhD in Biology or a related field by the start date. PREFERRED QUALIFICATIONS: - Demonstrated conceptual and technical strengths in host-parasite interactions, evolutionary ecology, evolutionary genetics, and/or dispersal biology - Experience in basic lab and molecular work - A strong background in experimental design, data analysis, and data management - Excellent written and oral communication, demonstrated by a strong publication record, consistent with the candidate's career stage, and presentations at conferences - Demonstrated ambition, creativity, independence, and ability to work well with others - Experience in and dedication to mentoring junior trainees APPLICATION PROCEDURE: Apply online https://uva.wd1.myworkdayjobs.com/UVAJobs/job/Charlottesville-VA/Research-Associate-in-Biology_R0084866. Attach a cover letter outlining your qualifications and motivation for pursuing the position, curriculum vitae, and contact information for three individuals who can provide professional reference letters. In the cover letter, please address your fit with the qualifications above and your experience in mentoring undergraduates. Please note that multiple documents can be uploaded in the box. APPLICATION DEADLINE: Review of applications will begin on August 30, 2026. The University will perform background checks on all new hires prior to employment. Anticipated start date for this position is January 2027, but the start date is flexible. This is a one-year appointment; however, appointment may be renewed for additional two, one-year increments, contingent upon available funding and satisfactory performance. For questions about the position, please contact Amanda Gibson, Associate Professor, at akg5nq@virginia.edu. For questions about the application process, please contact

Richard Haverstrom, Academic Recruiter, at rkh6j@virginia.edu. For information on the benefits available to postdoctoral associates at UVA, visit postdoc.virginia.edu and hr.virginia.edu/benefits. The University of Virginia is an equal opportunity employer. All interested persons are encouraged to apply, including veterans and individuals with disabilities. Click here to read more about UVA's commitment to non-discrimination and equal opportunity employment.

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UOstrava Czech Republic Virus Evolution and Host Interactions

Have you ever wondered how many viruses exist out there? Which species they can infect - and why some, but not others? And how do the viruses evolve to adapt to new host species?

We do. And we're looking for people to help us find out.

At my group "virus evolution and host interactions" at University of Ostrava (Czech Republic), we take an interdisciplinary approach – spanning bioinformatics and molecular biology – to answer these questions at scale, through international collaborations.

Postdoc position:

VP1 researcher (junior/postdoc) o University of Ostrava, Faculty of Science, Ostrava, Czechia

The official posting can be found here: <https://lerco.osu.eu/job-opportunitoes/?inzeratid=139> The Dean of the Faculty of Science of the University of Ostrava announces a selection procedure to fill the new job position - VP1 researcher (junior/postdoc) in the project LERCO - Type of position - postdoc I This is position filled in accordance with the conditions of the Life Environment Research Center Ostrava (LERCO) project (reg. no. CZ.10.03.01/00/22_03/0000003, *ResearchProgram1MolecularBiologyandGenomics*)

Workplace - Faculty of Science, Department of Biology and Ecology

Job description - Postdoc position in the newly established research group: Virus evolution & host interaction, group lead by dr. Pascal Mutz: <https://mutzp.github.io/vehi/home/> Responsibilities - Conduct independent research in the field of virus evolution and virus-host interactions - Analyze large-scale virus genomics datasets using bioinformatic and computational approaches - Train and run large language models to predict protein interactions - Contribute to the development of research projects and lead first-author publications in high impact journals - Present research findings at meetings and conferences - Collaborate with members of an interdisciplinary research team and across the institute - Assist in mentoring students and junior researchers

Research level - R2 - Recognized

The expected form of employment - 100

The expected start date - 1 October 2026 (or by agreement)

The language in which the selection procedure will be conducted - English

Documents required from the participant in Czech or English language - Curriculum vitae - Cover letter - Copies of documents on education

To apply for the recruitment process, please send us the completed application form and the required documents listed above:

- Please fill out and submit the Application Form: <https://forms.office.com/Pages/ResponsePage.aspx?id=BeoAsH4kSE6MkRzWDHSU7xXWsDSnFLxArIO6iefeeuVUM1RFR1Y3WjQ5UkpSRUo0S1o1M1VNVjQ0Si4u> - Upload all the required documents to the University share point: https://365osu-my.sharepoint.com/personal/driv_e_personalni_prf_osu_cz/_layouts/15/onedrive.aspx?p=26&s=aHR0cHM6Ly8zNjVvc3UtbXkuc2hhcmVwb2l

udC5jb20v0mY6L2cvcGVyc29uYWwvZmVfcGVyc29uYWxuaV9wcmZfb3N1X2N6L0lnQ3daZWJjVkcwQ1RJZzFPaIRu0XFYQkFiT05BMEZKUkxkEZ3pRVkFnUkVqSDZj For questions related to the application form and file upload please contact: personalni.prf@osu.cz.

Application deadline - 15 August 2026 (inclusive)

To ask further questions about the position and the research project contact pascal.mutz@gmx.de

Benefits - Vacation (6 weeks per year for non-academic positions, 8 weeks per year for academic positions) - 5 sick days for medical treatment (after trial period) - Flexible working hours - Occasional home office - Vaccination center of the Faculty of Medicine - Access to magnetic resonance imaging with an appointment within 14 days (City Campus of the University of Ostrava) - Multisport card - Discount on admission to the City Campus sports complex of the University of Ostrava - CZK 200 contribution for shared bikes - Access to Faculty of Arts concerts - Discount programs with partners - English language courses and other educational programs and courses - Free access to the University Library, including e-books on Bookport and the option of free interlibrary loan service - 15- Access to the SEDUO platform - Elanek kindergarten with a 50- Discount on rent at Heimstaden

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Vigo Spain Ancient DNA genomics of *Salmo salar*

Research Position Available Project: Testing Temporal Genomic Shifts in Exploited Fish Populations Using Ancient and Environmental DNA (ATRAE Programme; Ref. ATR2023-144170, funded by MICIU/AEI/10.13039/501100011033) We are seeking a postdoctoral researcher (Doctor FC3) to join an interdisciplinary project investigating temporal genomic shifts in exploited Atlantic salmon populations using ancient and historical DNA (OLDSALMO). The project is based at the ACUABIOTEC Lab, Institute of Marine Research (IIM-CSIC), Vigo, Spain. OLDSALMO is a four-year project funded by the ATRAE programme that uses Atlantic salmon as a model species to develop novel approaches for assessing the roles of overfishing and climate change in population declines. More information is available at: <https://oldsalmo.csic.es>. This is a one-year position, starting in January 2027. Requirements Applicants should hold a PhD in molecular ecology, population genomics, or a related discipline. Experience working with degraded DNA (ancient or environmental) and/or aquatic systems is desirable but not essential. The role The successful candidate will analyse existing ancient genomic datasets to investigate temporal changes in salmon populations, while also generating and analysing historical genomic and phenotypic data and relating these to environmental change. We are looking for an enthusiastic, collaborative, and adaptable researcher who is keen to learn new skills while contributing their own expertise to the project. The successful candidate will work closely with two PhD students based at IIM-CSIC and collaborate with researchers at Swansea University, the University of Cantabria (EvoAdapta & IIIPC), Harvard University (Reich Lab), the Regional Government of Cantabria (Dirección General de Montes y Biodiversidad), and the University of Vienna (Gelabert Lab). The postdoctoral researcher will be responsible for: - Generating and analysing genomic data. - Preparing manuscripts for publication. - Presenting project results at national and international conferences. - Participating in outreach and dissemination activities. - Contributing to the co-supervision of undergraduate and postgraduate students. How to apply To apply, please send your CV and a cover letter to Prof. Sofia Consuegra at sconsuegra@iim.csic.es. Application deadline: 14 August 2026 Interviews will be held online via Zoom during the first week of September 2026.

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Vigo-Spain-Institute of Marine-Research Ancient DNA Genomics Salmon

Research position available for the project: Testing temporal genomic shifts in exploited fish populations using ancient and environmental DNA (ATRAE programme; REF ATR2023144170 funded by MICIU/AEI/10.13039/501100011033)

We are looking for a postdoctoral researcher (Doctor FC3) to work on an interdisciplinary project on temporal genomic shifts in exploited salmon populations, using ancient and historical DNA (OLDSALMO). The project is based at the ACUABIOTEC Lab at the Institute of Marine Research (IIM-CSIC) in Vigo (Spain). OLDSALMO is a 4-year project funded by the ATRAE programme that is using Atlantic salmon as study species to develop novel approaches to assess the roles of overfishing and climate change in population declines (<https://oldsalmo.csic.es>).

