
E v o l D i r

July 3, 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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2026 Great Lakes Annual Meeting Evolutionary Genomics GLAM-EvoGen

2026 Great Lakes Annual Meeting of Evolutionary Genomics (GLAM-EvoGen) We are excited to announce that the 2026 Great Lakes Annual Meeting of Evolutionary Genomics (GLAM-EvoGen) will take place on Saturday, August 15, 2026 at the University at Buffalo. More information is available on our website: <https://gokcumenlab.org/glam2026/> Registration and abstract submission are now open and free: <https://forms.gle/84MRmLtMJgbTpY6DA> The abstract submission deadline is July 24; registration will remain open until August 10. As always, all presenters are trainees, and we warmly encourage you to support your students and postdocs in attending and presenting. – 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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Firenze Evolution2026 Sep6-10

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

————Early bird registration deadline extended————

Dear friends and colleagues of SIBE,

We are pleased to inform you that the early-bird registration deadline has been extended until June the 30th. We are also delighted to announce that an additional invited speaker will join our conference: Telmo Pievani will deliver a Plenary Lecture and Round Table entitled "Human Sociobiology: A Half-Century Debate", concluding the symposium "Evolutionary Roots of Behavioural Diversity."

There are still places available for the free crash course organized as part of the conference. The program can be found here, and registration is available through the dedicated form.

The scientific program will be organized around the following symposia:

Symposium 1 "Host-microbiome interactions" Symposium 2 "Evolutionary roots of behavioural diversity" Symposium 3 "Phylogeography and Conservation Genomics: understanding evolutionary history to sustain species resilience" Symposium 4 "Human evolution" Symposium 5 "The evolution of ecological diversification: mechanisms, interactions, and outcomes" Symposium 6 "Evolutionary biology without borders"

Each symposium will open with a plenary lecture by an international invited speaker, including Stephen Palumbi, Mihai Netea, David Caramelli, Martin Giurfa, Jacintha Ellers, Mirte Bosse, and Maurizio Mencuccini.

In addition to the scientific sessions, the congress will offer several events, including a dedicated poster session, a free crash course on wet-lab techniques in genomics, the meeting of the Italian Group for Conservation Genetics and Genomics, the original outreach theatre event "Botanica Queer", and a social dinner at

the Florence Botanical Garden.

The congress will take place across several venues in the city. All scientific sessions will be held in the Novoli district, at the University's Social Sciences Campus, while social events and the poster session will take place in the historic city centre. Participants may therefore choose to stay either in the city centre or in Novoli, two areas conveniently connected by the tram line.

Please note that the last tram runs at around 00:30; after this time, public transportation options become more limited. September is a high season for tourism in Florence, and other conferences are scheduled in the Novoli area during the same period. We therefore strongly recommend booking accommodation well in advance.

For further details about Evoluzione 2026, please visit the website: www.sibe-iseb.it/firenze2026 We look forward to welcoming many of you to Firenze, The Organizing and Scientific Committee

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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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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-

Online AnimalBehaviourLive2026 Nov12

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/1AQDEBXEKbz6SmZASCS8fxKl3u-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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Senckenberg Molluscan Genomics Aug30-Sep3

Dear mollusc fans There are less than two weeks to go until the registration and abstract deadline for the 2nd Molluscan Genomics Workshop 2026 at Senckenberg Nature Research in Frankfurt! When: 30 August - 3 September 2026 (Sunday-Thursday) Where: Senckenberg Museum, Frankfurt, Germany Registration and abstract deadline: 14 June 2026 Registration fee: 65 euro (flat rate for all participants) https://express.converia.de/frontend/index.php?folder_id=12190&page_id=12190 This is a focussed workshop to exchange current advances and adventures in the analyses of molluscan genomes. This conference is in person only. There is an absolute limit of 180 participants. We are grateful to the Deutsche Forschungsgemeinschaft (German Research Foundation [https://www.dfg.de/](https://www.dfg.de/jhttps://www.dfg.de/)) for conference funding as well as our sponsors Arima, PacBio, and Novogene for their support. We look forward to welcoming you in Frankfurt. Best wishes, Julia Sigwart & Carola Greve

Prof Dr Julia Sigwart Head of Section, Malacology Senckenberg Research Institute and Museum @sigwartae — bit.ly/SMFMalacology

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Switzerland Microbial Predation July27-31

Microbial Predation Conference 2026 Monte Verita, Switzerland – July 27-31, 2026 Join us in lovely Ticino, Switzerland to discuss what microbial predation looks like, how it originates and evolves, and how it shapes microbial communities. Researchers studying diverse aspects of microbial predation with different predator-prey systems will gather to promote conceptual synthesis across systems and questions. Submit abstracts and register by Friday, June 12th. Conference website: <https://microbialpredation.ethz.ch> Invited speakers include: Lutz Becks - University of Constance, Germany Antonis Chatzinotas - Helmholtz Center for Environmental Research, Leipzig, Germany Yen-Ping Hsueh - Max-Planck Institute for Biology, Tuebingen, Germany Andrew Lovering - University of Birmingham, UK David Queller - Washington University in St. Louis, USA Joan Strassmann - Washington University in St. Louis, USA Renske van Raaphorst - University of Groningen, The Netherlands With the Conference on Microbial Predation 2026, we seek to bring together microbial-predation researchers who rarely meet under a single scientific umbrella, including molecular microbiologists, ecologists, evolutionary biologists, theoreticians, and biocontrol researchers, promoting integration across microbial systems and connection with concepts largely associated with macroscopic predators. The conference provides a forum where diverse perspectives can converge to build shared conceptual frameworks, new interdisciplinary collaborations can be initiated, and the global community of microbial-predation researchers can more deeply interconnect. We welcome researchers working with animals who want to think more about microbial predation.

WE HAVE STUDENT SUPPORT FUNDS! Thanks to the Swiss National Science Foundation, we have received funds to support conference attendance by students from more financially limited contexts. We can provide support grants of 300 Swiss francs to each of 15 students. To be considered for a support grant, send an email to microbialpredation2026@ethz.ch Indicate your student status – Bachelor, Master or PhD – and institution, and a brief statement of how a grant would facilitate your participation.

Major themes: Behavior Ecology Evolution Molecular mechanisms Social aspects of predation Applications
 Scientific organizers: Marie Vasse, CNRS / University of Bordeaux, France Greg Velicer, ETH Zurich, Switzerland

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

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Ventura VA GordonResearchConference Urban Evolution and EcologyJan31-Feb5

Gordon Research Conference in Urban Evolution and Ecology Dear colleagues,

We are excited to announce the inaugural Gordon Research Conference in Urban Evolution and Ecology (<https://www.grc.org/urban-evolution-and-ecology-conference/2027/>) Jan 31-Feb, 2027 in Ventura, California.

You can check out the full program, list of speakers and discussion leaders following the link above, and you can already apply via the same website. Reviews of applications will start early September, and the application portal will stay open until Jan 3, 2027, unless the conference is full before this deadline.

Please forward this announcement to anyone who is interested in Urban Evolution, Urban Ecology, and/or Urban Evolutionary Ecology!

Best wishes, Anne Charmantier (co-chair) Marc Johnson (co-chair) Kiyoko Gotanda (vice-chair) Brian Verrelli (vice-chair)

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 UParisSaclay EvolutionaryEcology 8
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 VIB Ugent Belgium PhD Position Experimental Evolution and Bioinformatics 9
 Vienna Austria PhD Eco-Evolutionary Theory ??

Berlin Humboldt GraduatePosition PhD Animal Behaviour

GraduatePosition $_{PhD}$ AnimalBehaviourHumboldtBerlin

The DFG Emmy Noether project "Maintaining the balance of power in animal societies" investigates how

levelling processes, which may have different underlying mechanisms but exhibit functional convergence, constrain inequality in different species. Using long-term data (i), the PhD student will investigate the situational drivers of coalitionary formation in birds and mammals in collaboration with Eli Strauss (DomArchive) and Lauren Brent (Cayo Santiago, MacaqueNet). The PhD student project also involves collective movement experiments (ii) with robotic fish and small freshwater fish in the aquariums at the Humboldt Uni-

versity of Berlin, in collaboration with David Bierbach and Jens Krause. The PhD student will be supervised by the Emmy Noether Group Leader Danai Papageorgiou.

Deadline: July 6th 2026

See more on: <https://www.hu-berlin.de/en/university/working-at-the-hu/jobs/details/wissenschaftlicher-mitarbeiterin-m-w-d-im-bereich-tierverhalten-dr-103-26> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

ETHZurich Microbial PredatorPrey Coevolution

Comparative predator-prey co-evolution in complex microbial communities Applications are invited for a postdoc position and a PhD position in the group of Greg Velicer at ETH Zurich as part of our team researching predator-prey co-evolution in species-rich microbial communities.

Both positions will focus primarily on the evolution experiment MyxoEE-KillerProfiles, the first phase of which is visually summarized at <https://www.myxoe.org/newmyxoees>. In MyxoEE-KillerProfiles, highly diverse predators of microbes – Bdellovibrio-and-like-organisms, dictyostelids, nematodes and myxobacteria – are co-evolving with a 20-species synthetic community of bacterial prey in both single-predator and multiple-predator treatments. Among other questions, we are asking how different predators comparatively shape prey-community evolution and themselves comparatively evolve at predation-related traits. We also ask how combining multiple predators together alters the evolution of each predator and of the prey community. Evolved communities and organisms will be analyzed with various approaches addressing fitness, behavior, collective phenotypes, genomes, community composition and molecular-genetic mechanisms of adaptation. The postdoc who developed the protocols for and conducted the first phase of MyxoEE-KillerProfiles, Dr. Jos Kramer, has started his own group with an ERC Starting Grant on a different project. We seek candidates with a strong record of creative research from any relevant training background who thrive at both team and individual work in a scientifically and culturally diverse group. Relevant training areas include evolutionary community ecology, community metage-

nomics, experimental evolution, microbial ecology, microscopy, and molecular genetics. The selected postdoc will help mentor younger group members involved in the project. The postdoc will be supported from a Swiss National Science Foundation grant while a competitive fellowship (e.g. ETH, EMBO, MSCA) is sought, potentially for up to three years. To apply for one of the positions, send one file to Rita Jenny at rita.jenny@env.ethz.ch that includes a motivation statement (one page max), your CV and contact information for two persons who have agreed to serve as references. Review of applications will begin June 29th. Specify the relevant position with a subject line of either "predation postdoc" or "predation PhD". Informal inquiries can be sent to gregory.velicer@env.ethz.ch. Zurich, Switzerland has vibrant communities of ecologists, evolutionary biologists and microbiologists that offer many opportunities for interaction and collaboration. (<https://ibz.ethz.ch/research/eco-evo-zurich.html>) Background Velicer group research: <https://evo.ethz.ch/Myxobacteria> Evolution Experiments: myxoe.org New review article on microbial predation: <https://doi.org/10.1038/s41579-026-01299-7> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Germany Doctoral Researchers Plant Ecological Genetics

The SFB TRR 341 "Plant Ecological Genetics" is a collaborative research consortium based in Cologne and Dusseldorf, which extends across a total of 9 German institutions. This consortium brings together expert researchers across various disciplines in the plant sciences, with the aim of linking ecology and genetics to study plant adaptation. Our consortium is currently looking for 10 doctoral researchers (PhD students) to join us for our second funding phase on diverse projects investigating plant ecology and genetics. The successful candidates will be located where the project is based, i.e. one of the following institutions: Universities of Cologne, Dusseldorf (HHU), Bochum (RUB), Max Planck Institute for Plant Breeding Research (MIPZ, Cologne) or Julius-Kuhn Institute (JKI, Rostock). All doctoral researchers part of the TRR 341 will automatically be affiliated to the Graduate school for Ecological Genetics, which provides the opportunity for strong networking among researchers despite the physical distance. Please find the list of open projects here: <https://>

[//trr341.uni-koeln.de/join-us](https://trr341.uni-koeln.de/join-us) Please send your application by Friday 10th of July and find all the details here: <https://jobportal.uni-koeln.de/ausschreibung/renderFile/2632?propertyName=flyer> For further information, please feel free to contact trr341-office@uni-koeln.de

– Dr. Sophie-Asako XERRI Scientific coordinator for TRR 341 Graduate School for Ecological Genetics (GEcoGen) coordinator

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GraduatePosition PhD EvolutionaryGenomics NTNU Norway

The NTNU University Museum is seeking a highly qualified, ambitious, and motivated PhD candidate for a project focusing on the genomics of cryptic coloration in anurans. **** About the position **** Anurans display a diversity of colors and patterns that enable them to avoid detection by predators through background matching, masquerade (e.g., resembling leaves or bird droppings), or disruptive coloration. In many cryptically colored species, multiple color morphs co-occur within populations, and similar polymorphisms have evolved repeatedly across distantly related taxa. Proposed mechanisms for the maintenance of such polymorphisms include spatial and temporal variation in selection, heterozygote advantage, and pleiotropic effects linking coloration to other fitness-related traits. The PhD project will generate and analyze genomic and transcriptomic datasets derived from both samples collected in the field (e.g., Ethiopia, Borneo), and tissue collections in natural history museums. Using population and comparative genomics approaches, the candidate will have opportunities to investigate the evolutionary mechanisms underlying (i) the maintenance of cryptic color polymorphisms within species, and/or (ii) the repeated evolution of similar cryptic color traits across lineages. While the project will primarily be computational and lab-based, there will be opportunities to develop complementary field experiments. The focal study system will be defined in collaboration with the successful candidate. The successful candidate will be employed at the NTNU University Museum's Department of Natural History. The NTNU University Museum is the natural and cultural history museum of

the Norwegian University of Science and Technology in Trondheim. The Department of Natural History conducts research in systematics and taxonomy, evolutionary genomics, as well as in phylogeography, population genetics, and ecology with an emphasis on conservation biology. **** Selection criteria **** Prior to starting the PhD position, you must have obtained the equivalent of 120 course credits, corresponding to a five-year Norwegian master's level. We are looking for a student with a master's degree in biology or equivalent with specialization in population genetics, population genomics, evolutionary biology, or closely related fields. The master's degree must be obtained and documented before starting the position and no later than September 1st, 2026. Very good written and oral English language skills are necessary. Experience with modern statistical techniques using relevant scripting languages (R, python, bash, etc.), DNA extraction and genomic library preparation, or field work would be a plus. **** Application **** The application must include: A letter of motivation (max. 2 pages) stating specifically why you believe you meet the selection criteria Transcripts and diplomas for Bachelor's and Master's degrees CV, certified copies of certificates and diplomas Copy of Master's thesis. If you have recently submitted your Master's thesis, or are about to submit, you can attach a draft of the thesis. Documentation of a completed Master's degree must be presented before taking up the position. Publications or other relevant research work if you have such Names and contact information of two relevant referees

More information about the position and the application process can be found online: <https://www.jobbnorge.no/en/available-jobs/job/303353/phd-candidate-in-evolutionary-genomics-of-cryptic-coloration-in-frogs> Application deadline: 30 July 2026 If you have any questions about the position, please contact Sandra Goutte (sandra.goutte@ntnu.no).

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GraduatePosition UOxford PhD Evolutionary history of pathogens using aDNA

Reconstructing the evolutionary history of pathogens using ancient DNA

Are you interested in using ancient DNA to understand

the long-term evolution of infectious disease? This is an exciting opportunity to join the University of Oxford as a DPhil candidate, working at the intersection of ancient DNA, pathogen genomics, archaeology, and evolutionary medicine.

This four-year DPhil studentship is funded by the Royal Society for UK/home students, with fees covered at the home rate and a stipend provided at the UKRI rate. The successful candidate will join the DPhil in Genomic Medicine and Statistics programme, based at the Centre for Human Genetics, Nuffield Department of Medicine, University of Oxford. The project will also involve close collaboration with the ancient DNA laboratory at the School of Archaeology.

The successful candidate will use a combination of wet-lab and computational approaches. The laboratory work will involve ancient DNA methods, including target enrichment strategies designed to recover low-abundance pathogen DNA from archaeological samples. The computational work will involve genomic and evolutionary analyses of ancient pathogen sequences, with the aim of understanding how zoonotic pathogens have evolved across human and animal hosts.

<https://www.medsci.ox.ac.uk/study/graduate-school/courses/dtc-structured-research-degrees/genomic-medicine-statistics/gms-royal-society-studentship> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

LehighU EvolGenomics

The Schultz EvoGenome Lab at Lehigh University (Bethlehem, PA, USA) is recruiting a PhD student for Fall 2027, through the Department of Biological Sciences.

I'm looking for a motivated student excited about comparative genomics at chromosome scale and genome evolution across the tree of life, with a focus on animals and their close relatives. The lab spans genome assembly, computational analysis, and (for the curious) molecular/cell biology and marine fieldwork. Students develop their own dissertation projects that dovetail with these themes.

Ideal candidates would have: programming/bioinformatics experience, wet-lab molecular/cell biology, microscopy, or interest in cruise-based field-

work. Admitted PhD students receive a competitive 12-month stipend, normally for the duration of the program.