This is a one year position starting January 2027. Requisites: PhD in molecular ecology, population genomics or similar and, ideally but not necessarily, experience working with degraded DNA (ancient or environmental) and aquatic environments.

The position involves analysing ancient genomic data already available to assess population changes over time as well as producing and analysing historical genomic and phenotypic data and relate them to environmental change. We are looking for someone enthusiastic and flexible, looking to learn new things and contributing their expertise to the project in collaboration with 2 PhD students based at the IIM and collaborators at Swansea University, the University of Cantabria (EvoAdapta & IIIPC), the University of Harvard (Reich's lab), the regional government of Cantabria (Dirección General de Montes y Biodiversidad) and the University of Vienna (Gelabert's lab). The postdoctoral researcher will be responsible for data production and analyses, manuscript preparation, dissemination of project results in conferences (national and international) and outreach, and will have the opportunity to supervise undergraduate and postgraduate students.

To apply for this position, please send a CV and letter of intention to Prof Sofia Consuegra, sconsuegra@iim.csic.es. Deadline for applications is the 14 of August 2026 and interviews will take place the first week of September via zoom.

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VirginiaTech Population genomics and urban evolution

Position title: Postdoctoral Associate in Population Genomics and Urban Evolution

Position summary: The Urban Evolutionary Entomology Laboratory at Virginia Tech is seeking a highly motivated postdoctoral associate to investigate fundamental questions in population genomics and urban evolution using pest insect systems. Research will focus on understanding the genomic mechanisms underlying lineage establishment, persistence, adaptation, and extinction in highly inbred populations inhabiting urban environments. The successful candidate will address questions at the interface of evolutionary genetics, population genomics, and urban ecology, with broad implications for our understanding of adaptation in anthropogenic ecosystems and the evolution of economically important pest species.

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Crete 2027 EMBO Practical Workshop on Computational Molecular Evolution

Dear Colleagues,

Please pass the following info to PhD students and post-docs who may be interested in this workshop.

Applications are now open for 2027 EMBO Practical Workshop on "Computational Molecular Evolution" 9-20 May 2027, Heraklion, Greece.

Please follow the link for further information and to

apply:

<https://meetings.embo.org/event/27-comp-mol-evolution> Alexandros Stamatakis Aglaia (Cilia) Antoniou Adam Leache Ziheng Yang

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Erasmus BIP Nov-Dec2026

Registration open Reducing the gap between Linguistics and Genetics

Dear all,

We are happy to announce a new Erasmus BIP course "Finding a Common Ground: Reducing the Gap Between Linguistics and Genetics" organised by the University of Turku, Finland, in November and December 2026, in collaboration with the University of Tartu (Estonia) and Uppsala University (Sweden). International MA students may be eligible for an Erasmus+ short-term mobility grants by their home university. Please check with your local international office.

The course is aimed at MA students, PhD students and early-career researchers interested in interdisciplinary approaches to studying genes and languages. The topics incorporate the similarities between linguistics and genetics in terms of data, research questions, methods, and interpretations, and promote multidisciplinary collaborations. The course includes talks, interactive sessions, and group discussions. During the workshop, participants will have an opportunity to speak about their previous work in a special poster session, as well as establish or strengthen contacts with other participants and researchers in a networking event.

The on-site component of the course will be held at the University of Turku from November 30 to December 4, 2026. The on-site component will be preceded and followed by a series of online meetings.

The application form is now open and the deadline is September 7, 2026.

For more information, schedule, and registration, see: <https://sites.utu.fi/humandiversity/events/course-reducing-the-gap-between-linguistics-and-genetics/> Other links: General information on Erasmus+ short-term mobility grants: <https://erasmus-plus.ec.europa.eu/opportunities/individuals/students/studying-abroad> Information on the university course page (Peppi): <https://opas.peppi.utu.fi/en/course/KKLT0059/106526?period=2024-2027>

If you have any questions, please do not hesitate to contact me or Tatiana Kachkovskaia, University of Turku (tatiana.kachkovskaia@utu.fi) or Miina Norvik

(miina.norvik@utu.fi) for students enrolled at University of Tartu or Axel Palmer (axel.palmer@lingfil.uu.se) for students enrolled at Uppsala University.

Please share the course with your students, who might be interested in it and find attached the flyer of the course.

Kind regards, Tina Saupe

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FUBerlin

ProgrammingForEvolutionaryBiology- March2027

Course on Programming for Evolutionary Biology

When: March 5th - 22nd 2027

Location: Berlin, Germany

Detailed information about the course content and how to apply: <https://www.evop-bioinf.de/> Founded in 2012, our well established course is back with novel content! In this intensive 16 days course, students will learn how to survive in a Linux environment, get hands-on experience in two widely used programming languages (Python and R), and statistical data analysis. The classes will be given by experts in the field and consist of lectures and exercises with the computer. The aim of the course is to provide the students with the necessary background and skills to perform computational analyses with a focus on solving research questions related to genomics and evolution. The philosophy of the course will be "learning by doing", which means that the computational skills will be taught using examples and real data from evolutionary biology for the exercises. During the course, students will also propose projects of their own interest and perform them as final projects in small groups under the supervision of a teaching assistant. This course is open for students from all countries and targeted toward PhD students and postdocs of evolutionary biology or related research fields with no or little programming experience who want to become proficient in computational evolutionary biology in a couple of weeks.

The course takes place at the Free University of Berlin. For any questions related to the course, please send an email to: info@evop-bioinf.de

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Ithaca NY SLiMEvolModeling Oct5-9

SLiM is an evolutionary simulation framework; you can read about it at <https://messerlab.org/slim/>. There will be a SLiM workshop at Cornell in the fall of 2026:

Ithaca (New York, U.S.A.): October 5 - October 9, 2026
At Cornell University, in Ithaca, N.Y. Hosted by John Benning (Dept. of Ecology & Evolutionary Biology) and Erik Enbody (Dept. of Computational Biology).

This workshop is OPEN FOR REGISTRATION NOW. It will be free, and open to participants outside of the hosting institution. HOWEVER, registration is required, and a limited number of seats (30) are available. I expect this workshop to fill quickly, since it is the first workshop held in the U.S. since 2024, so you might want to register promptly. Note that half of the seats are first-come-first-served starting now, and the other half are reserved for priority registrations from people at the host departments for one month (to the end of 1 July 2026) and will then revert to first-come-first-served.

We will offer one fully funded scholarship – covering travel and lodging – for a participant who would otherwise be unable to attend. It's intended for graduate students, postdocs, and early-career researchers at institutions with limited resources, including those based in low- and middle-income countries. To apply for this scholarship: (1) apply to the workshop through the standard application form (see below); (2) in the comments field at the end of that form, note that you intend to apply for the travel scholarship; and (3) email John Benning (jbenning@cornell.edu; subject "SLiM Workshop Scholarship") with answers to two prompts (max 250 words each): (a) Describe the primary research question you're interested in using SLiM to address. (b) How would attending this workshop benefit your research and training, and why do you need financial support to attend? The award is selected by the organizers; financial need is self-reported and not verified. We book and prepay travel and lodging directly, so there's no out-of-pocket cost to you. Please apply only if you are reasonably certain you can attend if accepted: check the requirements and processing time for a U.S. visa from your country of residence, and make a realistic assessment of whether you can obtain one

before the workshop. If you accept and then have to withdraw late due to visa issues, the funding likely cannot be redirected to another applicant in time – so only apply if you're confident you can make it.

To apply to these workshops, please fill out the application form at <https://forms.gle/6LbcnCsS19DJHnig9>. Please read the form carefully. Note that there will be no automatic confirmation email after you submit the form; you will hear from me personally (bhaller@mac.com) by email once I have handled your application. I suggest that you whitelist my email address when you apply, so that you are sure to receive my emails; if I cannot communicate with you, your registration will be dropped (and yes, this has happened). Please do not make travel arrangements until you have been formally accepted to the workshop. Please do not apply to a workshop unless you are sufficiently serious that you will actually attend, if accepted. Please do not apply on behalf of someone else; only apply if you yourself will attend.

There are no strict prerequisites for the workshop, but it is recommended that all attendees have at least a little experience programming; if you have no programming experience, it is recommended that you complete an introductory R course beforehand. (SLiM does not use R, but it is similar.) Further information for attendees can be found at http://benhaller.com/workshops/workshops_attendees.html. Note that you will be responsible for arranging your own food, lodging, and transportation (unless you are awarded the scholarship mentioned above).

The plan is to cover all the major topics in the SLiM manual, starting with lots of introductory material to get beginners up to speed with SLiM and its associated scripting language Eidos, and ending up at advanced topics like non-Wright-Fisher models, tree-sequence recording, continuous-space models, nucleotide-based models, and multispecies models. We won't cover everything in the manual - that would be overwhelming! - but we'll try to cover all the big topics. There will also be time for attendees to work on their own models with help from me (most of the day Friday, typically), and we may also have time to explore some optional side topics that are of particular interest to those attending each workshop.

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Online Bayesian Modelling using INLA 21-25September2026

Bayesian Modelling Using R-INLA (BMIN04) - Applications for Evolutionary Biology

<https://prstats.org/course/bayesian-modelling-using-r-inla-bmin04/> Delivered by Dr. Virgilio Gomez-Rubio, author of Bayesian Inference with INLA and an internationally recognised expert in Bayesian statistics and spatial modelling. Learn how to build fast, flexible Bayesian models using R-INLA, with methods that are increasingly relevant across evolutionary biology, ecology, and population genetics. Bayesian modelling has become an essential tool for answering complex questions in evolutionary biology. While this course focuses on Bayesian modelling using R-INLA, the methods are highly transferable to studies of adaptation, population dynamics, comparative biology, phylogeography, quantitative genetics, and evolutionary ecology. R-INLA provides an efficient alternative to traditional MCMC methods, making sophisticated Bayesian analyses practical for large and complex biological datasets. What you'll gain - A strong understanding of Bayesian inference and prior specification - Practical experience fitting Bayesian models using R-INLA - Skills to build hierarchical, spatial, and spatio-temporal models - Understanding of model comparison and uncertainty quantification - Confidence in interpreting posterior distributions and Bayesian model outputs Course format - Live, instructor-led online training - Hands-on coding with real-world datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Evolutionary biologists and evolutionary ecologists - Population geneticists and quantitative biologists - Researchers working with comparative, ecological, or genomic datasets - PhD students and quantitative researchers - Anyone interested in applying modern Bayesian methods to evolutionary research Why take this course? Evolutionary datasets are often hierarchical, spatially structured, and characterised by multiple sources of uncertainty. Bayesian methods provide a powerful framework for modelling these complexities while allowing researchers to incorporate prior knowledge and quantify uncertainty throughout the analytical process. The techniques taught in this course are applicable to a wide range of evolutionary research

questions, including population dynamics, trait evolution, phylogeography, evolutionary ecology, comparative analyses, and quantitative genetics. By learning R-INLA, you'll gain the skills to fit sophisticated Bayesian models efficiently and apply modern Bayesian inference to challenging evolutionary datasets. Learn more & enrol PR Stats course page for Bayesian Modelling Using R-INLA (BMIN04) Questions? Email: oliver@prstats.org

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Online BayesianModellingUsingR-INLA

Bayesian Modelling Using R-INLA (BMIN04)

<https://prstats.org/course/bayesian-modelling-using-r-inla-bmin04/> Delivered by Dr. Virgilio Gomez-Rubio, author of Bayesian Inference with INLA and an internationally recognised expert in Bayesian statistics and spatial modelling. Learn how to build fast, flexible Bayesian models using R-INLA, a powerful alternative to traditional MCMC methods. Bayesian modelling has become an essential tool across ecology, epidemiology, environmental science, and many other research disciplines. This hands-on course introduces Integrated Nested Laplace Approximation (INLA), an efficient framework for fitting complex Bayesian models in R. You'll learn how to build, interpret, and compare Bayesian models while gaining practical experience with real-world datasets. What you'll gain - A strong understanding of Bayesian inference and prior specification - Practical experience fitting Bayesian models using R-INLA - Skills to build hierarchical, spatial, and spatio-temporal models - Understanding of model comparison and uncertainty quantification - Confidence in interpreting posterior distributions and Bayesian model outputs Course format - Live, instructor-led online training - Hands-on coding with real-world datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Statisticians and data scientists - Ecologists, epidemiologists, and environmental scientists - Researchers working with complex or hierarchical datasets - PhD students and quantitative researchers - Anyone interested in modern Bayesian modelling using R Why take this course? Bayesian methods provide a flexible framework for analysing complex datasets

while explicitly accounting for uncertainty. However, traditional Markov Chain Monte Carlo (MCMC) approaches can be computationally demanding, particularly for large or complex models. R-INLA offers a fast and practical alternative, allowing researchers to fit sophisticated Bayesian models efficiently without sacrificing statistical rigour. This course equips you with the practical skills needed to build, evaluate, and interpret Bayesian models, helping you apply modern Bayesian methods confidently across a wide range of research applications. Related PR Stats Courses If you're interested in Bayesian Modelling Using R-INLA (BMIN04), you may also find these PR Stats courses valuable. Upcoming Live Courses Spatial and Spatio-Temporal Modelling Using R-INLA (SSTM02) - Extend your INLA skills to spatial and spatio-temporal Bayesian models. <https://prstats.org/course/spatial-and-spatial-temporal-modelling-using-r-inla-sstm02/> Bayesian Statistical Modelling with Stan and brms (BMSB01) - Advanced Bayesian regression and multi-level modelling. <https://prstats.org/course/bayesian-statistical-modelling-with-stan-and-brms-bmsb01/> Species Distribution Modelling with Bayesian Statistics (SDMB08) - Bayesian SDMs using BART. <https://prstats.org/course/species-distribution-modelling-with-bayesian-statistics-sdmb08/> Spatial Phylogenetics and the Bayesian Phylogenetic Mixed Model (BPMM01) - Bayesian phylogenetic comparative methods and spatial evolutionary modelling. <https://prstats.org/course/spatial-phylogenetics-and-the-bayesian-phylogenetic-mixed-model-pmm-bpmm01/> Path Analysis, Structural Equations and Causal Inference for Biologists (PSCB04) - Causal modelling for biological systems. <https://prstats.org/course/path-analysis-structural-equations-and-causal-inference-for-biologists-pscb04/> Related Recorded Courses Introduction to Bayesian Statistics - Build a solid foundation in Bayesian inference. <https://prstats.org/recorded-courses/> Introduction to Mixed Models - Learn hierarchical and mixed-effects modelling. <https://prstats.org/recorded-courses/> Introduction to Generalised Linear Models - Master the regression techniques underpinning modern Bayesian modelling. <https://prstats.org/recorded-courses/> Species Distribution Modelling - Learn the principles of ecological prediction and habitat suitability modelling.

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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>

Online DataAnalysisWithR July

Dear all,

Whether you're cleaning complex datasets, building reproducible analyses, developing your own R packages, or exploring the latest AI tools, mastering R can dramatically improve the quality and efficiency of your research.

This July, Physalia is offering a series of live, hands-on online courses designed to help researchers and data scientists strengthen their R programming and statistical analysis skills.

Upcoming Courses - Advanced Multivariate Modelling in R (GLLMs) <https://www.physalia-courses.org/courses-workshops/gllvm/> online, 7-10 July Learn modern statistical approaches for analysing complex multivariate ecological and biological data.

- Dealing with Messy Data in R <https://www.physalia-courses.org/courses-workshops/messy-data/> online, 13-15 July Transform untidy, inconsistent datasets into clean, analysis-ready data using efficient R workflows.

- Time-series Analysis and Forecasting in R <https://www.physalia-courses.org/courses-workshops/time-series-in-r/> online, 20-24 July Model, visualise, and forecast temporal data using powerful statistical methods and R packages.

- Reproducibility with R <https://www.physalia-courses.org/courses-workshops/r-reproducibility/> online, 20-23 July Build transparent, reproducible workflows using Quarto, Git, project management, and workflow automation.

- Developing R/Bioconductor Packages <https://www.physalia-courses.org/courses-workshops/r-packages/> online, 27-31 July Learn how to create, document, test, and distribute professional R and Bioconductor packages.

- Integrating LLMs into R Workflows <https://www.physalia-courses.org/courses-workshops/llms-4-r-fsbi/> online, 4 August Discover how AI and Large Language Models can assist with coding, documentation, data exploration, and reproducible research—all from within R.