Deadline: January 1, 2027. Please email me before applying to discuss fit and ideas: dts@lehigh.edu

Lab: <https://evogeno.me/Bio>: <https://bio.cas.lehigh.edu/faculty-staff/darrin-schultz> Program: <https://bio.cas.lehigh.edu/graduate/applying-lehigh> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

UCL Social Evolution Microbes

We are recruiting for a PhD position at UCL funded by the Evolution Education Trust. The studentship comes with four years of funding, including generous allowances for research, travel, and conferences. Full details are available at:

<https://www.findaphd.com/phds/project/why-does-altruism-exist/?p197451> Please pass this along to anyone you know looking for a PhD position in social evolution (but note that full funding is only available to candidates who are eligible for UK 'home fees': UK citizens or pre/settled status). For further information etc. they can contact me (j.b.wolf@bath.ac.uk) or Chris Thompson (christopher.thompson@ucl.ac.uk).

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UParisSaclay EvolutionaryEcology

PhD position in Evolutionary Ecology at University Paris Saclay, France. Theoretical and statistical modeling of eco-evolutionary feedback loops from abundance-phenotype time series *** Scientific Context *** Eco-evolutionary feedback loops describe reciprocal interactions between the genetic adaptation of organisms and the biotic or abiotic environment in which they evolve. While environmental components such as temperature or competition impose natural selection on morphology, physiology, and behavior, organisms in turn modify the environment through their abundance

and traits, influencing ecosystem functioning and stability. Despite their theoretical and applied relevance, eco-evolutionary feedback loops remain poorly understood empirically. Few theoretical or statistical tools currently exist to detect them from observational data in the wild and to predict their consequences on population dynamics and trait evolution. *** Project overview ***

This project focuses on a potentially major feedback loop between body size and population density. Body size is a key ecological trait that may further influence individual reproductive output. In turn, population density also affects body size, either via plastic responses or by modifying the evolutionary optimum through competition intensity. The project has both a fundamental and a methodological purpose : (i) from a fundamental point of view, determining the conditions under which eco-evo feedback loops emerge under natural settings, and (ii) from a methodological point of view, assess the sampling strategy and modeling tools making it possible to detect such loops. The PhD student will develop a theoretical framework and exploit advanced statistical tools to detect eco-evolutionary feedbacks from abundance-body size time series. Specifically, the student will extend a base eco-evo model recently developed by our consortium to account for increasing biological complexity (e.g, overlapping generations, population structure) or specific sampling effects, such as a limited capture rate. *** Skills *** We are looking for a student with a Master degree in applied mathematics, theoretical biology, or ecology, attracted by fundamental questions in ecology and evolution. Solid training in programming (R, Python), and statistics (Bayesian and frequentist approaches, knowledge in machine learning would be appreciated) is required. Your Work Environment This PhD position is already funded as part of the collaborative BackOut ANR project (eco-evolutionary feedback loops out from the laboratory) running from 2025 to 2029, involving 6 national and international partners. The PhD student will be co-supervised by Arnaud Le Rouzic (CNRS researcher, EGCE, IDEEV, Université Paris-Saclay) and Eric Edeline (INRAE Research Director, DECOD, Rennes), and will benefit from interactions with other project partners (6 virtual meetings/year), including Julien Papaix (INRAE BioSP) and Willem Bonnafe (Oxford University). The student will be based at the EGCE research unit in Gif-sur-Yvette, 35 km south of Paris, on the new Paris-Saclay campus. EGCE is part of the Institute for Diversity, Ecology, and Evolution; Le Rouzic's "Genomes and Evolution" group hosts 8 researchers and 15 international students and postdocs. Frequent physical meetings with

the co-supervisor will be organised. *** Application *** A CV and a cover letter (mentioning two references) must be submitted through the CNRS application web site (<https://emploi.cnrs.fr/Offres/Doctorant/UMR9191-ARNLER-008/Default.aspx?lang=EN>), before June 22 2026. Preliminary enquiries can be e-mailed to Arnaud Le Rouzic (arnaud.le-rouzic@universite-paris-saclay.fr) and Eric Edeline (eric.edeline@inrae.fr).

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UppsalaU PopulationPalaeoGenomics

recruiting a new PhD student to join our team at Uppsala University, Sweden.

Deadline: Aug 7th

Apply here: <https://www.uu.se/en/about-uu/join-us/jobs-and-vacancies/job-details?query=944189> – Torsten Gunther Universitetslektor/Associate Professor Human Evolution Research Program, Department of Organismal Biology Evolutionary Biology Centre Uppsala University Sweden <https://www.gunther-lab.org> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

VIB UGent Belgium PhD Position Experimental Evolution and Bioinformatics

Yves Van de Peer (VIB-UGent, bioinformatics and evolutionary genomics)) and Olivier De Clerck (UGent, Phycology Research Group) are looking for a highly motivated PhD student to study the impact of genome duplication on volvocine algae, with a particular focus on *Chlamydomonas reinhardtii*. The project will investigate how genome dynamics and environmental conditions interact to shape the evolutionary success of polyploids using: *Experimental evolution approaches, including long-term laboratory experiments, strain maintenance, culturing, and phenotyping. These are labor-

Jobs

Bonn Germany LIB Curatorial Assistant biobank- Management of Cell Culture Laboratory	10	RZSS Edinburgh Zoo ConservationGenetics	13
Bonn Germany LIB Technical Assistance Molecular lab 11		Smithsonian NMNH CuratorsX3 Ornithology Herpetol- ogy Ichthyology	14
Cardiff UK National Museum Head of Botany	11	Taiwan NSYSU FacultyPosition Biology	15
Galapagos Field assistants needed Sea Lion Project	12	ULaval Canada FacultyPosition Cell BiologyMolecular- BiologyOrGenetics	15
Hamburg Germany LIB Curator Ornithology	12		

Bonn Germany LIB Curatorial Assistant biobank-Management of Cell Culture Laboratory

Curatorial Assistant at the biobank/ Management of the Cell Culture Laboratory (f/m/d) — We are looking for a candidate to start on August 1 on a fixed-term contract in accordance with the Part-Time and Fixed-Term Employment Act, initially ending on June 30, 2028, as Curatorial Assistant at the biobank/ Management of the Cell Culture Laboratory (f/m/d) in part-time (60

Link to the add: [https://8101202752.karriereportal.cloud/job/2026-13-Curatorial-Assistant-at-the-biobank_-Management-of-the-Cell-Culture-Laboratory-\(f_m_d\)](https://8101202752.karriereportal.cloud/job/2026-13-Curatorial-Assistant-at-the-biobank_-Management-of-the-Cell-Culture-Laboratory-(f_m_d))

Your Tasks: Laboratory work in our DNA and especially cell culture laboratories; data evaluation, literature research, establishment of (partly species-specific) protocols, particularly in the areas of cell culture and cryopreservation Management of biobank samples: documentation, quality control, data management, preparation, preservation, and depositions Selection of biobank samples for requests and applications, international communication regarding these, sample retrieval, and shipping Management of the cell culture laboratory; development and adaptation of laboratory safety concepts Supervision and guidance of users, interns, students, etc.; laboratory briefings

Your profile: Completed university degree in life sciences or relevant professional experience Extensive experience in cell culture laboratories, including developing and adapting cell culture protocols (especially for

different animal species) Experience with karyotyping is advantageous but not mandatory Experience in managing biobank samples Good IT skills (databases, spreadsheets) and solid English language skills for international correspondence Team orientation and strong social competence, meticulous and responsible work style, initiative, and problem-solving skills High flexibility regarding working hours (especially concerning cell culture)

We offer: An attractive position in an excellent research institution with a high degree of creative potential in a dynamic scientific and social environment Collaboration within an inclusive and dynamic LIB Biobank team, in a modern cell culture laboratory and cryorepository located on the Bonn-Poppelsdorf campus, at the interface of various biobank networks (e.g., GGBN Secretariat) Remuneration according to the collective agreement of the federal states (EG 10) with all the benefits of the public sector (company pension scheme, annual special payment, capital-forming benefits, collectively agreed vacation entitlement) Family friendliness certified by the "Work and Family Audit", offer of life coaching through professional family service the possibility of obtaining a job ticket A centrally located workplace with excellent transport links

Please send your complete application documents (including cover letter, CV, copies of certificates, max. 10 MB) by 21.06.2026 exclusively digitally via our career portal. [https://8101202752.karriereportal.cloud/job/2026-13-Curatorial-Assistant-at-the-biobank_-Management-of-the-Cell-Culture-Laboratory-\(f_m_d\)](https://8101202752.karriereportal.cloud/job/2026-13-Curatorial-Assistant-at-the-biobank_-Management-of-the-Cell-Culture-Laboratory-(f_m_d))/bewerben to Ms. Jennifer Scholze. For organizational reasons, only online applications will be accepted. We are a diverse institution and welcome our diversity. We would particularly like to encourage women to apply in order to actively promote equal opportunities. Severely disabled people will

be given preference if equally qualified. You can find more information about our institution on the Internet at: <https://leibniz-lib.de/>.

KONTAKT / CONTACT PERSONALADMINISTRATION Jennifer Scholze: +49 228 9122197 E-Mail: Beerbung@leibniz-lib.de

— The Leibniz Institute for the Analysis of Biodiversity Change (LIB) is one of the large, globally connected research museums of the Leibniz Association. In addition to excellent research on biodiversity and its change, we are advancing the further development of our extensive scientific collections with an international team and state-of-the-art technology. With our exhibition, knowledge transfer and communication work at our exhibition venues Museum Koenig Bonn and Museum der Natur Hamburg, we want to spread enthusiasm for nature and contribute with our research topics to current socio-political discussions on species loss, climate change and the protection of ecosystems. Become part of our institute in Bonn.

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

Stiftung des öffentlichen Rechts;

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Bonn Germany LIB Technical Assistance Molecular lab

Technical Assistance for our Molecular lab in Bonn (f/m/d) We are looking for a Technical Assistance for our Molecular lab in Bonn (f/m/d) in part time (29,87 h / week) at the Leibniz Institute for the Analysis of Biodiversity Change (LIB) Only online applications are accepted. Link to the add (in German): [https://8101202752.karriereportal.cloud/job/2026-17-Technische-Assistenz-im-Molekularlabor-\(w_m_d\)](https://8101202752.karriereportal.cloud/job/2026-17-Technische-Assistenz-im-Molekularlabor-(w_m_d))

– Stiftung Leibniz-Institut zur Analyse des Biodiversitätswandels Postanschrift: Adenauerallee 127, 53113 Bonn, Germany Stiftung des öffentlichen Rechts; Generaldirektion: Prof. Dr. Bernhard Misof (Generaldirektor), Adrian Gruter (Kaufm. Geschäftsführer) Sitz der

Stiftung: Adenauerallee 160 in Bonn Vorsitzender des Stiftungsrates: Dr. Michael H. Wappelhorst

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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.ciphr-irecruit.com/Applicants/vacancy/2682/Head-of-Botany-National-Museum-Cardiff?m=0> (to subscribe/unsubscribe the EvolDir send

mail to evoldir@evoldir.net) 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 experi-

ence 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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Hamburg Germany LIB Curator Ornithology

Curator Ornithology (m/f/d) in full-time at the Leibniz Hamburg Institute for the Analysis of Biodiversity Change (LIB) Become part of our institute in Hamburg. We are looking for the next possible date, limited according to the WissZeitVG for three years a scientist for a position as Curator Ornithology (m/f/d) in full-time 39.00 hours/week at LIB Hamburg, representing research at an internationally competitive level. The successful candidate will bring together the bird collection and ornithological research on biodiversity change

in space and time.

Link to the add: [https://8101202752.karriereportal.cloud/job/2026-18-Curator-Ornithology-\(m_f_d\)](https://8101202752.karriereportal.cloud/job/2026-18-Curator-Ornithology-(m_f_d))

Your Tasks: - Integrate into the Centre for Taxonomy and Morphology in Hamburg and play a strong role in advancing the LIB's reputation as a preeminent institution for the study of biodiversity change on a global scale - Conduct internationally recognised collection-based research and build a research group in Hamburg - Assume full curatorial responsibility for the ornithological collection housed by LIB Hamburg, including preparing for and relocating the ornithological collection into the new museum building (projected building completion: 2030-2032) - Additional curatorial duties such as collection management, provision of scientific services, expansion and digitization of the collection, and contributions to outreach activities - Promote and lead LIB-internal teamwork and external collaborations - Forge collaborations within the LIB (Hamburg and Bonn)

Your profile: The candidate's scientific expertise should include collection-based ornithological research and must cover at least one of the following research fields: - Systematics, taxonomy and phylogenetics - Evolution of phenotypic traits - Functional ecology - Biogeography - With a preference for methodologies such as morphometrics, bioacoustics or phylogenomics Requirements: - a PhD in zoology, biology or related areas with a focus on ornithology, - expertise in taxonomy and systematics in extant birds, - hands-on working experience with natural history collections, especially birds, - high quality publication record relative to opportunity - track record of third-party funding relative to opportunity - track record, or potential of developing a research group - track record of team-work and collaboration - demonstrate a vision for future research, collection development and third-party funding

What you get: - An attractive position in an excellent research institution with a high degree of creative potential in a dynamic scientific and social environment. This is a tenure-track position, initially limited for three years according to the WissZeitVG. Starting remuneration will be in pay group E13 according to the TV-L. After a successful tenure evaluation, the candidate will be classified in TV-L E14. - Remuneration according to the collective agreement of the federal states with all the benefits of the public sector (company pension scheme, annual special payment, capital-forming benefits, collectively agreed vacation entitlement) - Family friendliness certified by the "Work and Family Audit", offer of life coaching through professional family service

the possibility of obtaining a job ticket - A centrally located workplace with excellent transport links

Please send your complete application documents in english (CV, certificates, lists of publications and funding) and a concept for leading the Ornithology section should be submitted, max. 10 MB per document) by July 1, 2026 exclusively digitally via our career portal to Ms. Winkels. For organizational reasons, only online applications will be accepted. Apply online here: [https://8101202752.karriereportal.cloud/job/2026-18-Curator-Ornithology-\(m_f_d\)/bewerben](https://8101202752.karriereportal.cloud/job/2026-18-Curator-Ornithology-(m_f_d)/bewerben)

The Leibniz Association is committed to diversity and gender equity. The LIB strives to create a diverse, inclusive, welcoming and positive work environment. We are certified as a family-friendly institution. We strongly encourage individuals from diverse backgrounds, identities and abilities to apply. We particularly aim to increase the proportion of women in areas where women are under-represented and to promote their careers. Severely disabled people will be given preference if equally qualified.

KONTAKT / CONTACT PERSONALADMINISTRATION Josefine Winkels +49 228 9122 192 E-mail: bewerbung@leibniz-lib.de

You can find more information about our institution on the Internet at: <https://leibniz-lib.de/> —

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RZSS Edinburgh Zoo Conservation Genetics

Research Scientist - RZSS WildGenes Location: Royal Zoological Society of Scotland - Edinburgh Zoo

About Us The charity that owns both RZSS Edinburgh Zoo and RZSS Highland Wildlife Park are looking for committed, compassionate and conservation-minded individuals to join our expert staff team. RZSS aims to connect people with nature and safeguard species from extinction, a mission that sees us work both here in Scotland and in over 20 countries around the world. From inspiring the next generation about wildlife in our parks to protecting chimpanzees in the Ugandan

rainforest; looking after some of the world's most endangered species to saving the Scottish wildcat, RZSS is making a huge difference and we need your help to continue to grow.

The role An opportunity has arisen for a committed Research Scientist (Conservation Genetics) to join the Royal Zoological Society of Scotland's WildGenes team. Reporting to the Conservation Programme Manager (WildGenes), the Research Scientist will assist with the analysis of applied conservation genetic research data delivered by the RZSS WildGenes laboratory.

Who we are looking for The successful candidate will have a PhD in a relevant genetics discipline such as Conservation Genetics or Population Genetics/Genomics and a desire to work as part of our team to support conservation projects around the globe.

Interested? For full information on how to apply, please visit the RZSS vacancy page and follow the instructions: <http://www.rzss.org.uk/job-vacancies/> Closing date: Tuesday 23rd June 2026.

Invitation to interview will be by email/phone and interviews will take place during the 4th week of July.

For any questions and queries, please email Dr Alex Ball at aball@rzss.org.uk quoting "Research Scientist" as the subject.

Our mission is to connect people with nature and safeguard species from extinction.

The RZSS strives to be an equal opportunities employer. Registered Charity SC00406.

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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 year probationary period. The Smithsonian is not able to accommodate special requests.

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)

Taiwan NSYSU FacultyPosition Biology

Faculty position at the Department of Biological Sciences, National Sun Yat-sen University, Taiwan

The Department of Biological Sciences at National Sun Yat-sen University, Taiwan, invites applications for a tenure-track faculty position at the Assistant Professor level or above in Biology or a related field. Applicants of all nationalities are welcome.