We look forward to learning with you this summer! Best

wishes, Carlo ————— Carlo Pecoraro, Ph.D
Physalia-courses DIRECTOR info@physalia-courses.org

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Online DeepLearningforEvolutionaryGenomics 5-9October

Deep Learning for Evolutionary Genomics (DLEG01) - Applications for Evolutionary Biology <https://prstats.org/course/deep-learning-for-evolutionary-genomics-dleg01/> Delivered by experienced computational biologists, evolutionary geneticists, and deep learning researchers. Learn how to apply deep learning to genomic data, with methods that are transforming evolutionary biology, population genetics, and evolutionary genomics. Advances in sequencing technologies have produced genomic datasets of unprecedented size and complexity. Deep learning is rapidly emerging as a powerful approach for identifying complex patterns that are difficult to detect using traditional statistical methods, enabling researchers to investigate adaptation, natural selection, demographic history, population structure, speciation, and evolutionary processes with greater accuracy and flexibility. While this course focuses on deep learning for evolutionary genomics, the methods are applicable across a broad range of evolutionary research. What you'll gain - A strong understanding of deep learning concepts and neural network architectures - Practical experience applying deep learning to genomic datasets - Skills in supervised learning, classification, prediction, and feature extraction - Understanding of model training, optimisation, validation, and performance assessment - Confidence in interpreting deep learning models and applying them to evolutionary research Course format - Live, instructor-led online training - Hands-on coding with real-world genomic datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Evolutionary biologists and evolutionary ecologists - Population geneticists and evolutionary genomic researchers - Bioinformaticians and computational biologists - Researchers working with genomic and sequencing datasets - PhD students and quantitative life scientists Why take this course? Deep learning is opening new opportunities for evolutionary biologists to analyse genome-scale datasets and address questions that

were previously difficult to investigate using conventional analytical approaches. These methods are increasingly used to identify signatures of natural selection, infer demographic history, classify genomic variation, investigate adaptation, predict functional genomic elements, and uncover the evolutionary processes shaping genetic diversity. This course equips you with the practical skills needed to design, train, evaluate, and interpret deep learning models for evolutionary genomics. Whether you're studying adaptation, speciation, phylogeography, population divergence, or evolutionary history, you'll gain the computational toolkit needed to apply modern AI methods confidently to your own research. Learn more & enrol PR Stats course page for Deep Learning for Evolutionary Genomics (DLEG01) <https://prstats.org/course/deep-learning-for-evolutionary-genomics-dleg01/Questions?> Email: oliver@prstats.org

Oliver Hooker Managing Partner Advanced Training for Researchers in the Life Sciences coursesinfo@prstats.org — www.prstats.org (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Developing R-Bioconductor Packages for Genomics 27-31July

Dear all,

Have you ever wished you could turn your scripts into a polished, shareable Bioconductor package?

Join Developing R/Bioconductor Packages for Genomics (Online, 27-31 July) and learn the complete package development workflow—from writing robust functions and documenting code to testing, continuous integration, package websites, and publishing your package in Bioconductor.

Course website: <https://www.physalia-courses.org/courses-workshops/r-packages/>

Designed for biologists and bioinformaticians with basic R experience, this highly practical course combines expert-led lectures with hands-on exercises. By the end of the week, you'll have the skills and confidence to develop, maintain, and share professional-quality genomics software using Bioconductor best practices.

Turn your code into a reusable tool—and start contributing to the Bioconductor ecosystem.

For the full list of our courses and workshops, please have a look at: <https://www.physalia-courses.org/courses-workshops/> Best regards, Carlo

———— Carlo Pecoraro, Ph.D Physalia-courses
DIRECTOR info@physalia-courses.org

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Online Gaussian Processes with PyMC and LLMs

Hello EVOLDIR members

Model biological patterns while expressing uncertainty and testing model assumptions. Gaussian Processes with PyMC and LLMs led by Chris Fonnesbeck (PyMC Labs and Vanderbilt University Medical Center) is now available as an on-demand streaming seminar. Specify, fit, diagnose, compare, and scale Gaussian process models in PyMC for complex data. Evolutionary researchers can apply kernels, uncertainty estimates, multi-output models, and non-Gaussian likelihoods to genetic, trait, or time-series questions. Reproducible Python workflows can support model assessment, computational trade-offs, and publication-quality analyses.

Access this seminar (<https://instats.org/seminar/gaussian-processes-with-pymc-and-llms-1>) online at your convenience and we'd appreciate you sharing this with colleagues and students!

Best wishes

Michael Zyphur Professor and Director Instats — instats.org

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Online GenomeAssembly 9-13November

Dear all,

We are pleased to announce our upcoming online course, Eukaryotic Genome Assembly using PacBio and Hi-C (7th edition), taking place 9-13 November.

Course website:<https://www.physalia-courses.org/courses-workshops/pacbio/>

This five-day hands-on course provides a practical introduction to modern de novo genome assembly workflows using PacBio HiFi and Hi-C sequencing data. Participants will learn how to process sequencing reads, perform genome assembly, scaffold assemblies to chromosome level, assess assembly quality, and work with state-of-the-art bioinformatics tools through a combination of lectures and practical exercises.

The course is suitable for researchers interested in genome assembly, from beginners to more experienced users looking to strengthen their practical skills.

For the full list of our courses and workshops, please have a look at: <https://www.physalia-courses.org/courses-workshops/>

We would appreciate it if you could share this opportunity with anyone who may be interested.

Best regards,

Carlo ————— Carlo Pecoraro, Ph.D Physalia-courses
DIRECTOR info@physalia-courses.org

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ONLINE Genomic Prediction of Complex Traits 21-25Sept

Genomic Prediction of Complex Traits (GPCT01) - Applications for Evolutionary Biology <https://prstats.org/course/genomic-prediction-of-complex-traits-gpct01/> Delivered by Dr. Javier Fernandez-Gonzalez, a quantitative geneticist specialising in statistical genomics, genomic prediction, and computational methods for breeding and quantitative genetics. Learn how to build genomic prediction models for complex traits, with methods that are highly applicable to evolutionary biology, population genetics, and evolutionary genomics. Understanding the genetic basis of complex traits is central to modern evolutionary biology. Advances in genome sequencing now allow researchers to investigate how thousands of genetic variants collectively influence phenotypes, adaptation, fitness, and evolutionary potential. Although genomic prediction was originally developed for plant and animal breeding, these statistical approaches are increasingly being used to study natural populations, the evolution of quanti-

tative traits, genotype-phenotype relationships, and responses to environmental change. What you'll gain - A strong understanding of genomic prediction and quantitative genetics - Practical experience building genomic prediction models using modern statistical methods - Skills in predicting complex traits from genome-wide marker data - Understanding of model evaluation, validation, and prediction accuracy - Confidence in interpreting genomic prediction models within an evolutionary context Course format - Live, instructor-led online training - Hands-on coding with real-world genomic datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Evolutionary biologists - Population and quantitative geneticists - Evolutionary genomic researchers - PhD students and postdoctoral researchers - Anyone interested in applying statistical genomics to evolutionary research Why take this course? Many of the most important questions in evolutionary biology involve understanding how genetic variation contributes to phenotypic diversity, adaptation, and fitness. Genomic prediction provides a powerful statistical framework for modelling complex traits controlled by many loci, allowing researchers to investigate evolutionary potential, predict phenotypic variation, and better understand the genetic architecture of adaptive traits. These methods are increasingly being applied alongside GWAS, population genomics, and quantitative genetics to address fundamental evolutionary questions. This course equips you with the practical skills needed to develop, evaluate, and interpret genomic prediction models using modern statistical approaches. Whether you're studying adaptation, quantitative trait evolution, life-history variation, genotype-phenotype relationships, or evolutionary responses to changing environments, you'll gain the analytical toolkit needed to apply genomic prediction methods confidently in your own research. Learn more & enrol PR Stats course page for Genomic Prediction of Complex Traits (GPCT01) <https://prstats.org/course/genomic-prediction-of-complex-traits-gpct01/> Questions? Email: oliver@prstats.org

Oliver Hooker Managing Partner Advanced Training for Researchers in the Life Sciences coursesinfo@prstats.org — www.prstats.org (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net)

Online IntroductionToComputationalBiology 28September-2October

Dear all,

We would like to announce our upcoming online course "Introduction to Computational Biology", taking place 28 September-2 October.

Course website: <https://www.physalia-courses.org/courses-workshops/computational-biology/>

This hands-on course introduces modern computational approaches used in genomics, transcriptomics, and multi-omics research. Participants will gain practical experience working with real datasets through a combination of short lectures and guided group projects. Emphasis is placed on real-world datasets, current analytical workflows, and interpretation of biological results in research and applied contexts.

Topics covered include: - long-read genome assembly, - metagenomics and pangenomics, - single-cell RNA sequencing, - metabolomics and multi-omics integration.

The course is designed for PhD students, early-career researchers, life scientists transitioning into computational biology, and researchers seeking practical skills for analysing genomic and multi-omics data.

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

Best regards, Carlo ————— Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org

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Online IntroductionToDeepLearning

Dear all,

Are you interested in applying deep learning to biological data but unsure where to start?

Join our online course "Introduction to Deep Learning

for Biologists”, taking place 23-27 November.

Course website: <https://www.physalia-courses.org/courses-workshops/course67/> This five-day course will introduce the key concepts behind deep learning and provide hands-on experience developing predictive models for biological applications. Participants will learn how to build, evaluate and interpret deep learning models, with a focus on classification, regression and image segmentation using Convolutional Neural Networks (CNNs).

Topics covered include: - Fundamentals and building blocks of deep learning models - Data preparation, augmentation and model evaluation - Cross-validation, overfitting and model generalisation - CNN architectures for biological image analysis - Regression and segmentation approaches - Recurrent Neural Networks and applications to -omics data The course combines lectures, discussions and practical hands-on sessions using Python, Jupyter Notebooks and real biological datasets.

This course inspired the Deep Learning for Life Sciences book, written by the instructors and published as part of Physalia’s Decoding Evolution book series: <https://link.springer.com/book/10.1007/978-3-031-96852-5> 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

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Online Joint Species Distribution Modelling using HMSC 26-29Oct

Joint Species Distribution Modelling (JSDM) using HMSC: A Hierarchical Modelling Approach (JSDM01) - Applications for Evolutionary Biology <https://prstats.org/course/joint-species-distribution-modelling-jsdm01/> Delivered by Dr. Bastien Parisy, a community ecologist at the University of Helsinki whose research focuses on plant-soil interactions, community ecology, and environmental change. His work combines field ecology with advanced statistical methods, including Joint Species Distribution Models (JSDMs), Hierarchical Modelling of Species Communities (HMSC), and ecological network analysis.

Learn how to analyse complex biological communities using Joint Species Distribution Models (JSDMs) and Hierarchical Modelling of Species Communities (HMSC) in R, with methods that are highly applicable to evolutionary biology.

Evolutionary processes shape community composition through adaptation, niche evolution, phylogenetic history, species interactions, and environmental filtering. Traditional species distribution models treat species independently, often overlooking these important evolutionary relationships. Joint Species Distribution Models provide a powerful hierarchical framework for modelling entire communities simultaneously, allowing researchers to incorporate phylogenetic relationships, functional traits, environmental responses, and residual species associations to better understand the evolutionary processes underlying community assembly. This course provides comprehensive, hands-on training in HMSC, one of the leading frameworks for modern community and evolutionary ecology.

What you’ll gain

- A thorough understanding of Joint Species Distribution Modelling (JSDMs) and the HMSC framework
- Practical experience building hierarchical community models in R
- Skills in incorporating environmental variables, species traits, phylogenies, and spatial structure into community models
- Understanding of species co-occurrence, evolutionary relationships, and community assembly processes
- Confidence interpreting JSDM outputs and evaluating model performance

Course format

- Live, instructor-led online training
- Hands-on coding using real biological community datasets
- Interactive practical exercises throughout
- Strong focus on applied, research-ready workflows

Who is this course for?

- Evolutionary biologists and evolutionary ecologists
- Community ecologists
- Population and quantitative geneticists
- Researchers investigating trait evolution, adaptation, and phylogenetic community structure
- PhD students and quantitative life scientists

Why take this course?

Evolutionary biology increasingly seeks to understand how historical diversification, adaptation, ecological interactions, and environmental filtering combine to shape biological communities. JSDMs provide an integrated framework for investigating how species traits, shared evolutionary history, environmental gradients, and residual associations contribute to patterns of biodiversity. By incorporating phylogenetic information

directly into community models, researchers can test hypotheses about niche conservatism, adaptive divergence, trait evolution, and the evolutionary drivers of species distributions. This course equips you with the practical skills needed to construct, fit, interpret, and validate Joint Species Distribution Models using HMSC in R. Whether you're studying adaptive radiations, phylogenetic community structure, trait evolution, genotype-environment relationships, macroevolutionary patterns, or biodiversity responses to environmental change, you'll gain the analytical toolkit needed to confidently analyse complex biological communities using state-of-the-art hierarchical models.

Learn more & enrol

PR Stats course page for Joint Species Distribution Modelling (JSDM) using HMSC: A Hierarchical Modelling Approach (JSDM01) <https://prstats.org/course/joint-species-distribution-modelling-jsdm01/> Questions? Email: oliver@prstats.org

Oliver Hooker Managing Partner Advanced Training for Researchers in the Life Sciences coursesinfo@prstats.org — www.prstats.org (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Online LandscapeGenomics 13-17July

Dear all,

our online course "Landscape Genomics" is taking place on 13-17 July (2-6 PM Berlin time).

Course website: <https://www.physalia-courses.org/courses-workshops/course17>

This course introduces the field of landscape genomics, focusing on how genetic variation is distributed across space and how environmental factors can drive local adaptation. Participants will gain hands-on experience integrating environmental and genomic data to study spatial patterns of diversity and selection. The course covers the full analytical workflow, including acquisition and processing of environmental data from public databases, basic GIS operations, and the generation of environmental descriptors of landscapes. Participants will also learn how to analyse genetic variation and population structure in a spatial context, and apply key statistical approaches for detecting local adaptation, in-

cluding latent factor mixed models (LFMM), and redundancy analysis (RDA).

Finally, we will discuss interpretation and validation of results, as well as best practices for study design, including sampling strategies for landscape genomics experiments.

This course is aimed at biologists, ecologists, geneticists, and conservation scientists interested in applying landscape genomics approaches in their research.

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

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DIRECTOR info@physalia-courses.org

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Online Last chance Foundations of Bioinformatics for Evolutionary Genetics

Hello EVOLDIR members

Last chance - Build practical confidence for investigating genetic relationships with computational sequence methods. Foundations of Bioinformatics (Free Seminar) is a seminar livestreaming August 3 with Andres Zhou Tsang (Adelaide University). Analyse DNA, RNA, and protein sequences through alignment, genomic information retrieval, phylogenetic reconstruction, and sequence translation. Evolutionary researchers can apply these foundational tools to compare sequences, investigate relationships, and interpret genetic data. Open-access computational resources provide an entry point without prior programming experience.

Sign up today (<https://instats.org/seminar/foundations-of-bioinformatics-free-semin>) to reserve your place before it starts, and feel free to circulate this with colleagues and students!

Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online Last chance High-Performance Programming for Biology

Hello EVOLDIR members

Last chance - Make genome-scale computation faster, more reliable, and easier to reproduce. High-Performance Programming for Biology is a 2-day seminar livestreaming August 3 and 14 with Giulio Formenti (Vertebrate Genome Lab, The Rockefeller University). Write efficient C and C++ programs for genomic workloads by selecting suitable data structures, managing memory safely, and profiling performance bottlenecks. Apply multithreading, binary I/O, compression, indexing, and hashing to sequence data, genomes, reads, and k-mer analyses. Build reproducible, reliable software that supports scalable evolutionary and genetic research workflows.

Sign up today (<https://instats.org/seminar/high-performance-programming-for-biology>) to secure your spot, and please share this opportunity with colleagues and students who might benefit!

Best wishes

Michael Zyphur Professor and Director Instats — instats.org

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Online Last Chance Machine Learning for Computational Biology

Hello EVOLDIR members

Last chance - Extend evolutionary analyses with practical modelling approaches for complex genetic data. Machine Learning for Computational Biology 4.0 is a seminar livestreaming July 30 with Nikolay Oskolkov (Lund University). Implement neural networks, random forests, clustering, and MCMC in R and Python for genetic and genomic data. Build algorithms from scratch, troubleshoot model performance, and consider

ethical research practices. Apply these methods to evolutionary questions involving biological sequence, ecological, and genomic datasets.