Position summary: Tenure-track faculty position at the Assistant Professor level or above in Biology or a related field, beginning in the Spring semester of 2027.

Required qualifications: 1. Ph.D. degree in Biology or a related field. 2. At least 2 years of postdoctoral experience. 3. At least one year of experience studying or conducting research at research institution(s) outside Taiwan. 4. At least 3 publications, published between 2022 and 2026, in SCI-indexed journals, with the applicant as first author or corresponding author. 5. Certificate in EMI skills (English as a Medium of Instruction) in biology-related fields.

Application materials: 1. Curriculum vitae 2. Publication list Please indicate one paper as your primary publication and provide the impact factor and ranking for each publication. Impact factor information should be obtained from the most recent Journal Citation Reports. 3. Teaching statement 4. Research statement 5. Certificates of Ph.D. degree and postdoctoral experience 6. Electronic copy of all publications from 2022 to 2026 7. Completed CV Excel file, available at: https://docs.google.com/spreadsheets/d/12Ro-QhYoRZAqhJt79P_hpuJXvi_oil6s/edit?usp=drive_link&ouid=114732949523068693168&rtpof=true&sd=true 8. Three letters of recommendation, two of which should be provided by the applicant's Ph.D. and postdoctoral supervisors.

Please combine items 1-6 into a single PDF file and send it, together with the completed CV Excel file, to chlee@mail.nsysu.edu.tw by July 31, 2026.

The three letters of recommendation should be sent directly by the referees to chlee@mail.nsysu.edu.tw by July 31, 2026.

Contact: Prof. Che-Hsin Lee Department of Biological Sciences National Sun Yat-sen University Taiwan

Phone: +886-7-5252000 ext. 3620 Email: chlee@mail.nsysu.edu.tw Department website: <https://biology.nsysu.edu.tw/?Lang=en> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

ULaval Canada FacultyPosition Cell BiologyMolecularBiologyOrGenetics

The Department of Biology at Université Laval is seeking applications for a tenure-track faculty position in molecular biology, cell biology, or genetics. The successful candidate will be expected to develop an independent, externally-funded research program in molecular biology, cell biology, or genetics and to contribute to the recruitment and training of graduate students. In addition, the candidate will be expected to teach at the undergraduate and graduate levels in molecular biology, cell biology, or genetics. The Department of Biology at Université Laval is a premier center for education and research covering the fundamental fields of biology, ranging from cellular and molecular biology to genomics, physiology, animal ecology, marine ecology, freshwater ecology, plant ecology, conservation, and evolution. The Department is composed of a team of 22 faculty members who supervise 570 students, including 135 graduate students. The Department of Biology is a leader in northern research with recognized centers of excellence in non-human genomics, ecology and evolution, and oceanography. This research is supported by major infrastructure at Université Laval, including the Institute of Integrative Biology and Systems (featuring platforms for microscopy–fluorescence, confocal, and electron–genomic analysis, and bioinformatics), the scientific complex of the Institut nordique du Québec and the 11 research stations of the Centre for Northern Studies in Nunavik and Nunavut, as well as the research icebreaker NGCC Amundsen.

Position description 1. Teaching and mentoring at the undergraduate and graduate levels in cell biology, molecular biology, or genetics; 2. Development of an independent and externally-funded research program in molecular biology, cell biology, or genetics; 3. Participation in the educational and administrative activities of the Department of Biology, the Faculty of Science and Engineering, and Université Laval; 4. Participation in external academic activities that contribute to the university's reputation

Selection criteria 1. Hold a Ph.D. in biology or a discipline relevant to the field of molecular biology, cell biology, or genetics. Postdoctoral experience is desirable; 2. Proven ability to conduct academic research, demonstrated by publications in peer-reviewed journals in the relevant research field; 3. Potential to develop independent and original research in molecular biology, cell biology, or genetics; 4. Demonstrated aptitude or potential for university teaching at all three levels, for supervising graduate students, and for pedagogical innovation; 5. Ability to communicate and integrate into the institution's French-speaking environment (within two years); 6. Alignment of professional potential with the key competencies required for the professorial role: - Analytical skills, ability to synthesize information, and sound judgment; - Creativity and innovation; - Communication skills; - Interpersonal skills and openness; - Ability to work in a team and with partners; - Autonomy and a sense of responsibility; - Sense of ethics and duty;

Closing date : 4 September 2026

Start date: 1 May 2027

Nomination process Interested candidates should submit a complete application at <https://recrutement.fsg.ulaval.ca/en-US/>. The application package must contain the following items: 1. a letter of intent and motivation (no more than 2 pages); 2. a complete curriculum vitae; contact information for three referees; 3. a detailed document of no more than four (4) pages describing their teaching and research interests; 4. a de-

scription of no more than one (1) page explaining the contribution of their most relevant work to the field; 5. a self-declaration form

Universite Laval rejects all forms of discrimination, promotes excellence in research and research training, and guarantees equal opportunity to all applicants. It upholds the principle that excellence and equity are compatible and complementary. We welcome and encourage applications from people belonging to a visible minority, women, First Nations peoples (Indigenous peoples), people with disabilities, ethnic minorities, members of the 2SLGBTQIA+ community, as well as all qualified individuals with the skills and knowledge necessary to engage productively with diverse communities. Universite Laval also adheres to an equal opportunity employment program for women, members of visible or ethnic minorities, Indigenous peoples, and people with disabilities. In accordance with Canadian immigration requirements, priority will be given to qualified candidates who are Canadian citizens or permanent residents.

By choosing Universite Laval, you will be eligible for the following onboarding benefits: - orientation days for new faculty members; - free French language courses for you and your spouse;

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Other

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ESEB Under-represented ECR Achievement Award by 01 July

ESEB Under-represented ECR Achievement Award Two annual awards of EUR2,000 will highlight the achievements of under-represented early-career researchers (ECRs) who have faced difficult circumstances while conducting their work. Applicable difficult circumstances may be but are not limited to disabilities, social/cultural/political persecution, refugee status, single parenting or other caring responsibilities that have created unequal opportunities. This year's winners will also be invited to speak at the ESEB Hub Congress in 2027.

DEADLINE: 1 July 2026

Please find all further details about the application and previous winners at <https://eseb.org/prizes-funding/equal-opportunities-initiative/eseb-under-represented-ecr-achievement-award/> European Society for Evolutionary Biology (ESEB) Email: office@eseb.org Website: <https://eseb.org> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Evolving in microbiomes journal club

Hi,

We're introducing a new international journal club for research focussing on microbes evolving in a community or microbiome context. It can be your own published work, a paper you've been procrastinating to read, or unpublished work that you'd like to get feedback on. Our first paper is <https://www.science.org/doi/10.1126/sciadv.aeb8246> from Jeroen Meijer.

Schedule: Monthly, every second Wednesday (can be third if need be)

Time: 15:00 Central European Time CET/CEST, 09:00 Eastern Time ET/EDT. So for the time constant world, the meeting time will change every last weekend of March and October. <https://www.timeanddate.com/worldclock/converter.html> How to sign up? Email me: parab@mvp.lmu.de, subject line "Evolving in mi-

crobiomes journal club" and please send me the papers you'd like us to read! Or your own papers!

Regards Lavisha – Dr. Lavisha Parab Postdoctoral researcher - Wendling Group Max von Pettenkofer-Institute Ludwigs Maximilians University Munich

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Online RSP 2026 Photography Competition

Royal Society Publishing is delighted to announce that the 2026 Competition is now open for entries until 14 August for a chance to win GBP1000! The competition celebrates the power of photography in conveying the wonder of science happening all around us and photographs can be submitted in the categories of: Behaviour, Astronomy, Earth Science and Climatology, Ecology and Environmental Science, and Microimaging.

The competition is free to enter and open to anyone studying or working in science at graduate level or above. Category winners will receive a one-year membership to the Royal Photographic Society and the overall winner will receive a grand prize of GBP1,000. Find out more at Royal Society Publishing Photography Competition 2026 (<https://royalsociety.org/journals/publishing-activities/photo-competition/>).

Many thanks and we look forward to hearing from you.

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Online Talk-by-Silvia-De-Monte 25-06-2026

Dear evoldir community,

Here's a reminder for Silvia De Monte's online talk on Thursday as a part of the seminar series "Adaptive Behaviour in Non-neuronal Systems" that will interest some of you. More information on the talk below, and registration for the series, here: <https://www.royalsocietypublishing.org/journal/rsos>

[//groups.google.com/g/adabiosys-lectures](https://groups.google.com/g/adabiosys-lectures)
 How can collective functionality structure species-rich communities? June 25, 17:00-18:00 CEST Zoom link: <https://umontpellier-fr.zoom.us/j/98560358832>

Abstract: Random matrices have been widely used to represent the effect of nonlinearities in communities composed of a large number of species, when the details of interactions are unknown. Models such as the disordered Lotka-Volterra equations, despite being simplistic, adequately describe a range of statistical patterns of microbial communities, such as abundance distributions. However, microbial communities are typically structured by species traits, for instance, through the utilization of common resources, by the existence of functional groups, or by phylogenetic distance. I will use a set of high-dimensional models that admit effective, low-dimensional descriptions to address two complementary questions. First, what is the effect of low-dimensional features on the dynamics of otherwise disordered communities? And second, what is the possible evolutionary origin of the structure that underpins community function?

About the speaker: Silvia De Monte is a researcher at the Institute of Biology of the Ecole Normale Supérieure in Paris, France, in the Eco-Evo Math group and at the Department for Evolutionary Theory at the Max Planck Institute for Evolutionary Biology in Plön, where she leads the research group "Dynamics of Microbial Collectives". Her research is focused on the ecological processes underpinning evolution in phenotypically and genetically heterogeneous cellular assemblies. Detailed information about her various research projects is available on her website - <https://www.bio.ens.psl.eu/~demonte/>. Please do share and spread the word, the more the merrier! And in case of any questions, please don't hesitate to contact me at gautham [dot] ganesh [at] cbs [dot] cnrs [dot] fr.

Best, Gautham

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Online Talk by Silvia De Monte
25-06-2026

Hello all,

We are organising an online talk on Thursday next week as a part of the seminar series "Adaptive Behaviour in Non-neuronal Systems" that will interest some of

you. More information on the talk below, and on the series, here: <https://groups.google.com/g/adabiosys-lectures> How can collective functionality structure species-rich communities? June 25, 17:00-18:00 CEST Zoom link: <https://umontpellier-fr.zoom.us/j/98560358832> Abstract: Random matrices have been widely used to represent the effect of nonlinearities in communities composed of a large number of species, when the details of interactions are unknown. Models such as the disordered Lotka-Volterra equations, despite being simplistic, adequately describe a range of statistical patterns of microbial communities, such as abundance distributions. However, microbial communities are typically structured by species traits, for instance, through the utilization of common resources, by the existence of functional groups, or by phylogenetic distance. I will use a set of high-dimensional models that admit effective, low-dimensional descriptions to address two complementary questions. First, what is the effect of low-dimensional features on the dynamics of otherwise disordered communities? And second, what is the possible evolutionary origin of the structure that underpins community function?

About the speaker: Silvia De Monte is a researcher at the Institute of Biology of the Ecole Normale Supérieure in Paris, France, in the Eco-Evo Math group and at the Department for Evolutionary Theory at the Max Planck Institute for Evolutionary Biology in Plön, where she leads the research group "Dynamics of Microbial Collectives". Her research is focused on the ecological processes underpinning evolution in phenotypically and genetically heterogeneous cellular assemblies. Detailed information about her various research projects is available on her website - <https://www.bio.ens.psl.eu/~demonte/>. Please do share and spread the word. In case of any questions, contact me at gautham [dot] ganesh [at] cbs [dot] cnrs [dot] fr.

Best, Gautham

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Royal Society Publishing 2026
Photography Competition

Royal Society Publishing is delighted to announce that the 2026 Competition is now open for entries until 14 August for a chance to win GBP1000! The competition celebrates the power of photography in conveying

the wonder of science happening all around us and photographs can be submitted in the categories of: Behaviour, Astronomy, Earth Science and Climatology, Ecology and Environmental Science, and Microimaging.

The competition is free to enter and open to anyone studying or working in science at graduate level or above. Category winners will receive a one-year membership to the Royal Photographic Society and the overall winner will receive a grand prize of GBP1,000. Find out more at Royal Society Publishing Photography Competition 2026 (<https://royalsociety.org/journals/publishing-activities/photo-competition/>).

Many thanks and we look forward to hearing from you.
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Survey definitions of sex

Contribute to the Tree of Sex consortium research survey on how sex is defined in biology

I am a member of the Tree of Sex consortium (<https://www.treeofsex.org/>), a collaborative, international initiative to compile a database on reproductive systems across all eukaryotes. Sex is an important component in many aspects of biological research. However, the meaning of "sex" is the subject of increasing debate in both scientific and social contexts. We are conducting a survey to find out about how scientists define sex. We hope you will take the survey and share with your colleagues.

Contribute to the Definitions of Sex survey <http://univie.questionpro.eu/definitionsurvey>
<http://univie.questionpro.eu/definitionsurvey>
The survey consists of 17 scientific questions (14 multiple choice and 3 short open responses) as well as questions about your experiences and background. You can start and then save to continue later. Participation should present no greater risk than every day use of the internet. All questions are optional to answer and survey responses are confidential. This study was approved by the Ethics Review Board at the University of Vienna (reference number 01453) and adheres to the European Union general data protection regulations. Full participant information can be found at the Tree of Sex GitHub (<https://github.com/Tree-of-Sex/Ethic>

[s_and_Inclusivity](#)).

Please forward this email and share the survey with your colleagues, trainees, collaborators, departments and networks.

We appreciate your time and contribution toward identifying the ways scientists understand sex!

On behalf of the Tree of Sex 2.0: Definitions of Sex Research Team ToS.DefinitionSurvey@protonmail.com

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Tomorrow Joan Roughgarden Stanford Theoretical Microbiology Holobionts Lytic-Lysogenic Switch and Merger vs Major Transition

(Please circulate this announcement)

Joan Roughgarden Professor Emerita, Department of Biology, Stanford University and Adjunct Researcher, Hawaii Institute of Marine Biology, University of Hawaii, USA

"Theoretical Microbiology: Holobionts, Lytic/Lysogenic Switch, and Merger vs Major Transition"

Online talk, PhilInBioMed Seminar Series

June 8, 2026, 5pm-6:30pm (Paris time, UTC+2)

Abstract of the talk: Microbiology has traditionally been exclusively experimental. Yet the functioning of holobionts with their hologenomes, the switch of virus from a parasitic lytic stage to a commensal or mutualistic lysogenic stage, and the assembly of microbes and hosts into holobionts are all phenomena that invite a theoretical ecological and evolutionary perspective. Holobiont assembly suggests a concept of an ecological merger that may be more useful than the concept of a major evolutionary transition.