Sign up today (<https://instats.org/seminar/machine-learning-for-computational-biology-4>) to join before enrollment closes, and please pass this to colleagues and students who may be interested! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online Longitudinal Analysis in Biostatistics

Hello EVOLDIR members

Tracking changes in biological systems over time requires robust statistical methodologies. Longitudinal Analysis in Biostatistics led by Md Tuhin Sheikh (Biostatistics, College of Health Solutions, Arizona State University) is now available as an on-demand streaming seminar. This on-demand seminar provides comprehensive training in advanced modeling frameworks, multi-level analysis, and missing data strategies using R. Evolutionary biologists and geneticists can apply these longitudinal methods to track phenotypic changes across generations, model evolutionary trajectories, and analyze time-series genomic data. By mastering these biostatistical tools, researchers can robustly handle missing data and hierarchical structures to uncover deeper insights into temporal biological processes.

Access this seminar (<https://instats.org/seminar/longitudinal-analysis-in-biostatistics>) online at your convenience and we'd appreciate you sharing this with colleagues and students!

Best wishes

Michael Zyphur Professor and Director Instats — instats.org

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Online Machine Learning for Computational Biology Jul30

Hello EVOLDIR members

Enhancing your analytical toolkit with advanced computational methods can significantly accelerate your ongoing evolutionary research. Machine Learning for Computational Biology 4.0 is a seminar livestreaming July 30, led by Nikolay Oskolkov (Lund University). This workshop provides evolutionary biologists and geneticists with hands-on training in implementing machine learning algorithms from scratch using R and Python. By mastering neural networks, random forests, and Markov Chain Monte Carlo (MCMC) methods, researchers can more effectively analyze complex genomic datasets, model evolutionary pathways, and perform population genetic clustering. These practical computational skills will enable you to resolve intricate biological patterns and accelerate your research in molecular evolution and genomics.

Sign up today (<https://instats.org/seminar/machine-learning-for-computational-bio-4>) to register, and we would appreciate you sharing this with colleagues and students who might benefit!

Best wishes

Michael Zyphur Professor and Director Instats — instats.org

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Online Machine Learning for Multi-Omics Integration 21-23September

Dear all, We would like to share an upcoming online course focused on Machine Learning for Multi-Omics Integration, taking place on 21-23 September.

More information about the programme and registration is available here: <https://www.physalia-courses.org/courses-workshops/multiomics/> The

rapid growth of genomics, transcriptomics, proteomics, metabolomics, and single-cell datasets is creating new opportunities and challenges for biological data analysis. Machine learning methods are increasingly being used to integrate these diverse data types, identify complex patterns, and generate biologically meaningful insights.

This course is aimed at researchers working with omics data and combines lectures with hands-on practical sessions covering both established and emerging approaches for multi-omics integration.

Topics covered include: - Machine learning concepts for biological data integration - Feature selection and supervised integration approaches using LASSO, PLS, LDA, mixOmics, and DIABLO - Unsupervised integration with MOFA1 and MOFA2 - Deep learning approaches, including autoencoders - Single-cell multi-omics integration methods, including UMAP, Seurat CCA, Dynamic Time Warping (DTW), Weighted Nearest Neighbours (WNN), and batch correction approaches Participants will gain practical experience with commonly used computational tools and workflows for multi-omics analysis.

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

— Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org

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Online Multivariate Trait Evolution Sep15-24

Dear colleagues, Transmitting Science is offering a new edition of the course "Modelling and analysing multivariate traits evolution using R". Course webpage: <https://www.transmittingscience.com/courses/evolution/modelling-and-analysing-multivariate-traits-evolution-using-r/> The aim of this course is to introduce participants to methods for modelling and analysing the evolution of multivariate traits using the mvMORPH R package. By the end of the course, students will be able to: - Understand multivariate trait evolution models. - Apply comparative methods using R. - Interpret evolutionary patterns in multivariate datasets. The course comprises lectures, hands-on computational exercises and guided examples. For any questions, please write to

courses@transmittingscience.com Best regards,
 Haris – Haris Saslis, PhD Course Coordinator Trans-
 mitting Science www.transmittingscience.com
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Online Path Analysis Structural Equations and Causal Inference 19-30Oct

Path Analysis, Structural Equations, and Causal Inference for Biologists (PSCB04) - Applications for Evolutionary Biology <https://prstats.org/course/path-analysis-structural-equations-and-causal-inference-for-biologists-pscb04/> Delivered by Prof. Bill Shipley, Professor Emeritus at the University of Sherbrooke, internationally recognised for his pioneering work in causal inference, path analysis, and structural equation modelling in biology. He is the author of the widely used textbook Cause and Correlation in Biology and has published over 170 peer-reviewed papers.

Learn how to use path analysis, structural equation modelling (SEM), and causal inference to test complex evolutionary hypotheses using observational and experimental data.

Evolutionary biology seeks to understand how multiple ecological, genetic, developmental, and environmental factors interact to shape phenotypes, fitness, adaptation, and diversification. Traditional regression approaches often fail to capture these interconnected causal relationships. Path analysis and structural equation modelling provide a powerful framework for testing evolutionary hypotheses, quantifying direct and indirect effects, and evaluating competing causal models. This course provides comprehensive hands-on training in modern causal modelling using R, with a strong emphasis on evolutionary applications and reproducible analytical workflows.

What you'll gain

- A strong understanding of path analysis, structural equation modelling, and causal inference - Practical experience fitting piecewise and covariance-based SEMs in R - Skills in constructing, testing, and interpreting causal models using evolutionary datasets - Understanding of latent variables, d-separation, multigroup models, and model comparison - Confidence in applying

causal modelling techniques to evolutionary research

Course format

- Live, instructor-led online training - Hands-on coding with real-world biological datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows

Who is this course for?

- Evolutionary biologists and evolutionary ecologists - Population and quantitative geneticists - Researchers studying adaptation, life-history evolution, and phenotypic evolution - PhD students and quantitative life scientists - Anyone interested in applying causal modelling to evolutionary research

Why take this course?

Many of the most important questions in evolutionary biology involve complex networks of interacting processes rather than simple cause-and-effect relationships. Structural equation modelling enables researchers to investigate how genetic, ecological, developmental, and environmental factors jointly influence phenotypes, fitness, adaptation, and evolutionary change through both direct and indirect pathways. It has become an increasingly important framework for testing mechanistic hypotheses in evolutionary research.

This course equips you with the practical skills needed to construct, evaluate, and interpret causal models using modern R-based workflows. Whether you're studying natural selection, adaptation, phenotypic plasticity, life-history evolution, genotype-phenotype relationships, or evolutionary responses to environmental change, you'll gain the analytical toolkit needed to apply path analysis and structural equation modelling confidently to your own research.

Learn more & enrol

PR Stats course page for Path Analysis, Structural Equations, and Causal Inference for Biologists (PSCB04) <https://prstats.org/course/path-analysis-structural-equations-and-causal-inference-for-biologists-pscb04/> Questions? Email: oliver@prstats.org

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Online Population Genomics 21-25 September

Dear all,

We are pleased to announce the upcoming online course Population Genomics Using Ancient DNA Data, taking place from 21-25 September.

Course website: <https://www.physalia-courses.org/courses-workshops/adna-popgen>

This five-day course will introduce participants to the generation, processing, authentication, and population genomic analysis of ancient DNA data, combining lectures with hands-on computational exercises based on real research questions.

The course will cover: - Processing and authentication of ancient DNA data, including contamination and postmortem DNA damage - Pseudo-haploid variant calling from low-coverage aDNA data - Population structure using PCA and MDS - Coalescent theory and demographic inference - Historical population dynamics, bottlenecks, and population expansions - D and F statistics for studying population affinity and gene flow - Relatedness and kinship analysis - Population genetics simulations and hypothesis testing - Detecting signals of natural selection using ancient DNA data

The course is aimed at graduate students and researchers in genetics, genomics, ecology, evolutionary biology, and anthropology interested in using aDNA data for population genetic inference. Although examples will primarily focus on the human genome, the methods and approaches discussed are broadly applicable to other organisms for which ancient DNA data are available.