Two recommended papers for this talk: Roughgarden J (2026) Evolutionarily Optimal Phage Life-History Traits: Burst Size vs. Lysis Time. <https://doi.org/10.1101/2025.04.16.649164> Roughgarden J (2023) Holobiont Evolution: Population Theory for the Hologenome. The American Naturalist 201:763-778. <https://doi.org/10.1086/723782> Details & Zoom

link: <https://philinbiomed.cnrs.fr/event/joan-roughgarden/> More on the speaker: Joan Roughgarden is an evolutionary biologist and ecologist. Her work bridges biology, behavior, and social theory. Over her career, she has contributed foundational research in evolutionary ecology, population genetics, and the evolution of social behavior. Roughgarden is widely known for her critiques of sexual selection theory and for advancing social selection as an alternative framework emphasizing cooperation and diversity in reproduction. Her books, including *Evolution's Rainbow* (2004) and *The Genial Gene* (2009), have shaped ongoing debates about sex, gender, and sexuality in both biology and society, positioning her as a leading voice in expanding evolutionary perspectives on diversity. She has written more than 200 scientific papers, including:

Akçay E, Van Cleve J, Feldman MW, Roughgarden J (2009) A theory for the evolution of other-regard integrating proximate and ultimate perspectives. *Proceedings of the National Academy of Sciences* 106:19061-19066. <https://doi.org/10.1073/pnas.0904357106> Connolly SR, Roughgarden J (1999) Theory of Marine Communities: Competition, Predation, and Recruitment-Dependent Interaction Strength. *Ecological Monographs* 69:277-296. [https://doi.org/10.1890/0012-9615\(1999\)069](https://doi.org/10.1890/0012-9615(1999)069)

Folse HJ, Roughgarden J (2010) What is an Individual Organism? A Multilevel Selection Perspective. *The Quarterly Review of Biology* 85:447-472

Hughes TP, Baird AH, Bellwood DR, et al (2003) Climate Change, Human Impacts, and the Resilience of Coral Reefs. *Science* 301:929-933. <https://doi.org/10.1126/science.1110105>

<https://doi.org/10.1126/science.1085046> Roughgarden J (2009) Is there a general theory of community ecology? *Biol Philos* 24:521-529. <https://doi.org/10.1007/s10539-009-9164-z> Roughgarden J (2012) The social selection alternative to sexual selection. *Philos Trans R Soc Lond B Biol Sci* 367:2294-2303. <https://doi.org/10.1098/rstb.2011.0282> Roughgarden J (2020) A Mathematical Theory of Holobiont Evolution. *bioRxiv* 2020.04.10.036350. <https://doi.org/10.1101/2020.04.10.036350> Roughgarden J (2023) Holobiont Evolution: Population Theory for the Hologenome. *The American Naturalist* 201:763-778. <https://doi.org/10.1086/723782> Roughgarden J (2024) Lytic/Lysogenic Transition as a Life-History Switch. *Virus Evol* 10:veae028. <https://doi.org/10.1093/ve/veae028> Roughgarden J (2026) Evolutionarily Optimal Phage Life-History Traits: Burst Size vs. Lysis Time. 2025.04.16.649164

Roughgarden J, Gilbert SF, Rosenberg E, et al (2017) Holobionts as Units of Selection and a Model of Their Population Dynamics and Evolution. *Biol Theory* 1-22. <https://doi.org/10.1007/s13752-017-0287-1> Roughgarden J, Oishi M, Akçay E (2006) Reproductive Social Behavior: Cooperative Games to Replace Sexual Selection. *Science* 311:965-969. <https://doi.org/10.1126/science.1110105> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

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BangorU UK **AmphibianHostMicrobeInteractions**

The Osborne group at Bangor University is recruiting a 3-year postdoc in amphibian host-microbiome interactions, based in the Molecular Ecology and Evolution group in the School of Environmental and Natural Sciences, Bangor University. The post is part of a UK-US collaborative project led by Bangor University and George Washington University (US), including partners from the Smithsonian's National Zoo and Conservation Biology Institute (US) and Tropical Research Institute (Panama), funded by BBSRC (UK) and NSF (US). The project will investigate the role of amphibian skin microbiomes and skin-resident immune components in determining species-specific outcomes of infection by the fungal pathogen *Batrachochytrium dendrobatidis* (Bd). Invasive fungal diseases are rising globally, causing catastrophic declines in wildlife populations and posing severe threats to animal and human health. Bd is a leading cause of global amphibian biodiversity loss. Both the amphibian skin microbiome and resident immune components are known to influence infection outcomes, but the mechanisms that govern interactions between the immune system, microbiome and disease remain poorly understood. This project will investigate the central hypothesis that species-specific interactions between skin-resident microbiomes and immune components critically define Bd infection outcomes in amphibians. This hypothesis will be explored through experimental manipulation of microbiomes and skin-resident immune components in Bd-susceptible and Bd-tolerant

frog species. The post holder will be responsible for planning, conducting, analysing and contributing to the publication of the microbiome-related components of the project. This will include leading 16S metabarcoding, shotgun metagenomic and bacterial genome sequencing activities, integrating microbiome datasets with infection, immune and transcriptomic data generated by the wider project team, and liaising with UK, US and Panama-based project partners. Deadline: 8 July 2026 For full details, and to apply, see here: <https://www.jobs.ac.uk/job/DRW850/postdoctoral-research-officer-in-amphibian-host-microbiome-interactions> Informal enquiries can be made by contacting: Owen Osborne o.osborne@bangor.ac.uk

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Bordeaux Philosophy of **Cancer-Theoretical approaches to** **cancer**

Call for Applications: Postdoctoral Position in Philosophy of Cancer at the University of Bordeaux, France

All information here: <https://philinbiomed.cnrs.fr/jobs/postdoctoral-position-in-philosophy-of-cancer/> (Please circulate this announcement)

Applications are invited for a two-year postdoctoral position in conceptual, theoretical, or philosophical approaches to cancer, starting Fall 2026 (precise starting date is flexible), at ImmunoConcept (CNRS & Univer-

sity of Bordeaux, France).

This position is part of the research project COCO-CAN (Cancer: Between Competition and Cooperation—The Complex Interactions Between Host Cells, Tumors, and the Microbiome), co-directed by Thomas Pradeu and Fridolin Gross, and funded by the French National Research Agency (ANR) and the Region Nouvelle-Aquitaine.

Project Overview COCO-CAN investigates cancer from a conceptual, theoretical, and philosophical perspective, with a particular focus on the interplay between competition and cooperation in oncological processes. While empirical research increasingly highlights the importance of cooperative phenomena in cancer (e.g., among tumor cells, between tumors and host tissues, or involving the microbiome), this evidence remains fragmented. The project aims to develop a coherent conceptual framework capable of integrating these insights and clarifying their implications for our understanding of cancer.

Postdoctoral Project The successful candidate will develop an independent research project aligned with COCO-CAN's themes. The precise topic is flexible, provided it engages with the broader question of cooperation and competition in cancer biology.

Possible research questions include (but are not limited to):

- What roles do cooperative interactions play in processes such as metastasis?
- Do the conditions of cancer coincide with the conditions of multicellularity?
- How do interactions between the organism, cancer cells, and the microbiome affect intra-host cooperation?

Candidate Profile: We welcome applications from candidates with backgrounds in philosophy, the biological and biomedical sciences, or related fields. Applicants should demonstrate a strong interest in conceptual, theoretical and/or philosophical issues in cancer biology, as evidenced by their previous research.

What We Offer: A stimulating interdisciplinary research environment of philosophers of science embedded in a biology lab Collaboration with philosophers of biology and medicine, along with scientists and MDs working on cancer Full-time funding for two years

Application Details: Please send your resume and a cover letter with a brief (2-4 pages) description of your project idea(s) to fridolin.gross@u-bordeaux.fr and thomas.pradeu@u-bordeaux.fr. The application deadline is July 30, 2026.

Sincerely, Thomas Pradeu.

– Thomas Pradeu CNRS Research Director in Philos-

ophy of Science Immunology Unit ImmunoConcEpT, UMR5164, CNRS & University of Bordeaux Presidential Fellow, Chapman University, CA, USA Team Leader Conceptual Biology and Medicine Team Coordinator of the Philosophy in Biology and Medicine Network (PhilInBioMed)

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CambridgeUK Disease Evolution

Applications are invited for a Postdoctoral Research Associate position to work on a NERC-funded project investigating the evolutionary dynamics of virus resistance in wild animal populations. The post will be based in the Pathogen Dynamics Unit within the Department of Genetics at the University of Cambridge and be co-supervised by Professor Frank Jiggins and Professor Henrik Salje in collaboration with Prof Jon Slate at the University of Sheffield and Dr Joel Alves at the University of Oxford.

The Pathogen Dynamics Unit at the University of Cambridge consists of 15-20 researchers at different stages of their career using experimental, mathematical and computational research to help our understanding of how pathogens spread in populations. This post will work closely with the Slate group, which uses genomics approaches to study the evolution of quantitative traits.

The project will consist of the analysis of data from a population of wild rabbits in Australia that have been followed and sampled regularly for 25 years. During this period there have been regular outbreaks of Rabbit Haemorrhagic Disease Virus (RHDV), a highly contagious, often fatal virus. This project will use advanced quantitative genetics and epidemiological modelling to explore the evolution of resistance in the rabbit population and coevolution with the virus. This will include analysing several thousand host genomes from the 25-year period allowing us to investigate the evolution of host immunity from a quantitative genetic perspective. The project promises to provide fundamental insight into our understanding of disease ecology and evolution by exploring the interplay between host immunity and virus across long timeframes.

The applicant will have strong quantitative skills. The project will require the development of computationally intensive models and analysis of large genomic datasets,

and therefore applicants should have experience in coding and a good understanding of probability, likelihoods and Bayesian analysis.

Full details: <https://www.jobs.ac.uk/job/DRS051/research-associate-fixed-term> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

CNRS Toulouse France Genomics and forest ecology

Dear colleagues, I would like to share a postdoctoral opportunity in genomics and forest ecology In Toulouse (France). The aim of the project is to understand the eco-evolutionary dynamics of European beech at the margins of its distribution range in the Pyrenees. Applications must be submitted here (a detailed description of the position is also available) : <https://emploi.cnrs.fr/Offres/CDD/UMR5300-ROMBER-003/Default.aspx?lang=EN>The deadline of the application is July 5th, 2026 and the postdoc is expected to start the September 1st, 2026. Best regards, Romain Bertrand

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ETHZurich Microbial PredatorPrey Coevolution

Comparative predator-prey co-evolution in complex microbial communities Applications are invited for a postdoc position and a PhD position in the group of Greg Velicer at ETH Zurich as part of our team researching predator-prey co-evolution in species-rich microbial communities. Both positions will focus primarily on the evolution experiment MyxoEE-KillerProfiles, the first phase of which is visually summarized at <https://www.myxoe.org/newmyxoees>. In MyxoEE-KillerProfiles, highly diverse predators of microbes – Bdellovibrio-and-like-organisms, dictyostelids, nematodes and myxobacteria – are co-evolving with a 20-species synthetic community of bacterial prey in both single-predator and multiple-predator treatments. Among other questions,

we are asking how different predators comparatively shape prey-community evolution and themselves comparatively evolve at predation-related traits. We also ask how combining multiple predators together alters the evolution of each predator and of the prey community. Evolved communities and organisms will be analyzed with various approaches addressing fitness, behavior, collective phenotypes, genomes, community composition and molecular-genetic mechanisms of adaptation. The postdoc who developed the protocols for and conducted the first phase of MyxoEE-KillerProfiles, Dr. Jos Kramer, has started his own group with an ERC Starting Grant on a different project. We seek candidates with a strong record of creative research from any relevant training background who thrive at both team and individual work in a scientifically and culturally diverse group. Relevant training areas include evolutionary community ecology, community metagenomics, experimental evolution, microbial ecology, microscopy, and molecular genetics. The selected postdoc will help mentor younger group members involved in the project. The postdoc will be supported from a Swiss National Science Foundation grant while a competitive fellowship (e.g. ETH, EMBO, MSCA) is sought, potentially for up to three years. To apply for one of the positions, send one file to Rita Jenny at rita.jenny@env.ethz.ch that includes a motivation statement (one page max), your CV and contact information for two persons who have agreed to serve as references. Review of applications will begin June 29th. Specify the relevant position with a subject line of either "predation postdoc" or "predation PhD". Informal inquiries can be sent to gregory.velicer@env.ethz.ch. Zurich, Switzerland has vibrant communities of ecologists, evolutionary biologists and microbiologists that offer many opportunities for interaction and collaboration. (<https://ibz.ethz.ch/research/eco-evo-zurich.html>) Background Velicer group research: <https://evo.ethz.ch/Myxobacteria> Evolution Experiments: myxoe.org New review article on microbial predation: <https://doi.org/10.1038/s41579-026-01299-7> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Galapagos Ecuador Post-doctoral Position Recent Vertebrate Paleobiology

The Charles Darwin Foundation for the Galapagos Islands is seeking a Vertebrate Paleobiologist <https://www.darwinfoundation.org/en/about/careers/>

Role: Vertebrate Paleobiologist Place: Galapagos, Ecuador Type of work: Full-time Deadline: July 7th, 2026 Duration: Annual, renewable for second year (up to September, 2028)

Introduction The Charles Darwin Foundation for the Galapagos Islands (CDF), in collaboration with The California Academy of Sciences (CAS), is recruiting a Terrestrial Vertebrate Paleobiologist to work on a collaborative, multi-institutional project to study the pre-human faunal baselines for the islands. Recently, CAS received funding from the Global Environment Fund to participate in a multiorganization effort to restore extirpated species to island ecosystems in the Galapagos. The project focuses on the islands of Floreana, Santiago, Santa Fe, Pinzon, and Rabida, which have already seen extensive work to eradicate invasive vertebrate species, and the project includes partners from Fundacion Jocotoco, Durrell Wildlife Conservation Trust, and Island Conservation, working in partnership with the Galapagos National Park. The primary objective of this project is to increase knowledge of recent vertebrate assemblages in order to help inform species translocation efforts and improve ecosystem and to understand the causes and timings of local vertebrate extinction events. Secondary objectives include building significant paleobiology collections and reference bone collections on the islands to increase the local capacity for future paleobiological work.

Position Objective The Terrestrial Paleobiologist will support the development and implementation of research activities in the Galapagos Islands, in alignment with program commitments and in collaboration with CDF's regional research partners. This includes organizing and carrying out fieldwork and collecting on focal islands, as well as labwork at CDF to study and curate the collections. The position reports to the Principal Coordinator of the Natural History Collections at CDF (Miguel Pinto) and to the PI from CAS (Jack Dumbacher) and will work with staff from the Galapagos National Park Directorate (GNPD), as well as

with other researchers, students and volunteers, and scientific, logistical, and administrative support staff, to successfully achieve the project's objectives and expected outcomes. Activities The main responsibilities of the position include: - Collaborate on and conduct scientific research and data analyses that improve baseline understanding of the pre-human vertebrate fauna of the Galapagos islands: - Organizing expeditions to the project focal islands of Floreana, Santiago, Santa Fe, Pinzon, and Rabida; - Identifying and developing sites with paleobiology deposits and potential for pre-human and early-human remains; - Identifying bones and bone fragments to species using morphological and genetic techniques from paleobiology specimens; - Characterization of early island fauna assemblages; - Additional studies of sites and materials to infer information about the timing and causes of faunal changes; - Other related scientific studies as appropriate. - Increase capacity and develop scientific infrastructure that will support paleobiological work into the future: - Collecting, preparing, cataloging, and curating bones, other paleo remains, and geological specimens for the permanent collections of the CDF; - Collecting and preparing bone reference collections for the vertebrate fauna of the Galapagos, using salvaged and/or collected voucher specimens of species as permitted. - In coordination with the PIs and the CDF Scientific Directorate, plan and organize fieldwork and provide support to visiting international expeditions as needed, including occasional extended fieldwork periods on remote islands. - In coordination with the PIs, manage and prepare quarterly and annual progress reports and accounting reports for the funders and for the Galapagos National Park. - Generate educational materials and actively participate in outreach related to CDF, CAS, Galapagos National Park, as well as with Galapagos authorities, regional project partners, and the local community. - Produce technical and scientific reports, including at least one peer-reviewed publication (as lead or co-author) submitted annually to scientific journal(s) to contribute to the knowledge and management of vertebrate ecosystems on the islands. - Provide mentorship and support to CDF students and volunteers throughout the program. - Support the development of additional funding proposals. **Minimum Requirements** - PhD or Master's degree in paleobiology, geology, evolutionary biology, or related fields. - At least two years of experience (PhD) or five years (Master's) working in vertebrate paleobiology science-related fields.

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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(at)helsinki.fi) and Dr. Tutku Aykanat (tutku.aykanat(at)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-T-hree-post-doc-positions-in-salmonid-fish-ecological-and-evolutionary-genomics-and-conservation/1365060357/?feedId=350602&utm_so

[urce=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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HomLab UMississippi microbial co-evolution

Postdoctoral Research Associate: Experimental Co-Evolution of Microbial Mutualisms The Hom Lab at the University of Mississippi (UM) is recruiting a postdoctoral researcher to further develop a model experimental system for observing microbial mutualisms evolve in real time. Funded by a new NSF award and connected to an ongoing collaboration with the Kryazhimskiy Lab at UC-San Diego, this project uses synthetic microbial communities, custom strain engineering, lineage tracking, and long-term experimental evolution to ask how cooperative species interactions originate, stabilize, diversify, and fail. The work will build on the study by Venkataram et al. (2023) Nat Ecol Evol 7:143-154 and the synthetic mutualism created in the Hom Lab between *Chlamydomonas reinhardtii* and *Saccharomyces cerevisiae*. The postdoctoral associate will extend this system to dissect how microbial ecosystems co-evolve under controlled laboratory conditions. We are particularly interested in recruiting someone who wants intellectual ownership. Our NSF project provides a strong experimental foundation, but the postdoctoral associate will also have substantial freedom to pursue new questions that align with the lab's broader mission to understand how biotic and abiotic factors shape the formation, persistence, and evolution of species interactions, especially symbioses and mutualisms. More about the lab can be found at

<https://darwinsdaemon.com>. The postdoctoral associate will lead experiments, publish first-author papers, present at national and international meetings, and develop toward an independent scientific career. They will also have opportunities to mentor graduate, undergraduate, and high-school students (e.g., through the ARISE@UM program), and to help develop a course-based undergraduate research module associated with the NSF award. For many students in this region, where research opportunities are scarce, this may be their first real opportunity to find out what research is like, and a big reason why our lab takes outreach as seriously as the science. What we are looking for: Applicants should have a Ph.D. by the time of appointment in molecular biology, molecular genetics, synthetic biology, microbiology, evolutionary biology, or a related field. We do not expect any one candidate to have all the skills below, but strong candidates will bring deep expertise in at least one relevant area and a clear appetite to learn the others; competitive applicants will have some combination of: - Strong wet-lab expertise in molecular genetics, genetic engineering, synthetic biology, microbial genetics, or a related area - A working knowledge of evolutionary biology, population genetics, microbial ecology, and/or experimental evolution - Experience constructing, validating, maintaining, and analyzing engineered microbial strains. Experience with *Chlamydomonas* and/or budding yeast is a plus - A record of scientific productivity, such as peer-reviewed publications, preprints, or manuscripts in preparation - Strong scientific writing and communication skills - Evidence of ownership and follow-through on complex research projects - Interest in mentoring junior scientists and contributing to a collaborative lab culture Experience with genome sequencing, lineage tracking, barcode sequencing, population-genomic analysis, high-throughput phenotyping, natural products, biosynthetic gene clusters, metabolomics, and/or mass spectrometry would be welcome but is not required.

Environment and support The Hom Lab is based UM's Insight Park Innovation Hub, a building that houses academic labs, startups, businesses, UM's office of commercialization, and state/regional offices for economic development.

Oxford, Mississippi is a lively college town with a vibrant collegiate sports culture, a celebrated literary and music scene, excellent food, and a cost of living that compares favorably with many major US research hubs. It can genuinely be a good place to do hard science and still have a life.

The position is funded for 2.5 years at 62,000/year, with full health and retirement benefits.

To apply Please submit: 1. a cover letter describing your fit and interest 2. a CV 3. contact information for at least three references Optional supporting materials, such as preprints or manuscripts in preparation, are welcome. Questions and application materials may be sent to homlab.postdoc26@protonmail.com with the subject line "Postdoc26 - Coevolution". Review of applications begins immediately and will continue until the position is filled. We warmly welcome applications from women and others underrepresented in the sciences. The University of Mississippi is an equal-opportunity employer.

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HUNGARY MICROBIAL ECOLOGY

POST-DOCTORAL POSITION IN MICROBIAL ECOLOGY OF SHOREBIRDS

POSITION OVERVIEW. We are seeking a motivated and talented field biologist to join our team. The post-doc will carry out field investigations of breeding and non-breeding shorebirds and combine this with microbial sampling. We seek applicants with strong background in evolutionary biology, animal behaviour or ecology, and willingness to learn microbial ecology. The position is part of a collaborative project "The role of migratory birds in spreading antimicrobial resistance" funded by the Hungarian Research agency (HUN-REN). This is a joint project with Prof Sam Sheppard (Oxford University).

ABOUT US: The position is based at University of Debrecen (Hungary) where our team has PhD students, postdocs and collaborating academics. The post-doc will be mentored by an international team of scientists. We continue to aim high profile publications (see below). Beyond significance in ecology, animal behaviour and evolution, our research has direct implications for biodiversity conservation by preserving species and by working with local communities to protect shorebird habitats. We work globally using an in-

ternational network of scientists and conservationists, see www.szekelylab.com

FURTHER DETAILS. The main task of the post-doc is to carry out field investigations of both breeding and non-breeding shorebirds, use efficient microbiological sampling protocols in the field, carry out data analyses and publish papers. In addition, s/he will advise research of MSc and PhD students and possibly contribute at modest level to postgraduate teaching (all in English).

We seek applicants with strong research background in one (or more) of the following fields: behavioural ecology, population ecology, field biology, wildlife conservation, disease ecology and microbiology. Applicants should have a Ph.D. in animal ecology, behavioural ecology, population demography or a related field, and background in quantitative analyses. Good communication and interpersonal skills are essential. Knowledge of programming languages such as R is required, and experience with biostatistics or demography is desirable. Proficiency in English is essential as is research track matching the career stage of the applicant. Field experience, bird ringing licence and full driving licence are essential.

DURATION: The position is available immediately and the contract will be offered until 31 December 2027.

SALARY: The gross salary is up to 800,000 HuF per month (approx 2,200 EURO). Living in Hungary is substantially cheaper than in Western Europe, and the salary we offer is equivalent of an assistant professorial salary in Hungary. Social and health insurance contributions are independent of salary and paid by the employer.

RESEARCH ENVIRONMENT: The position is based in Debrecen: a vibrant and liveable city in eastern Hungary with large international student community. Debrecen has good public services, and rental housing and food are affordable. The post-doc will be based at the Department of Evolutionary Zoology. Our research team works closely with Hortobagy National Park - a UNESCO Heritage Site just outside Debrecen.

HOW TO APPLY: Please send i) a cover letter explaining your research interests and suitability for the position, ii) your CV with a list of scientific publications, and iii) contact information of two referees to Ms Rita Nagy nagy.rita@science.unideb.hu

Please use the subject line "HU-RIZONT post-doc application." Only shortlisted candidates will be contacted for an interview. Application deadline: 18 July 2026.

Selected recent publications by our team: Prof T Szekely (Debrecen/Bath) and Prof Sam Sheppard (Oxford). For our complete track record, please see GoogleScholar and ResearchGate. Amano, T., T. Szekely, ..2018. Successful conservation of global waterbird populations depends on effective governance. *Nature* 553: 199-202. Kubelka, V.R. Freckleton, T. Szekely. 2018. Global pattern of nest predation is disrupted by climate change in shorebirds. *Science* 362: 680-683. McDonald, G. C., .T. Szekely..2023. Remating opportunities and low costs underlie maternal desertion. *Evolution* 77: 97-109. Mourkas, E., ..T. Szekely .. & S. K. Sheppard. 2024. Proximity to humans is associated with anti-microbial resistant enteric pathogens in wild bird microbiomes. *Current Biology* 34: 3955-3965. Szekely, T. 2019. Why study plovers? The significance of non-model organisms in avian ecology, behaviour and evolution. *Journal of Ornithology* 160: 923-933. Szekely, T... 2023. The causes and implications of sex role diversity in shorebird breeding systems. *Ibis* 166: 357-385.

T.Szekely@bath.ac.uk

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HUNGARY MICROBIAL ECOLOGY2

POST-DOCTORAL POSITION IN MICROBIAL ECOLOGY OF SHOREBIRDS

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IRBCroatia Genomics of repetitive elements in bivalves

Postdoctoral Position in Genomics / Molecular Evolution - Ruder Boskovic Institute (Zagreb, Croatia)

We are inviting applications for a Postdoctoral Researcher position within the project GENREP - The impact of repetitive sequences on the molecular evolution and architecture of bivalve genomes at the Ruder Boskovic Institute, Division of Molecular Biology. Duration: 13 months

The project focuses on understanding how repetitive DNA sequences, particularly satellite DNAs and transposable elements, contribute to genome architecture, chromosome organization, and molecular evolution in bivalve mollusks. The research combines genomics, bioinformatics, and molecular biology approaches to explore the structure, dynamics, and evolutionary roles of repetitive elements in complex genomes. Bivalves represent fascinating model systems due to their repeat-rich genomes, providing opportunities to study genome plasticity, repeat evolution, and the interaction between different classes of repetitive elements.

Project description: https://lnkd.in/dVE3p6_3 Location: Zagreb, Croatia Institution: Ruder Boskovic Institute - Division of Molecular Biology Research area: genomics, molecular genetics, evolutionary biology, repeatomics

Croatian Science Foundation Administrative Requirements: The employment contract must end no later than 30 November 2027. If the contract starts after October 2026, the duration of the postdoctoral appointment will be shortened accordingly. The candidate must have been awarded an official PhD diploma. The candidate must not have more than ten years of research experience counted from the start of their doctoral studies (with possible extensions for maternity/parental leave or long-term illness). The total duration of postdoctoral employment throughout the candidate's career must not exceed four years. If the candidate has previously held a postdoctoral position (in Croatia or abroad), the combined duration of all previous postdoctoral appointments and the appointment under this project must not exceed four years.

Application details (position II.11):

HR: <https://lnkd.in/dqkxYWP5> (Please also pay attention to the additional points listed below the general section of the call - "Selection Criteria for the Associate Position" for position no. 11).

EURAXESS: <https://lnkd.in/d3hafyjW> Applications with all the docs listed in the call: natjecaji.pi.sarnica@irb.hr More info: esatovic@irb.hr

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LehighU AAndGenomics

The Schultz EvoGenome Lab at Lehigh University (Bethlehem, PA, USA) seeks a candidate to co-develop an NSF Postdoctoral Research Fellowship in Biology (PRFB) proposal, with me as sponsoring mentor. This year's competition (NSF 26-504) focuses on the intersection of AI and biological sciences. Example directions: - AI for comparative genomics - AI-driven genome assembly/annotation tools - LLMs for genome analysis - Genome rearrangements, including in cancers Other ideas at the interface of evolution, chromosome biology, gene provenance, and human health are welcome. Note: the fellow is the applicant/PI; I am the host. Eligibility: PhD by start date, and U.S. citizen/national/permanent resident at submission. Deadline: 29 Sept 2026. Reach out now to leave time to write a strong proposal. PRFB: <https://www.nsf.gov/funding/opportunities/prfb-postdoctoral-research-fellowships-biology/nsf26-504/solicitation> Lab: <https://evogeno.me>/Bio: <https://bio.cas.lehigh.edu/faculty-staff/darrin-schultz> Contact: Darrin Schultz, dts@lehigh.edu

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LehighU EvolGenomics

The Schultz EvoGenome Lab at Lehigh University (Bethlehem, PA, USA) is hiring a Postdoctoral Research Associate in Evolutionary Genomics and Molecular Evolution.

I'm seeking someone to lead projects in comparative genomics at chromosome scale, exploring genome evolution

across the tree of life with a focus on animals and their close relatives. The ad is intentionally broad: I hope the postdoc will dovetail with ongoing lab research while bringing their own project ideas.

Qualifications: - Strong genomics and programming/bioinformatics skills (required) - A completed PhD and a record of peer-reviewed publication - A plus: molecular biology, cell biology, biochemistry, microscopy, FACS, protein purification, invertebrate transgenics, aquaculture, or cruise-based fieldwork (AAUS scuba / research-cruise experience especially welcome)

Terms: Two-year appointment with possible renewal. Salary around 62,232/yr plus benefits. On-campus presence required, with willingness to join marine research experience 30 days). Open until filled.

To apply, submit a cover letter, CV, contact information for 2-3 references, and one representative publication via the posting below. Interested candidates are welcome to reach out to DTS by email prior to applying.

Lab: <https://evogeno.me>/Ad: <https://www.higheredjobs.com/faculty/details.cfm?JobCode=179371422> email: dts@lehigh.edu

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Leipzig Germany Helmholtz Centre Environmental Research Postdoc(f-m-x) Ecological Integrity Assessment (Statistical Modelling)

Postdoc (f/m/x) in Ecological Integrity Assessment (Statistical Modelling) What: Postdoc position Where: Helmholtz Centre for Environmental Research (UFZ), Department of Computational Landscape Ecology, Leipzig Start: 01.09.2026 Application deadline: 28.06.2026 This position aims to advance assessments of ecological integrity by contributing to the development of a novel approach rooted in community ecology. Key targets will be to establish an approach that (i) focuses on ecosystem functionality, (ii) operates without the definition of reference states and (iii) is applicable across ecosystem types. A core part of your work will be to advance and test conceptual frameworks using biodiversity, trait and phylogenetic datasets from aquatic

and terrestrial ecosystems.

You will be part of an interdisciplinarity team working on ecological integrity assessments across multiple departments at Helmholtz Centre for Environmental Research-UFZ. The core team at the UFZ will be supported by a larger synthesis group (with researchers from University College London, Senckenberg Biodiversity and Climate Research Centre, Bristol University, and University of Giessen) who will assist in conceptual development and provide data from a range of different ecosystem types. An important feature of this project is its strong linkages to applied conservation work and policy design. In the second year of the project, we will hence organize a workshop that interlinks researchers with local and national conservation practitioners and environmental policy professionals. Key targets of this workshop will be to evaluate potential applications of developed approaches and reflect on conservation values that are implicitly intertwined with their implementation. Your tasks - Statistical modelling: Analyses of long-term time-series and spatial datasets of community composition, linking community to trait and phylogenetic data - Data curation: Quality control of individual datasets, linking and comparing different datasets - Coordination with project partners: Taking over communication task with scientific and non-scientific project partners We offer - An international and welcoming research environment at the UFZ in Leipzig, a city widely considered for its high living quality and its social and cultural diversity - A wide range of options for balancing care responsibilities and work through our family office - The option to dedicate part of the work time for follow up grant applications - A range of possibilities to engage in career development and training programmes, including the option to develop teaching skills through the support of selected university courses - Excellent computational research infrastructure and data management support - Competent support and advice for international colleagues arriving at the UFZ from the 'International Office' - Special annual payment, capital-forming benefits and subsidised Deutschland-Job-Ticket Your profile - Completed Doctorate in ecology, environmental, or a closely related field in the natural or social sciences - Good understanding of ecological theory, especially in community ecology - Strong knowledge of statistical, data-driven analyses and programming skills, preferably in R or Python - Willingness to contribute to the management of the research network supporting this project - Ability to work in a team, excellent communication skills, and strong scientific writing skills - Very good command of English Your contact for any questions you may have about the job: alfred.burian@ufz.de, julia.pasqualini@ufz.de

Postdoc (f/m/x) in Ecological Integrity Assessment (Statistical Modelling) - <https://recruitingapp-5128.de.umantis.com/Vacancies/3403/Description/2> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

LSU NewOrleans Avian Comparative Genomics

The Claramunt lab at LSU New Orleans (<https://claramuntlab.org>) is seeking a postdoctoral researcher to work on the project "Genomic drivers of climate adaptability and evolutionary diversification in a radiation of Neotropical passerine birds," funded by the Louisiana Board of Regents. The focus of the position is the generation and analysis of high-quality genomes for the family Furnariidae, including genome assembly, annotation, and comparative analyses across lineages.

Responsibilities - Assemble and curate genomes from short- and long-read data (e.g., PacBio HiFi) - Develop and implement assembly and annotation pipelines - Conduct comparative genomic analyses in a phylogenetic framework - Write a manuscript

Qualifications - Ph.D. in genomics, bioinformatics, evolutionary biology, or related field - Experience with genome assembly and/or large genomic datasets - Strong computational skills (Unix/Linux, scripting in R/Python) - Publication record in peer-reviewed journals

Position details - Start date: 1st July 2026 (negotiable) - Duration: 1 year - Location: New Orleans, Louisiana - Competitive salary

To apply:

The official application portal will be available soon at <https://www.uno.edu/careers>. Until then, prospective applicants are encouraged to contact Dr. Santiago Claramunt at sclaramu@uno.edu to express their interest and request additional information about the position.

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Munich LMU PostDoc Evolutionary Genetics

Postdoctoral Researcher in Evolutionary Genetics

Location: University of Munich & MPI-BI, Munich, Germany Duration: 3 years initial Salary: 100Target Start Date: Autumn 2026

We are recruiting a postdoctoral scientist to join our international research team in Munich. Whether you are completing your PhD or finishing a first postdoc, this fully funded, long-term position offers a great opportunity to make an impact in evolutionary genetic research and establish a career in science.

The position. We are seeking a highly motivated, creative and skilled scientist with a strong background in evolutionary genetics and a passion for understanding the mechanisms that generate biological diversity. The successful candidate has expertise in evolutionary genetic theory and demonstrated proficiency in population and comparative genomic data analyses. They will develop and apply innovative computational approaches to existing data sets and will contribute to the design and development of future research directions. Beyond research, the candidate will take an active role in maintaining the lab's computational infrastructure and contribute to teaching in BSc and MSc courses aligned with the lab's expertise and research profile (4 hours per week during the semester).

Research. Research in the lab combines evolutionary theory with field work, lab work and large-scale computational approaches to investigate fundamental evolutionary processes in natural and experimental populations (e.g. 1-3). A central goal is to understand the evolutionary processes and molecular mechanisms involved in adaptation and speciation. We integrate diverse sequence-based datasets (WGS, ATAC-seq, RNA-seq, WGBS, EM-seq) from ancient and modern samples with quantitative phenotypes, which we have begun characterizing using AI-based approaches. Study systems range from yeast to whales with primary focus on vertebrates and current emphasis on avian host-parasite systems such as cuckoos and indigobirds (4, 5). The successful candidate is expected to contribute to the lab's ongoing research and will have creative freedom to develop complementary research directions aligned with the broader goals of the lab.

Environment. The Wolf lab is located at LMU Munich and Max-Planck Institute of Biological Intelligence (MPI-BI) and maintains close ties to a growing evolutionary genetics community representing the breadth of the field (EvoGenMunich). With the Leibniz Supercomputing Centre (LRZ) and its local partners, we have access to state-of-the-art computing facilities. Through our EES Master's program and our partnership with the MEME program, we are fortunate to attract exceptional talent, giving you the unique opportunity to work with passionate, enthusiastic students from around the world. Munich is Bavaria's capital combining living traditions with a relaxed, high-quality lifestyle. If you enjoy the outdoors, the Alps and many lakes are just a short train or bike ride away.