For the full list of our courses and workshops, please have a look at: <https://www.physalia-courses.org/courses-workshops/> Best regards,

Carlo ————— Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org

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Online Population Genomics and Structure Analysis 28Sep-2Oct2026

Population Genomics and Structure Analysis (PGSA01) - Applications for Evolutionary Biology

<https://prstats.org/course/population-genomics-and-structure-analysis-pgsa01/> Delivered by Dr. Nikolay Oskolkov, a computational biologist and bioinformatician with expertise in population genomics, evolutionary biology, machine learning, and statistical genomics.

Learn how to analyse population structure using modern genomic tools, with methods that are central to evolutionary biology, population genetics, and evolutionary genomics.

Population structure inference lies at the heart of evolutionary biology. Modern genomic technologies now allow researchers to investigate population divergence, demographic history, gene flow, adaptation, admixture, and introgression at unprecedented resolution. This hands-on course provides practical training in the statistical and computational methods used to analyse modern and ancient genomic datasets, helping researchers answer fundamental questions about evolutionary processes.

What you'll gain - A strong understanding of population genomics and population genetic theory - Practical experience analysing genomic variation using modern software tools - Skills in population structure, ancestry inference, and clustering analyses - Understanding of demographic history, gene flow, admixture, and introgression - Confidence in interpreting genomic patterns within an evolutionary framework

Course format - Live, instructor-led online training - Hands-on coding with real-world genomic datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows

Who is this course for? - Evolutionary biologists and population geneticists - Evolutionary ecologists and comparative biologists - Bioinformaticians and computational biologists - Researchers working with SNP, RAD-seq, whole-genome, or ancient DNA datasets - PhD students and quantitative life scientists

Why take this course? Understanding how populations evolve through time is fundamental to evolution-

ary biology. Population genomic methods enable researchers to reconstruct demographic history, quantify gene flow, detect natural selection, identify hybridisation events, and investigate the evolutionary forces shaping genetic diversity. These approaches have become indispensable for studying adaptation, speciation, phylogeography, and the genetic basis of evolutionary change. This course equips you with the practical skills needed to analyse population genomic datasets using widely adopted tools such as ANGSD, ADMIXTURE, STRUCTURE, NGSadmix, ChromoPainter, fineSTRUCTURE, and F-statistics. Whether you're investigating population divergence, admixture, evolutionary history, or adaptation, you'll gain the analytical toolkit needed to extract robust evolutionary insights from genomic data.

Learn more & enrol PR Stats course page for Population Genomics and Structure Analysis (PGSA01) <https://prstats.org/course/population-genomics-and-structure-analysis-pgsa01/> Questions? Email: oliver@prstats.org

Oliver Hooker Managing Partner Advanced Training for Researchers in the Life Sciences coursesinfo@prstats.org — www.prstats.org (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Online Python For Biologists October November

Dear all,

Ready to level up your Python skills for biology and life sciences?

Whether you're completely new to programming or already have some Python experience and want to take your skills further, we have two online courses designed to help you build practical, research-focused skills.

1) Introduction to Python Programming for Biologists - 19-22 October — Online <https://www.physalia-courses.org/courses-workshops/python24/> Perfect for biologists and life scientists with little or no prior programming experience. Learn the foundations of Python programming and how to apply them to real biological problems, with hands-on projects covering: - Biological data manipulation and analysis - Data analysis and statistics - Data visualisation - Writing organised and reusable code

2) Advanced Python for Data Science & Bioinformatics - 3-6 November — Online <https://www.physalia-courses.org/courses-workshops/advanced-python/>

This course is designed for participants with some prior programming and basic Python experience. Explore: - Data wrangling with Pandas - Bioinformatics with Python - Machine learning fundamentals - Complete end-to-end data science projects

Both courses are highly practical, combining expert-led teaching with hands-on exercises and projects focused on biology and life sciences.

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

Best wishes, Carlo ————— Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org

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Online RNAseqWithR 9-18November

Dear all, We are pleased to announce the online course "Introduction to RNA sequencing data analysis with R/Bioconductor" (7th edition), running on 9, 11, 13, 16, 17, and 18 November (3-6 PM Berlin time).

Course website: <https://www.physalia-courses.org/courses-workshops/course19/>

This course is designed for biologists and bioinformaticians who want to build practical and rigorous skills for analysing high-throughput transcriptomic data. Starting from core statistical concepts, participants will learn how to perform a complete RNA-seq workflow in R using Bioconductor—from data import and visualization to differential expression and gene set analysis.

Topics include hypothesis testing, genomic data handling, RNA-seq processing, differential expression (DESeq2, edgeR, limma/voom), and pathway enrichment analysis.

This course is organized in collaboration with Bioconductor Training and Physalia Courses.

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

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evoldir@evoldir.net) evoldir@evoldir.net)

Online SmallRNAseq 6-9October

Dear all,

Our new online course, MicroRNA Annotation and Small RNA-Seq Analysis (6-9 October), provides a practical, hands-on introduction to the complete workflow—from raw sequencing reads to high-quality microRNA annotations.

Course website: <https://www.physalia-courses.org/courses-workshops/smallrnaseq/>

Using real datasets and published studies, participants will learn how to: Process and quality-control small RNA-seq data Retrieve and reproduce analyses from published research Perform microRNA annotation using current best practices Critically evaluate predicted microRNAs and avoid common annotation pitfalls Apply widely used tools including miRTrace, MirMachine, and MirMiner Designed for PhD students, postdoctoral researchers, and scientists working in genomics, molecular biology, and bioinformatics, the course combines theory with extensive practical exercises that participants can immediately apply to their own research.

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

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Online Spatial Phylogenetics and Bayesian Phylogenetic MixedModel 22-24September2026

Spatial Phylogenetics and the Bayesian Phylogenetic Mixed Model (BPMM01)

<https://prstats.org/course/spatial-phylogenetics-and-the-bayesian-phylogenetic-mixed-model-pmm-bpmm01/> Delivered by Dr. Ignacio Morales-Castilla, a leading researcher in macroecology, biogeography, and spatial phylogenetics.

Learn how to integrate phylogenetic comparative methods, Bayesian Phylogenetic Mixed Models (BPMMs), and spatial analysis to answer complex evolutionary and ecological questions.

Species do not represent statistically independent observations—they share evolutionary histories that influence their traits, distributions, and ecological interactions. Likewise, many ecological datasets exhibit strong spatial structure. This hands-on course teaches you how to combine phylogenetic and spatial information within modern Bayesian modelling frameworks, allowing you to account for both evolutionary relatedness and spatial autocorrelation in your analyses.

What you'll gain

- A strong understanding of phylogenetic comparative methods and Bayesian Phylogenetic Mixed Models (BPMMs)
- Practical experience implementing phylogenetic models in R
- Skills to incorporate phylogenetic and spatial structure into ecological analyses
- Understanding of model interpretation, diagnostics, and uncertainty
- Confidence in analysing comparative datasets using modern Bayesian workflows

Course format

- Live, instructor-led online training
- Hands-on coding with real-world evolutionary and ecological datasets
- Interactive practical exercises throughout
- Strong focus on applied, research-ready workflows

Who is this course for?

- Evolutionary biologists and evolutionary ecologists
- Comparative biologists and macroecologists
- Population geneticists and quantitative biologists
- Researchers working with phylogenetic, trait, or spatial datasets
- PhD students and quantitative life scientists

Why take this course?

Accounting for shared evolutionary history is fundamental to comparative biology. Ignoring phylogenetic relationships can lead to biased estimates and incorrect biological conclusions, while failing to account for spatial structure can further compromise ecological inference.

This course brings together phylogenetic comparative methods, Bayesian modelling, and spatial analysis into a single, coherent workflow. Whether you're studying trait evolution, species distributions, macroecology, community ecology, or biodiversity patterns, you'll learn how to build robust statistical models that properly account for both evolutionary relationships and spatial dependence.