How to apply. Applicants holding a PhD with a proven publication record in a relevant field are encouraged to apply. Applications including a statement of motivation, a CV and the contact details of at least two references should be sent as a single .pdf file to evolution@bio.lmu.de subject term 'EvoGen postdoc'. The position is open until filled with an anticipated start date in autumn 2026. For more information consult the university page here: <https://job-portal.lmu.de/jobposting/7a6500c7ad2bc0b593cc9ab6d39943fb09a516640?ref=homepage> 1. J. W. Poelstra et al., Science. 344, 1410-1414 (2014). 2. C. R. Peart et al., Nat. Ecol. Evol. 4, 1095-1104 (2020). 3. S. Tusso, B. P. S. Nieuwenhuis, B. Weissensteiner, S. Immler, J. B. W. Wolf, Nat. Ecol. Evol. 5, 338-349 (2021). 4. J. Merondun et al., Sci. Adv. 10, ead15255 (2024). 5. J. Merondun et al., Science. 390, 527-532 (2025).

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Postdoc UC Davis Population Genomics Informatics

Postdoctoral Fellow - Population Genomics Informatics Location: Vector Genetics Laboratory (VGL), University of California, Davis / Davis, CA / USA Duration: 2 years with possibility of extension Start Date: July 2026 Application Review: Rolling until filled

Position Overview We invite applications for a Postdoctoral Fellow in Population Genomics Informatics to join a multidisciplinary program preparing for the first-ever field release of a low-threshold genetically modified

fied mosquito. This fellowship offers a rare opportunity to contribute to a globally visible translational milestone by developing the data and informatics systems that underpin large-scale population genomics, field ecology, and mosquito borne disease control innovation. The successful candidate will lead research at the intersection of genomics, data science, ecological monitoring, and regulatory-grade data governance, shaping the informatics backbone of a pioneering field trial. Key Responsibilities - Develop and evaluate integrated data architectures linking field entomology, ecological covariates, sample metadata, and genomic outputs - Build reproducible, scalable workflows supporting multi-site field operations and high-throughput sequencing - Implement FAIR -aligned data governance frameworks - Prototype and test tools for field-data capture, metadata validation, and cross-dataset integration - Publish high-impact research on informatics methods, standards, and population-genomics data systems and how these relate to the overall VGL mission concerning malaria - Provide scientific mentorship to all VGL personnel who generate or handle data, including Postdoctoral Fellows, Staff Research Associates and students. - Collaborate closely with field, wet-lab, and computational teams across partner institutions Required Qualifications - PhD in bioinformatics, computational biology, population genetics, information science, or a related field - Demonstrated experience with large-scale genomic or ecological datasets - Strong programming skills (e.g., Python, R, SQL) and experience with Linux/Unix command-line environments and Bash scripting - Familiarity with workflow managers (Nextflow, Snakemake, CWL) and interactive data visualization tools like QuickSight (currently in use in our lab) - Experience with cloud computing and reproducible research practices - Strong communication skills and ability to work across multidisciplinary teams Preferred Qualifications - Experience with field-site data, ecological covariates, or vector biology - Knowledge of ontologies, metadata standards, and semantic data models - Experience with LIMS, REDCap, ODK, or similar data-capture systems - Background in translational research, global health, or gene-drive-related data systems Why Join Us This fellowship provides the opportunity to contribute to a first-in-the-world field trial, shaping the scientific and operational foundations of a transformative vector-control strategy. The fellow will gain experience in multi-site data integration, regulatory-grade data systems, and high-impact translational genomics—while building a strong publication record in an emerging, high-visibility domain. For additional information see VGL website: <https://vectorgeneticslab.ucdavis.edu/How to Apply> Please submit the following materials as a single

PDF: - Cover letter describing research interests and relevant experience - Curriculum vitae - Contact information for three references Submit applications and address inquiries with the subject line "INFORMATICS POSTDOC APPLICATION '26" to: Mrs. Christine Coleman Executive Assistant Vector Genetics Laboratory cmhandy@ucdavis.edu

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Postdoc U Exeter Badger-bovineTB EcoEvo Genomics Ageing

We are recruiting two postdoctoral researchers for a NERC Large Grant project on the eco-evolutionary dynamics of badger - bovine tuberculosis (bTB) interactions. The project builds on an amazing dataset: 50 years of longitudinal data from the Woodchester Park project, incl. bTB infection, life history, behavioural / movement, physiological / immunological and fitness data, paired with medium coverage whole-genome sequencing data for 2,500+ badgers across the study period.

One of the roles focuses on the evolutionary genomics of badger - bovine TB interactions, using the WGS data to understand how genetic variation influences bTB susceptibility, disease progression and transmission, to examine the role of inbreeding and gene flow in shaping disease dynamics, to quantify how bTB has driven evolutionary change in the population over five decades, and to test evolutionary hypotheses for the maintenance of genetic variation in disease susceptibility (e.g. resistance-reproduction trade-offs, fluctuating selection), among others. You can find the link to the evolutionary genomics position here: <https://careers.exeter.ac.uk/vacancies/847/postdoctoral-research-associate--fellow.html> The other position will combine concepts and analytical approaches from evolutionary ecology and quantitative genetics to investigate the evolutionary mechanisms that maintain senescence in natural populations, the inter-generational effects of senescence (parental age effects) and their evolution, the effects of senescence on bTB dynamics susceptibility, progression and transmission, and the mechanisms that underpin these effects, among others. You can find the link to the senescence position here: <https://careers.exeter.ac.uk/vacancies/822/postdoctoral-research-associate--fellow.html>

ml The wider project includes five postdocs with complementary expertise, along with research faculty from the Universities of Exeter (Barbara Tschirren, Andy Young, Dave Hodgson, TJ McKinley), Sheffield (Jon Slate) and Edinburgh (Matt Silk), and project partners from the Animal and Plant Health Agency (APHA), DEFRA and the Office for Environmental Protection. The positions are based at the Centre for Ecology and Conservation at the University of Exeter's Penryn Campus in Cornwall, UK, and are funded for 4 and 3.5 years, respectively, with an October 2026 starting date (flexible).

Contact b.tschirren@exeter.ac.uk for more information about the genomics position and a.j.young@exeter.ac.uk for more information about the ageing position.

Deadline: June 30 2026 Please refer to the Person Specification PDF in the advertisements and explain in your application how you meet the criteria.

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PurdueU USA population genomics and or epigenetics

Job Title: Postdoctoral Research Assistant City: West Lafayette Job Description: Job Summary A postdoc position is available immediately in Andrew DeWoody's lab at Purdue University (West Lafayette, Indiana, USA). The successful applicant will collaborate on several different projects in population genomics and/or in the deployment of epigenetic clocks. Requisite skills include basic bioinformatics, DNA extractions (ideally from noninvasive sources), PCR, sequencing and statistical modeling (e.g., simple regression). Desired skills include the analyses of whole genome sequence data, qPCR, and/or bisulfite sequencing as well as elastic net regression or other statistical techniques suitable for use with high-dimensionality data. The initial appointment is for 12 months with the possibility of an extension. Experience A PhD is required. For more information, see BOTH of these websites: <https://www.purdue.edu/fnr/sites/dewoody/lab-members/potential-students/> and

https://careers.purdue.edu/job/Post-Doc-Research-Assistant/42765-en_US/?st=09562B93BB96A38F9C7BEFD0EA05FB1D79640FAB If interested, send a

PDF of your CV directly to dewoody@purdue.edu.

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SenckenbergFrankfurt Macrogenetics

Senckenberg - Leibniz Institution for Biodiversity and Earth System Research (SGN), headquartered in Frankfurt am Main, is seeking to fill the following position in the Department of Genomic Biomonitoring at the Senckenberg Research Institute and Natural History Museum Frankfurt, starting as of 01.10.2026:

Postdoctoral Researcher in Macrogenetics (f/m/d)

(Full-Time / Part-Time)

Location: Frankfurt Employment scope: Full-Time / Part-time options are available Type of contract: Limited to 21 months Remuneration: Collective agreement of the state Hesse (TV-H) / E13

Senckenberg is one of the world's leading research institutions in the field of Biodiversity and Earth System Research, with eight research institutes and three natural history museums across Germany and scientists from over 40 nations. Our headquarter is located in the thriving commercial metropolis of Frankfurt in the heart of Germany, which also hosts one of our most famous facilities, the Senckenberg Natural History Museum.

This project will focus on improving our understanding and protection of multispecies genetic diversity patterns through macrogenetic synthesis (see Leigh et al., 2021 NRG) and population genetic simulations.

Islands are nature's natural laboratories and have long been used to fuel and test evolutionary thought. In this postdoctoral project you will synthesize population-level data from islands to characterize genetic diversity's relationship with geological, climatic, and biotic variables. You will explore if relationships on islands are consistent or opposed to those found at a global scale, generating essential information for island nations interested in biodiversity protection and management. This information will parameterize realistic simulations that explore the broader impact of the severe genetic erosion occurring on islands (e.g. Leigh et al., 2019) to gain insight into system stability.

We seek a candidate interested in moving fluidly be-

tween big-picture questions and practical implementation. We are particularly interested in candidates who combine deep scientific curiosity with a motivation to translate ideas into real-world impact. You will work in the Genomic Biomonitoring Lab at Senckenberg (Prof. Dr. Deborah Leigh; Frankfurt, Germany) and have the chance to work within an established network of international collaborators, offering a great opportunity to grow as a scientist. The working language of the lab is English.

Your tasks - Collate and enrich published nuclear genetic and genomic datasets in a macrogenetic database - Conduct large-scale synthesis analyses - Simulate realistic genetic data in SLiM - Publish findings in high-quality peer-reviewed scientific journals and present results at international conferences - Supervise MSc and/or BSc students and their thesis Your tasks - PhD in Population Genomics, Bioinformatics, Macroecology, Digital twin development - Good knowledge of fundamental population genetic theory and analyses - Basic understanding of different molecular data types - Experience working in a reproducible manner on remote computing clusters with large-scale biodiversity, macroecological, or genomic datasets - Statistical modelling and inference skills - Collaborative, collegial, organized working style - Excellent communication and scientific writing skills in English Desirable skills - Strong programming skills (typically Python and/or R) - Experience publishing in scientific journals and presenting at conferences - Experience simulating data using SLiM (or similar tools) - Interest in conservation biology and biodiversity protection - Understanding of island biogeographic theory We offer - access to an international network of scientists, policymakers and research organizations - an attractive job within the inspired and dynamic working environment of an internationally recognized research institution - flexible working hours - mobile working options - employee ID card with free admission to Senckenberg museums - annual special payment - collectively agreed vacation entitlement - company pension plan Senckenberg is committed to diversity. We benefit from the different expertise, perspectives and personalities of our staff and welcome every application from qualified candidates, irrespective of age, gender, ethnic or cultural origin, religion and ideology, sexual orientation and identity or disability. Applicants with a severe disability will be given special consideration in case of equal suitability. Senckenberg actively supports the compatibility of work and family and places great emphasis on an equal and inclusive work culture.

Hot to apply?

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TexasAM PlantSystematics Phylogeography

The Integrative Plant Systematics Lab at Texas A&M University is recruiting a postdoctoral research associate for Fall 2026. This two-year position will focus on plant phylogeography, taxonomy, genomics, and phenomics, centered on an integrative phylogeographic study of a focal grass clade.

The position will involve laboratory and herbarium work, with opportunities for fieldwork. The postdoc will use and develop skills in spectral reflectance, trait prediction, phylogenomics, spatial data analysis, and scholarly writing while working closely Dawson White. There will also be opportunities to develop related projects in other focal clades and geographic regions. Desired start date: August 1 or September 1, 2026. Applicants should have a PhD by the start date, experience with phylogenetics, population genomics, comparative methods, herbarium collections, plant taxonomy, trait datasets, biodiversity informatics, and/or R, and interest in a collaborative, collections-centered research environment.

See the job ad and instructions for applying here: <https://whiteplantsystematics.org/join.html> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UAlabama Biodiversity Taxonomy-Systematics NaturalHistory

The Department of Biological Sciences at The University of Alabama invites applications for a Postdoctoral Fellowship sponsored by the Edward O. and Irene K. Wilson Endowed Fund for Biological Research and Education. The endowment provides fellowships for postdoctoral scholars in taxonomy, museum collections, curation, and the science of natural history. Fellows

will work under the supervision of one or more Biological Sciences faculty conducting relevant research (<https://bsc.ua.edu/directory/>).

Qualifications A Ph.D. with relevant research experience in taxonomy and/or systematics, museum collections, curation, and/or the science of natural history is required. All formal requirements for the doctoral degree must be completed before the start of the fellowship, though degree receipt may be forthcoming. The position is open to both U.S. and non-U.S. citizens. The University of Alabama will not sponsor employment-eligible immigration statuses for this position.

Evaluation Criteria Applications will be evaluated by the selection committee based on a strong academic record in taxonomic, systematic, and/or natural history research, as well as demonstrated experience working in natural history collections. Competitive applicants will present a fully developed research proposal with clearly defined outcomes and anticipated products that incorporate museum collections and associated curation of specimens. Proposals that leverage an integrative approach combining traditional morphological methods with modern molecular or imaging techniques are especially encouraged. Preference will also be given to projects with a high likelihood of resulting in the discovery and formal taxonomic description of new species, and/or the characterization of intraspecific diversity, biogeography, or other natural history components of species supported by collections. Strong interpersonal skills to facilitate effective collaboration with academics, scientists, and students. Exhibit outstanding capabilities in personal responsibility, taking initiative, problem solving, and communication proficiency.

Application Requirements A complete application includes (1) a one-page cover letter that describes how the applicant's past experiences will contribute to the execution and success of the proposed project and how the project promotes collections-based science at The University of Alabama; (2) a research proposal, limited to four single-spaced pages, that outlines the scope and research questions, describes the approach and methods, explains how existing UA collections will be used and expanded with new specimens, details research infrastructure and consumable needs, identifies proposed UA faculty sponsor(s), and lists likely products, including publications, to be completed during the first year of the fellowship; (3) a one-page research budget that itemizes anticipated research and travel costs, not to exceed 10,000 per year; (4) a curriculum vitae limited to two pages;

To apply, go to <http://careers.ua.edu/cw/en-us/job/529577>, complete the online application,

and upload all required documents. Questions about the position may be addressed to Dr. Phillip Harris (pharris@ua.edu). Review of applications will begin 15 July 2026 and will continue until the position is filled. For more information about the department, visit <http://bsc.ua.edu>. Prior to hiring, the final candidate will be required to pass a pre-employment background investigation. The start date is negotiable with sponsoring faculty member.

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UFlorida US Bioinformatics

BIOINFORMATICS POSTDOCTORAL ASSOCIATE

***Position Summary:** The newly established multidisciplinary Plant-Nematode-Microbe Interactions Laboratory at the University of Florida seeks a highly motivated recent Ph.D. graduate with a strong publication record in bioinformatics, computational biology, or molecular biology. The successful candidate will analyze multi-omics datasets to uncover molecular mechanisms underlying plant-nematode-microbe interactions and develop hypotheses for experimental validation. This postdoctoral position is based in the Department of Entomology and Nematology on UF's Gainesville campus and provides access to world-class computational resources, including the HiPerGator supercomputing cluster (4th generation NVIDIA Blackwell architecture), NaviGator AI, and the University's emerging agricultural AI center. The successful candidate will also have opportunities to publish independently, mentor students, develop grant-writing skills, and establish an independent research profile. ***Expected Start Date:** Fall 2026 or Spring 2027 ***Position Duration:** Initial appointment for one year with expectation of renewal for up to three years contingent upon satisfactory performance and funding availability. ***Minimum Qualifications:** - A recent Ph.D. degree (within 3 years) in Bioinformatics, Computational Biology, Genomics, Molecular Biology, Plant Sciences, Microbiology, or a closely related field. - Experience and expertise in nematology is not required but preferred. - Strong track record of lead author publication in computational analyses of omics data. - Experience programming in Python, R, Perl, and/or C++ with the proposed pipeline. - Experience with NGS workflows, such as sequencing and statistical analysis of omics data. - Experience with several of the following tools and workflows: Bowtie2, GATK, FastQC, edgeR, DESeq2, HISAT2,

Scanpy, MaxQuant, or equivalent bioinformatics software. - Experience with high-performance computing environments, workflow management systems, or reproducible research practices is desirable but not required. - Strong written and verbal communication skills in English. - Ability to work independently and collaboratively in a multidisciplinary research environment. - Demonstrated interest in integrating molecular biology experiments with computational analyses.

***Application Process:** Applicants should submit the following materials to Dr. Haarith via email only (deepakrajendran@ufl.edu):

1. Cover letter outlining the candidate's interest and fit for the advertised position.
2. Curriculum vitae (CV) with a clear peer-reviewed original research publication record.
3. Unofficial transcripts for all the University degrees earned.
4. A 2-page research statement outlining the candidate's research interests relevant to the laboratory. Applicants are encouraged to review resources for prospective lab members at deepakhaarith.com prior to preparing their research statement.
5. Contact information of at least 3 references. For further policy information on salaries, benefits and compensation, please read: <https://postdoc.aa.ufl.edu/policies--hiring/benefits-compensation-and-taxes/>

Deadline to apply (via email only): All applications need to be sent in via email only (deepakrajendran@ufl.edu). Applications will remain open until 1 of August 2026 or until the position is filled. Incomplete applications and applicants not meeting the minimum requirements will not be considered.

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UGuam marine eDNA

Postdoctoral Researcher - eDNA Specialist

Project: NAVFAC - Marine Biodiversity Surveys at Joint Region Marianas Administered and Leased Submerged Lands Duration: 1-3 years Salary: 67,000/year Location : University of Guam Marine Laboratory and Guam Center for Biodiversity Research

Relocation to Guam is required. International applicants are encouraged to apply. Position Description

The University of Guam Marine Laboratory and the

Guam Center for Biodiversity Research are seeking a highly motivated postdoctoral researcher to join a multidisciplinary team focused on advancing marine biodiversity monitoring using environmental DNA (eDNA) approaches, including metabarcoding and quantitative PCR (qPCR).

The successful candidate will contribute to marine biodiversity surveys and the development of eDNA-based monitoring strategies in tropical marine ecosystems. Primary responsibilities include collection and processing of water, sediment, and Autonomous Reef Monitoring Structure (ARMS) samples for eDNA analyses, as well as molecular laboratory work including DNA extraction, qPCR assays, sequencing library preparation, and metabarcoding workflows.

The position will support project objectives including:

- Detection and monitoring of scalloped hammerhead sharks using qPCR approaches;
- Broad-scale marine biodiversity assessments and invasive species detection using metabarcoding; and
- Development and evaluation of eDNA-based biodiversity assessment and targeted monitoring strategies.

Additional responsibilities include:

- Assisting with field deployment, recovery, and processing of ARMS units;
- Leading or contributing to technical reports, manuscripts, and project documentation;
- Supporting molecular laboratory organization and management;
- Coordinating with administrative and grants personnel to procure laboratory reagents, supplies, and equipment;
- Assisting with biodiversity and ARMS-focused workshops and training activities; and
- Supporting additional eDNA and biodiversity survey activities associated with field programs in Guam and the broader Mariana Islands, including potential travel to Saipan and Tinian.

Preferred Qualifications

- Ph.D. in molecular ecology, marine biology, environmental science, genetics, bioinformatics, or a related field;
- Experience with eDNA workflows, metabarcoding, qPCR, or molecular biodiversity assessments;
- Experience conducting fieldwork in marine or aquatic environments;
- Strong organizational and communication skills;
- Ability to work independently and collaboratively in interdisciplinary research settings.

Application Instructions

To receive full consideration in the first round of review, please submit the following materials by 25 June 2026:

- Curriculum vitae (CV) - Cover letter - Letters of recommendation

Apply online for position number RC-26-35 here: <https://www.uog.edu/rcuog/job-annou>

ncements For additional information, please contact Robert Lasley at lasleyr@triton.uog.edu.

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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/postdoctoral-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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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 re-

search. 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 maintaining laboratory colonies, and experimental design in behavioral studies.
- Preferred experience in sexual selection, mating systems, mate choice and/or parental care behavior.
- Preferred skill in working with live animals, especially insects.

Application Materials:

To Apply, submit the following:

- 1) Cover letter describing background and research experience, research focus and future goals, competencies, and relevant skills. Additionally, what you hope to gain from this position and how it will support your long-term development as a scientist.
- 2) Curriculum vitae
- 3) 1-2 first author representative publication (published or in press)

APPLY HERE:

https://erecruit.umsystem.edu/psc/tamext/COLUM/HRMS/c/HRS_HRAM_FL.HRS_CG_SEARCH_FL.GBL?Page=HRS_APP_SCHJOB_FL&Action=U JOB ID: 59959

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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/qualification, field of study*
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UNorthCarolina ChapelHill PopulationGenetics

Postdoctoral Research Associate Position Population Genetics University of North Carolina, Chapel Hill

The Johri Lab is seeking a postdoctoral researcher to join us at the University of North Carolina, Chapel Hill. Our research interests involve understanding how evolutionary processes like selection, mutation, recombination, and historical population size changes shape patterns of genomic variation. Projects can involve employing computational and theoretical approaches or statistical method development or using an empirical approach to ask fundamental questions in population genetics. More information about our research interests is provided at <https://www.johrilab.org/>.

The position is best suited for someone trained in population genetics/evolutionary genomics and/or someone with a quantitative background (such as statistics, computer science, bioinformatics) and an interest in population genetics. A Ph.D. in a relevant field will be required by the start date. Informal inquiries about your fit to the lab are very welcome!

Start date is flexible. Salaries will follow recommendations by the NIH.

We are located in the intellectually vibrant Research Triangle area where there are many excellent faculty studying evolutionary biology and genomics both at UNC and neighboring institutions, providing a fantastic opportunity for postdocs to interact with other labs.

How to Apply:

Interested candidates should send the following materials to Parul Johri (pjohri@unc.edu):

-CV -Contact information of two references -A brief explanation of your research interests and why you are interested in joining the lab. [No more than one page.]

Review of applications will begin immediately and continue until a suitable candidate fills the position.

Parul Johri (pjohri@unc.edu),

(to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UNorthCarolina USA Multi-Omics Integration Single Cell Analysis

Postdoctoral Research Associate -Multi-Omics Integration/Single Cell Analysis University of North Carolina at Charlotte (Department of Biological Sciences; School of Data Science)

We are seeking a highly motivated and independent postdoctoral researcher to lead data-driven projects in plant systems biology, with a focus on wild legumes, plant resilience, and multi-omics integration. Research Focus Projects integrate evolutionary genomics, transcriptomics, proteomics, metabolomics, and emerging single-cell approaches to understand plant responses to biotic (e.g., nematodes) and abiotic (e.g., drought, salinity) stresses. Current systems include wild soybean and wild sand bean. What You Will Do Lead analysis and interpretation of single-cell and multi-omics datasets Develop publication-ready figures and manuscripts Drive at least 1-2 first-author papers within 12-18 months Collaborate with a focused research team What We Are Looking For PhD in plant biology, genomics, bioinformatics, or related field Demonstrated ability to write and publish scientific papers Experience with single-cell and omics data analysis (RNA-seq required; multi-omics preferred) Strong organizational and project management skills Ability to work

independently and meet deadlines Highly Preferred Experience with legume genomics Experience integrating multi-omics datasets Familiarity with R/Python and statistical analysis What We Offer Access to rich multi-omics datasets ready for analysis Clear, focused projects with strong publication potential A collaborative and efficient research environment How to Apply Please upload your application package: CV, personal statement, and Names for three references to <https://jobs.charlotte.edu/postings/67133> If you have any questions, please contact bsong5@charlotte.edu (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

UOxford UK Evolution of sex chromosomes

Postdoctoral Research Associate, University of Oxford, UK

The Department of Biology, University of Oxford is seeking to recruit a Postdoctoral Research Associate (PDRA) on 20 months' project funded by a grant to Prof Filatov from the BBSRC. The project will focus on the analysis of sex chromosome evolution, but may also extend to evolution of other types of chromosomes mainly in plants. The PDRA will be encouraged to collaborate on other related projects to help improve their publication record and maximize the chances of future employability in academia. The PDRA on this project will be responsible for lab work, data analysis and preparation of papers for publication. Most of the work in the project is expected to be computer-based, with the focus on evolutionary genetic analyses of genome and transcriptome sequence data. Closing date: 29-Jun-2026 For more details and formal application go to: <https://www.ox.ac.uk/about/jobs> then click "Search all vacancies" and select vacancy ID: 186626

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UWisconsinMadison Avian Transcriptomics and Conservation

We are hiring a 2-year Postdoctoral Research Associate to investigate the sub-lethal effects of rodenticide exposure in wild owls using transcriptomic approaches. This work is part of a collaborative project funded through the California Department of Fish and Wildlife's Cannabis Restoration Grant in partnership with the Hoopa Valley Tribe. The project involves leading an RNA-seq study designed to identify genome-wide

amenable to simulation, novel methodology, or *Drosophila* genomic analysis. * The population genomics of admixture/introgression between partially isolated fly populations and species. * Using multi-omic data to investigate the evolution of maternal investment and reproductive tradeoffs in a challenging environment. * Analyzing genomic variation within laboratory fly strains to uncover their cryptic history, and developing new cutting-edge population genomic resources.

Our lab currently includes 1 masters-level lab manager with a diverse skill set, 1 recently arrived postdoc, 2 advanced PhD students (with a couple rotating first year PhD students to in the fall), and several undergraduates. Lab alumni include 6 postdocs and 5 PhD recipients. Further lab info: <http://www.johnpool.net> UW-Madison offers a superb scientific environment with a vast biological research community and a supportive, collaborative, and egalitarian culture. Numerous labs focus on population genetics, evolutionary genomics, and *Drosophila* research: <https://genetics.wisc.edu/evolutionary-and-population-genetics/><https://evolution.wisc.edu/people/faculty/><https://genetics.wisc.edu/drosophila-and-other-insects/> Madison offers an exceptional quality of life in a beautiful landscape, and has been ranked as both the best US city for young adults and the best for raising a family. <http://www.visitmadison.com/media/rankings/> Downtown and campus are bordered by lakes, it's easy to get around by bike or bus, and Madison features diverse art, music, cultural, and culinary offerings.

We welcome applicants from all backgrounds, including those poised to add unique or rare perspectives to our field and our community.

Start dates are flexible. Salary follows the NIH scale. Benefits include individual or family health insurance.

Applications are due by [July 7]. However, earlier applications are welcome, and later applications may still be considered. Informal inquiries are also welcome at any time.

To apply, send a statement of research interests (up to 1 page) addressing the intersection between your own scientific interests and the Pool lab's research in terms of potential projects, along with a CV and contact info for 3 references.

John Pool Professor of Genetics Director of Wisconsin Evolution (The J. F. Crow Institute) University of Wisconsin - Madison jpool@wisc.edu

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UWyoming US Amphibian disease microbiome genetics interaction

Postdoctoral Researcher Wyoming Toad Recovery Challenge Grant University of Wyoming — Laramie, Wyoming
Background The Wyoming toad (*Anaxyrus baxteri*) is a critically endangered species endemic to the Laramie Basin. Once abundant through the 1950s and 1960s, the species underwent severe population declines beginning in the 1970s until the last known wild individuals were brought into captivity in the 1990s to establish a managed breeding program. Although individuals from the captive breeding program have been reintroduced into the wild, self-sustaining wild breeding populations have not yet been reestablished. Ongoing research and monitoring are assessing the status of wild populations, including the ecological effects of vegetation management treatments. This position offers an exceptional opportunity to lead novel scientific inquiry contributing directly to the recovery of one of North America's rarest amphibians. Location This position is based at the University of Wyoming in Laramie, Wyoming. Field research will be conducted at Mortenson Lake National Wildlife Refuge (approximately 15 miles southwest of Laramie) and at multiple Safe Harbor reintroduction sites throughout the Laramie Basin. Position Description The Postdoctoral Researcher will lead field and laboratory research efforts focused on Wyoming toad population ecology, disease dynamics, and reintroduction success. This is a research leadership role requiring independent scientific research, strong publication record, and demonstrated ability to supervise field personnel. Specific responsibilities include: - Leading and developing field research protocols, including

population monitoring, survival analyses, and assessment of implementation outcomes. - Leading disease ecology scientific investigations, including experimental *Batrachochytrium dendrobatidis* (Bd) exposure trials, treatment protocols, and culture maintenance)

- Directing on-site toad Bd exposure, treatment, and microbiome inoculation to assist recovery efforts. - Conducting and supervising systematic surveys for non-captive Wyoming toads across refuge and Safe Harbor sites - Overseeing Bd swabbing protocols and conducting laboratory analyses (Bd and microbiome) - Mentoring and supervising field technicians; providing leadership and quality control for all data collection; potential to mentor undergraduate researchers

- Managing data pipelines, ensuring data integrity, and leading quantitative analyses - Preparing peer-reviewed manuscripts, technical reports, and recovery documents - Communicating and collaborating with USFWS, Wyoming toad recovery partners, and cooperating landowners - Contributing to strategic planning for Wyoming toad species recovery - Other research duties as assigned Required Qualifications - MS (researcher) or PhD (postdoc) in wildlife biology, ecology, conservation biology, herpetology, or a closely related field * NOTE this position is listed as either a Researcher position (MS required) or Postdoctoral researcher (PhD). Preference is to fill the position as a postdoctoral researcher, with pay, expectations, and independence commensurate with postdoc position.

- Peer-reviewed publication(s) demonstrating independent research contributions and scientific writing. - Demonstrated experience leading field research and supervising field and/or lab employees. - Strong background in amphibian ecology, wildlife biology, and/or disease ecology - Proficiency in quantitative methods and statistical analysis relevant to wildlife research - Excellent written and verbal communication skills, including experience preparing scientific manuscripts and technical reports - Valid driver's license with a clean driving record; ability to lift up to 40 lbs - Ability and willingness to work extended hours including weekends and holidays, as determined by animal care and field needs - Capacity to work effectively in challenging field conditions (temperature extremes, wind, rain, biting insects, mud) while maintaining rigorous data quality standards - Ability to work in confined spaces at site while caring for animals. Preferred Qualifications - Experience with amphibian husbandry, captive breeding programs, or reintroduction biology - Population and/or conservation genetics laboratory work. - Familiarity with chytrid fungus (Bd) biology, culture techniques, and disease management - Experience working with federal and state wildlife agencies and recovery teams - History of successful grant acquisition or contribution to funded research programs - Knowledge of the ecology of the Laramie Basin or the broader Rocky Mountain West Compensation & Position Details

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XTBG TropicalPlantEvolutionConservation

Postdoctoral Researcher We are currently seeking postdoctoral researchers in the Tropical Plant Diversification and Ex-Situ Conservation research group, which is closely affiliated with the Applied Research Center for Tropical Plant Conservation at the Xishuangbanna Tropical Botanical Garden (XTBG) in Yunnan, China. Both the research group and the conservation center are newly established multidisciplinary teams formed by merging several smaller research teams for the purpose of addressing major environmental and conservation issues in tropical China and more generally in Southeast Asia.

Given the multidisciplinary nature of ongoing and anticipated projects, we are inviting applications from researchers with expertise and ambition in a number of different fields, including computer modeling of plant

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AntCourse 2026Mexico

Applications are now open for the Ant Course, an intensive international field course focused on ant biology, systematics, and ecology.

Information on location, dates, instructors, and how to apply, can be found here: <https://www.antcourse.org/>

The Ant Course is a globally recognized training program that brings together students, researchers, and professionals to learn directly from leading myrmecologists through a combination of lectures, laboratory work, and hands-on field experience. Participants gain practical skills in ant identification, sampling, specimen

curation, and the study of ant diversity, behavior, and their roles in ecosystems.

The course emphasizes: - Ant phylogeny, diversity, and classification - Social behavior and colony biology - Field collection and biodiversity sampling methods - Specimen preparation and identification techniques The program is designed for a broad audience, including students, postdocs, professors, researchers, and motivated participants from diverse backgrounds in biology; prior specialization in ants is not required.

Please feel free to share this announcement widely with interested students and colleagues.

Best regards, Marek Borowiec

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Course OnlineClusteringHigh-DimensionalData Jun16

Hello EVOLDIR members Last chance - We are pleased to announce an upcoming livestream seminar designed to enhance your data analysis workflows. Clustering High-Dimensional Data 3.0 is a seminar livestreaming June 16 with Nikolay Oskolkov (Lund University). This upcoming seminar provides researchers in evolutionary biology and genetics with the practical skills to analyze complex, multi-dimensional genomic and phenotypic datasets. Participants will learn to implement advanced dimensionality reduction and clustering algorithms in R and Python to identify distinct evolutionary lineages and genetic patterns. By mastering these unsupervised learning techniques, you can extract meaningful biological insights from high-throughput sequencing and population data to advance your research. Sign up today (<https://instats.org/seminar/clustering-high-dimensional-data-30>) to register now, and we'd 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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FUBerlin AgentBasedModellingUsingNetlogo 24-28August

Dear all,

the registration deadline for our course "Agent-based and Individual-based Modelling using NetLogo" is June 30th, and a few seats are still available.

Dates: Berlin, 24-28 August - Freie Universitat Berlin (Biology, Dahlem)

Course website: <https://www.physalia-courses.org/courses-workshops/course52/>

This intensive 5-day course introduces the principles and practice of agent-based and individual-based mod-

elling (ABMs/IBMs) using NetLogo. Participants will learn how to design, implement, and analyse simulation models relevant to ecology and beyond, guided by leading experts Prof. Volker Grimm and Prof. Steve Railsback.

Expect a highly hands-on format combining lectures, coding tutorials, and independent project work. By the end of the week, you will be able to build, test, and evaluate your own ABMs and apply best practices in model design and analysis.

Looking forward to welcoming you in Berlin this August.

Best regards, Carlo

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

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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 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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OhioStateU FloraPalooza Aug17-20

If you are or want to be working on applying AI/ML to digitized herbaria, plant and plant community images, including in combination with hyperspectral and other remote sensing modalities, the following workshop may be of particular interest to you.