Learn more & enrol

PR Stats course page for Spatial Phylogenetics and the Bayesian Phylogenetic Mixed Model (BPMM01) <https://prstats.org/course/spatial-phylogenetics-and-the-bayesian-phylogenetic-mixed-model-bpmm01/> Questions? Email: oliver@prstats.org

Oliver Hooker Managing Partner Advanced Training for Researchers in the Life Sciences coursesinfo@prstats.org — www.prstats.org (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

ONLINE SpeciesDistributionModellingwithBayesianStatistics Oct6-8

Species Distribution Modelling with Bayesian Statistics (SDMB08) - Applications for Evolutionary Biology <https://prstats.org/course/species-distribution-modelling-with-bayesian-statistics-sdmb08/> Delivered by Dr. Marcia Barbosa, a biogeographer and macroecologist with extensive expertise in species distribution modelling, ecological niche modelling, GIS, and biodiversity forecasting. Learn how to build Bayesian Species Distribution Models (SDMs) using Bayesian Additive Regression Trees (BART), with methods that are highly applicable to evolutionary biology, biogeography, and macroevolutionary research. Species distributions reflect both contemporary environmental conditions and evolutionary history. Bayesian species distribution modelling is increasingly used to investigate historical range dynamics, ecological niches, adaptation, diversification, and the processes shaping biodiversity across space and time. This hands-

on course introduces Bayesian SDMs using BART, providing a practical workflow for building, validating, and interpreting predictive distribution models while explicitly accounting for uncertainty. What you'll gain - A strong understanding of Bayesian species distribution modelling - Practical experience building SDMs using BART in R - Skills in model validation, cross-validation, and performance assessment - Understanding of prediction uncertainty and credible intervals - Confidence in interpreting variable importance, partial dependence plots, and habitat suitability maps Course format - Live, instructor-led online training - Hands-on coding with real-world ecological datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Evolutionary biologists and evolutionary ecologists - Biogeographers and macroecologists - Researchers investigating adaptation, speciation, and historical biogeography - PhD students and quantitative life scientists - Anyone interested in combining Bayesian modelling with evolutionary research Why take this course? Species distribution models have become an important component of modern evolutionary biology, allowing researchers to investigate how environmental factors influence species ranges, ecological niches, and diversification. Bayesian approaches provide an important advantage by quantifying uncertainty while producing robust predictions, making them particularly valuable for studying historical distributions, niche evolution, climate change, adaptive divergence, and the ecological processes that drive evolutionary change. This course equips you with the practical skills needed to develop, evaluate, and interpret Bayesian species distribution models using BART. Whether you're studying niche evolution, phylogeography, adaptive radiation, historical range shifts, or the impacts of past and future climate change on biodiversity, you'll gain the knowledge and confidence to apply modern Bayesian SDM methods to your own evolutionary research. Learn more & enrol PR Stats course page for Species Distribution Modelling with Bayesian Statistics (SDMB08) <https://prstats.org/course/species-distribution-modelling-with-bayesian-statistics-sdmb08/> Questions? Email: oliver@prstats.org

Oliver Hooker Managing Partner Advanced Training for Researchers in the Life Sciences coursesinfo@prstats.org — www.prstats.org (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Online TransposableElements 2-6November

Dear all, We are pleased to announce the online course "Bioinformatic Analysis of Transposable Elements", taking place 2-6 November (7th edition).

Course website: <https://www.physalia-courses.org/courses-workshops/course24/>

Transposable elements (TEs) are major drivers of genome evolution and structural variation, yet their rapid evolution and repetitive nature make them challenging to identify and analyse—particularly in non-model organisms. This course provides a practical introduction to TE biology and computational analysis, equipping participants with the skills needed to tackle these challenges.

Through a combination of lectures and hands-on practical sessions, participants will learn to: - Discover and annotate TEs in genome assemblies - Build and curate de novo TE libraries - Classify and manually curate TE sequences - Analyse TE insertion polymorphisms and transcriptomic data - Interpret computational results in the context of TE biology

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

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UAuckland Australia Summer Institute in Statistical Genetics

The Summer Institute in Statistical Genetics (SISG) has been offered annually in the US since in 1995. It is now directed by Greg Gibson at the Georgia Institute of Technology in Atlanta. We are delighted that for the 3rd time in its history, a version of SISG will be run in New Zealand, hosted by Waipapa Taumata Rau - University of Auckland. Questions? Please con-

tact Prof Bruce Weir and Assoc Prof Anna Santure: bsweir@uw.edu; a.santure@auckland.ac.nz

Registration page : <https://events.humanitix.com/southern-ssig-auckland-2026> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UKonline PRStats RNA-seqAnalysis 7-10September2026

RNA-Seq Analysis (RNAA02) <https://prstats.org/course/rna-seq-analysis-rnaa02/> Delivered by experienced bioinformaticians and computational biologists specialising in transcriptomics and sequencing data analysis. Delivered online over 4 days, 18:00-21:00 UK time. Learn how to analyse RNA-Seq data using modern transcriptomic workflows in R. RNA sequencing (RNA-Seq) has become one of the most powerful technologies for studying gene expression, enabling researchers to investigate biological processes across a wide range of organisms and experimental systems. This hands-on course provides a practical introduction to RNA-Seq data analysis, covering quality control, differential expression, visualisation, and functional interpretation using reproducible workflows in R. ***What you'll gain*** - A strong understanding of RNA-Seq experimental design and transcriptomic workflows - Practical experience analysing RNA-Seq data in R - Skills in quality control, read alignment, differential expression analysis, and visualisation - Understanding of functional enrichment and pathway analysis - Confidence in interpreting transcriptomic results and communicating biological findings ***Course format*** - Live, instructor-led online training - Hands-on coding with real-world RNA-Seq datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows

Who is this course for? - Bioinformaticians and computational biologists - Molecular biologists and geneticists - Researchers working with transcriptomics or sequencing data - PhD students and life scientists - Anyone interested in modern genomic data analysis

Why take this course? RNA-Seq has become the standard approach for investigating gene expression across diverse areas of biology, from development and evolution to disease, physiology, agriculture, and conservation. As sequencing technologies continue to advance,

researchers are generating increasingly large and complex transcriptomic datasets that require robust statistical analysis and reproducible computational workflows. This course equips you with the practical skills needed to move confidently from raw sequencing data to biological insight. You'll learn modern RNA-Seq analysis workflows, develop a strong understanding of best practices, and gain the tools to analyse and interpret transcriptomic datasets for a wide range of research applications. ***Learn more & enrol*** PR Stats course page for RNA-Seq Analysis (RNAA02) <https://prstats.org/course/rna-seq-analysis-rnaa02/>***Questions?*** Email: oliver@prstats.org (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

ZJU Hangzhou China 5th YoungTalentSymposiumEvolBiol

The 5th Young Talent's Symposium of Evolutionary Biology Date: September 29, 2026 Location: Zhejiang University, Hangzhou, China Host: Center for Evolutionary & Organismal Biology

About the Forum Dedicated to supporting early-career scholars, this forum offers a premier platform to foster academic exchange, connect with peers, and explore ca-

reer advancement in evolutionary biology. Since 2022, we have welcomed scholars from across the globe (including China, the US, UK, Germany, and France) to discuss cutting-edge topics ranging from molecules to ecosystems—including phylogenetics, computational biology, comparative genomics, ancient DNA, and more. Remarkably, many of our past participants have successfully secured faculty positions at institutions across China following the forum.

Call for Speakers We invite postdoctoral researchers and senior PhD candidates worldwide working at the frontiers of evolutionary biology to share their research works. Candidates who are interested at working in China in future are preferred, and selected candidates will receive support for travel and accommodation. - Format: 30-minute presentation followed by a Q&A discussion. - Audience: Peers and distinguished senior professors/experts from across China.

How to Register We warmly encourage all scholars passionate about evolutionary biology to join us! - Option 1: Visit the link (<https://forms.gle/qrpgr7K6J3MTccqP7>) to apply. - Option 2: Send your CV or questions directly to evolution@zju.edu.cn. (We will contact you shortly with further details.)

Review Panel Members: Luonan Chen (Shanghai Jiao Tong University) Xionglei He (Sun Yat-sen University) Jianquan Liu (Lanzhou University) Bing Su (Kunming Institute of Zoology)

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Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to evoldir@evoldir.net. 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 evoldir@evoldir.net. In addition, if it originates from 'blackballed' addresses it will be sent to evoldir@evoldir.net. 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 notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to evoldir@evoldir.net. 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@evoldir.net`. Do not include encoded attachments and do not send it as Word files, as HTML files, as $\text{\LaTeX}$ 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 formatted) the message will be sent to `evoldir@evoldir.net` 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 preformatting 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 $\text{\LaTeX}$ do not try to embed $\text{\LaTeX}$ or $\text{\TeX}$ in your message (or other formats) since my program will strip these from the message.