FloraPalooza 2026 - Call for Participation

The Imageomics Institute is hosting a 3.5-day workshop offering a unique opportunity to develop proof-of-concepts demonstrating how the application of computer vision techniques can transform plant imagery analyses such as biodiversity assessment, plant-insect interaction studies, and trait data extraction. This event will bring together an interdisciplinary group around a shared interest of analyzing plant imagery (e.g., herbarium, in-situ, hyperspectral, remote sensing images) with AI/ML, including ML researchers, ecologists, biologists, software developers, and data engineers. Participants will work in small groups to collaboratively develop FAIR data products, tutorials, tools, workflows, and other products targeting the motivating challenge.

The event will take place August 17-20 at Hyatt House Columbus/OSU near The Ohio State University in Columbus, OH, USA. To apply to participate, please fill out the FloraPalooza 2026 Application for Participation by the end of June 25, 2025 here: <https://forms.gle/fVcrmbvYQDdWKMSA> Funds to assist with travel expenses are available but limited, as is

space. We expect to notify applicants about acceptance by July 2, 2025.

A full Call for Participation, including motivation, goals, and who should attend, is posted here: <https://github.com/Imageomics/FloraPalooza-2026/blob/main/CfP.md> Organizing Team

Elizabeth Campolongo (The Ohio State University & Imageomics Institute) Jeannine Cavender-Bares (Harvard University Herbaria) Jianyang Gu (The Ohio State University & Imageomics Institute) Hilmar Lapp (Neuromatch & Imageomics Institute) Dylan MacArthur-Waltz (University of Maine, Department of Wildlife, Fisheries, and Conservation Biology) William Weaver (University of Michigan, Michigan Institute for Data and AI in Society)

On behalf of the organizing committee:

Hilmar Lapp (Neuromatch & Imageomics Institute; first.last at gmail.com)

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actionable conservation recommendations.

- o Coverage of cutting-edge topics such as genetic load, demographic inference, and SNP panel design.

- o Discussion of methodological limitations and decision-making under uncertainty.

- o Integration of international conservation frameworks, including CBD, CITES, IUCN, and EU legislation.

- o Interactive debates and case studies connecting science, management, and policy.

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 Advanced Conservation Genomics 28 September-1 October

Dear all,

We are pleased to announce our upcoming online course Advanced Conservation Genomics (28 September - 1 October), designed for researchers and professionals seeking to apply genomic data directly to biodiversity conservation and management.

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

This training focuses on how genomic evidence can inform real-world conservation decisions, management actions, and policy frameworks. Participants will learn how to interpret effective population size, assess genetic load, develop SNP panels for conservation applications, and critically evaluate the role of genomics in legislation and institutional decision-making. The course is intended for PhD students, postdoctoral researchers, conservation geneticists, and professionals working in conservation agencies, NGOs, and wildlife management.

Key strengths of the course include:

- o A strong focus on translating genomic results into

Online AgenticAIForLifeSciences 6-7 July

Dear all, We are pleased to announce the course "Agentic AI for Life Sciences", taking place online on 6-7 July.

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

Agentic AI is rapidly transforming research workflows, moving beyond chat-based assistants to systems that can support coding, data analysis, and multi-step scientific pipelines. This hands-on course provides practical training on how to effectively integrate these tools into real life sciences research.

Participants will learn how to: - Use modern AI tools for data analysis and coding tasks - Improve outputs through effective prompt and context design - Build interactive data applications and reproducible workflows - Connect AI tools to external knowledge sources - Apply best practices for responsible use in research The course is aimed at life sciences researchers (ecologists, biologists, bioinformaticians, data scientists) with basic programming experience. No prior experience with AI tools is required.

If you want to learn about AI-Assisted Coding for Bioinformatics with Python, have a look at our course as well:

<https://www.physalia-courses.org/courses-workshops/ai-powered-python/>

Best regards, Carlo —————

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

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Online AI-Assisted Systematic Reviews Jun10-12

Hello EVOLDIR members

Last chance - Keeping pace with the rapidly expanding volume of scientific literature is a growing challenge for researchers. AI-Assisted Systematic Reviews and Meta-Analysis is a 2-day seminar livestreaming June 10 and 12 with Moses Boudourides (Data Science Graduate Program, School of Professional Studies, Northwestern University). This upcoming livestream seminar introduces a no-code workflow for leveraging large language models and bibliographic APIs to automate literature screening and data extraction. Evolutionary biologists and geneticists can apply these AI-driven methods to rapidly synthesize vast bodies of literature on gene families, phylogenetic analyses, or population genetics. By mastering these reproducible workflows, researchers can efficiently map historical evolutionary debates and extract structured phenotypic data to accelerate their own meta-analyses.

Sign up today (<https://instats.org/seminar/ai-assisted-systematic-reviews-and-meta>) 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 Bayesian Analysis on July1 LastChance

Hello EVOLDIR members

Last chance - Enhance your quantitative research toolkit with advanced statistical methods designed to resolve complex analytical challenges. Introduction to Bayesian Analysis 2.0 is a seminar livestreaming July 1 with Centre for Applied Statistics Courses (CASC) (University College London). This upcoming livestream seminar offers evolutionary biologists and geneticists a robust framework for integrating prior evolutionary knowledge into statistical models. By mastering Bayesian inference, researchers can more accurately estimate ancestral states, model phylogenetic uncertainty, and interpret complex genomic datasets. Participants will gain the practical skills needed to compute posterior distributions and critically evaluate Bayesian methodologies in published evolutionary literature.

Sign up today (<https://instats.org/seminar/introduction-to-bayesian-analysis-20>) to register now, and we'd 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 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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Online BigDataPhylogeny and ComparativeMethods 23-26June

Dear all, We are pleased to announce that only 3 seats are still available for the upcoming online course: Big Data Phylogeny and Comparative Methods: From Theory to Practice

Dates: 23-26 June

More information and registration details can be found here: <https://www.physalia-courses.org/courses-workshops/bigphylogenies/>

This 4-day hands-on course provides a comprehensive introduction to phylogenetic and comparative evolutionary analyses, covering tree construction, trait evolution, ancestral state reconstruction, comparative genomics, and advanced topics such as species delimitation and phylogenetic networks.

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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OnlineCourse Build Autonomous AI Agents for Scientific Research

Last chance: Online Course: Build Autonomous AI Agents for Scientific Research Hello EVOLDIR members

Last chance - Modern scientific workflows are rapidly evolving with the integration of advanced computational tools. Building Autonomous AI Agents for Scientific Research is a 2-day seminar livestreaming June 26-27 with Renan Maestri (Department of Ecology, Universidade Federal do Rio Grande do Sul). By learning to build autonomous AI agents in R, evolutionary biologists can automate complex comparative genomic analyses and phylogenetic workflows. These agentic systems allow researchers to orchestrate multi-step data retrieval and code execution tasks securely, ensuring reproducibility in large-scale evolutionary studies. This training provides the practical skills needed to deploy local or cloud-based agents that can accelerate literature synthesis and data-intensive modeling in your own research.

Sign up today (<https://instats.org/seminar/building-autonomous-ai-agents-for-scient>) 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 DemographicInferenceInPopulationGenomics 20-24July

Dear all, Are you interested in learning how to infer population history, structure, and gene flow from genomic data?

Join our upcoming online course: Model-Based Demographic Inference from Population Genomic Data

Dates: 20-24 July — Online

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

This course provides an introduction to the theory and practice of evolutionary demographic inference using population genomic data. Participants will explore key approaches based on both frequency-based data (e.g. SNPs and site frequency spectra) and haplotype-based data (e.g. whole genomes), combining lectures with hands-on practical sessions using real and simulated datasets.

Topics covered include: - Population genomic data and summary statistics - Coalescent theory and site frequency spectrum (SFS)-based inference - Demographic modelling and model comparison - Isolation-with-migration frameworks - Sequentially Markovian Coalescent (SMC) methods - Practical applications using tools such as fastsimcoal, PSMC, MSMC2, IMA3, and others The course is aimed at graduate students, postdoctoral researchers, and scientists interested in population genomics and statistical inference.

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 Dimensionality Reduction with UMAP

Hello EVOLDIR members

Analyzing complex, high-dimensional datasets presents unique challenges for researchers across the biological sciences. Dimensionality Reduction with UMAP and Beyond 2.0 led by Nikolay Oskolkov (Lund University) is now available as an on-demand streaming seminar. This hands-on workshop provides a comprehensive foundation in linear and non-linear dimensionality reduction techniques, including PCA, t-SNE, and UMAP. Evolutionary biologists and geneticists can apply these advanced methods to simplify complex genomic datasets, allowing for clearer visualization of population structures and evolutionary trajectories. By mastering these tools in R and Python, you will be able to extract meaningful patterns from high-dimensional biological data to accelerate your research.

Access this seminar (<https://instats.org/seminar/dimensionality-reduction-with-umap-and-b-1>) on demand at your own pace, and please pass this to colleagues and students who may find it useful! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online Evolutionary macroecology in R exploring biodiversity patterns at large scales

Online live course: Evolutionary macroecology in R: exploring biodiversity patterns at large scales Dear colleagues, There are two spots available for the course "Evolutionary macroecology in R: exploring biodiversity patterns at large scales". Dates & schedule: June 8th-12th, 2026 from 13:00-17:30 (Madrid time zone). Course webpage: <https://www.transmittingscience.com/courses/ecology/macroecology-in-r-exploring-biodiversity-patterns-at-large-scales/> The aim of this course is to introduce participants to

macroecological analyses using R to explore large-scale biodiversity patterns and ecological processes. By the end of the course, students will be able to: Generate geographic maps of biodiversity. Construct biogeographic regions while accounting for the evolutionary relationship of species. Integrate tools of macroevolutionary dynamics, such as estimating ancestral areas and ancestral traits, with community phylogenetic metrics.

Instruction will combine lectures, hands-on computational exercises, and guided examples. Language of instruction: English. For any questions, please write to courses@transmittingscience.com Best wishes Sole – Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online GLMMsInR September21-24

Dear all,

Interested in "Generalized Linear Mixed Models (GLMMs) in R"?

You can still join us for our GLMMs in R course in September (21-24): <https://www.physalia-courses.org/courses-workshops/glms-in-r/>

This course provides a practical and applied introduction to specifying, interpreting, and validating GLMMs in R, with a strong focus on real research applications.

Participants will work with the lme4 and glmmTMB packages and learn how to incorporate random effects, variance structures, and correlation structures (including spatial and temporal autocorrelation) into their models. We will also cover model interpretation, diagnostics (using DHARMA), and best practices for building defensible statistical analyses.

The course is aimed at graduate students and researchers with prior experience in generalized linear models in R who wish to extend their skills to mixed modelling frameworks.

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

- Build and interpret GLMMs for real-world data
- Include random effects, heteroscedasticity, and correlation structures
- Select appropriate model structures for applied research questions
- Evaluate model assumptions and performance using diagnostic tools in R

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 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, including 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

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

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Online Last-Chance Learn Python and AI for Data Analysis

Hello EVOLDIR members

Last chance - Streamlining your research workflow has never been more accessible with modern computational tools. Using AI to Learn Python for Data Analysis is a 2-day seminar livestreaming June 23 and 26 with Peter Gruber (Faculty of Economics, USI Università della Svizzera Italiana). By leveraging AI assistants to write and debug Python code, evolutionary biologists can rapidly build custom pipelines for processing large genomic datasets. This approach allows researchers to transition away from restrictive point-and-click software toward fully reproducible workflows for phylogenetic and population genetic analyses. Participants will gain the practical skills needed to automate data cleaning, run complex statistical models, and ensure their evolutionary research meets the highest standards of replicability.

Sign up today (<https://instats.org/seminar/using-ai-to-learn-python-for-data-analysis>) 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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OnlineLiveCourse Geometric Morphometrics inR

Dear colleagues, Registration is open for the Transmitting Science online course "Geometric Morphometrics in R" (12th edition). Dates & Schedule: July 20th, 21st, 22nd, 23rd, 24th, 27th, and 28th, 2026, from 12:00 to 17:00 (Madrid time zone). Course webpage: <https://www.transmittingscience.com/courses/geometric-morphometrics/geometric-morphometrics-r/>Instructor: Dr. Julien Claude, author of the book "Morphometrics with R" (Institut des Sciences

de l'Evolution de Montpellier, France). Geometric morphometrics provides a powerful quantitative framework for analyzing phenotypic evolution by capturing and statistically comparing shape variation across organisms in a rigorous and reproducible manner. Concepts in geometric morphometrics will be taught using a series of original data sets and working in R for solving a series of tasks. The course will start with an introduction to R and will rapidly go into shape analysis with measurements, landmark data and outlines. Participants are welcome to bring their own data and problems so that we may find R solutions. Best wishes Sole Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

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 Evolutionary Genomics MLEG01

Machine Learning for Evolutionary Genomics (MLEG01) <https://prstats.org/course/machine-learning-for-evolutionary-genomics-mleg01/> Delivered by experienced computational biologists, evolutionary geneticists, and machine learning researchers. Learn how to apply Machine Learning (ML) and Artificial Intelligence (AI) methods to evolutionary and population genomic data. The rapid growth of genomic datasets has created new opportunities and challenges for evolutionary biologists. Machine learning methods are increasingly being used to identify adaptive variation, detect signatures of selection, classify populations, predict evolutionary processes, and uncover complex patterns hidden within large genomic datasets. This hands-on course provides a practical introduction to machine learning workflows for evolutionary genomics using real-world examples and datasets. Machine learning is becoming a major tool in evolutionary genomics, particularly for population genetics, demographic inference, and selection detection. What you'll gain - A strong understanding of machine learning concepts in evolutionary biology - Practical experience applying machine learning methods to genomic datasets - Skills in predictive modelling, classification, and pattern recognition - Understanding of supervised and unsupervised learning approaches - Ability to evaluate model performance and avoid common pitfalls - Confidence in interpreting machine learning outputs in an evolutionary context

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

Who is this course for? - Evolutionary biologists and population geneticists - Bioinformaticians and computational biologists - Researchers working with genomic and sequencing datasets - PhD students and quantitative life scientists - Anyone interested in applying AI and machine learning to biological questions

Why take this course? Modern genomic datasets often contain millions of genetic variants and increasingly complex biological signals. Traditional analytical methods can struggle to identify subtle patterns associated with adaptation, demographic history, and evolutionary

processes. Machine learning provides powerful tools for extracting information from these large datasets, enabling researchers to tackle questions involving population structure, natural selection, genomic prediction, and evolutionary inference. Recent advances have demonstrated the growing importance of machine learning and deep learning methods across population genetics, evolutionary genomics, and comparative biology. This course equips you with the practical skills needed to apply machine learning methods confidently to evolutionary genomic data, helping you generate new biological insights and build reproducible analytical workflows.

Learn more & enrol PR Stats course page for Machine Learning for Evolutionary Genomics (MLEG01) <https://prstats.org/course/machine-learning-for-evolutionary-genomics-mleg01/> Questions? Email: oliver@prstats.org

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

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 Transmitting Science www.transmittingscience.com (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Online Phylogenetic Comparative Methods In R 15-19 June

Dear all,

Are you interested in Phylogenetic Comparative Methods in R? We are pleased to announce the 6th edition of this online Physalia course, which will run from June 15th to 19th. Course website: <https://www.physalia-courses.org/courses-workshops/course44/> This course provides a hands-on introduction to how phylogenetic comparative methods can be used to study trait evolution and diversification using time-calibrated phylogenies.

Over five days, participants will combine lectures and practical sessions to learn how to: - Build and interpret ultrametric phylogenies (chronograms) - Reconstruct trait evolution across lineages - Explore models of diversification and evolutionary rates - Apply phylogenetic comparative methods in R The course is aimed at advanced students, researchers, and professionals with a basic background in evolutionary biology and some familiarity with R. Participants are also welcome to bring their own datasets for discussion and practical guidance.

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 Population Genomics With Low Coverage WGS 26-29 October

Dear all, registration is now open for the Physalia online course: Population Genomic Inference from Low-Coverage Whole-Genome Sequencing Data

Dates: 26-29 October

Course website: <https://www.physalia-courses.org/courses-workshops/course64/>

Low-coverage sequencing is a powerful and cost-effective approach for population and evolutionary genomics, but it requires probabilistic methods that properly account for genotype uncertainty. This course focuses on practical inference using genotype likelihood frameworks and the ANGSD ecosystem.

You will learn how to: - Analyse low-coverage sequencing data in population genomics - Use genotype likelihoods for SNP calling and allele frequency estimation - Infer population structure, demography, and inbreeding - Detect selection using genome-wide summary statistics

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 Population Modeling Sept8-Dec20

Learn techniques for integrated population modeling in this online course from Center for Wildlife Studies.

DESCRIPTION: This course provides a thorough introduction to integrated population models, i.e. population dynamics models in which the parameters are estimated using two or more datasets. We show how to use Bayesian methods to fit a wide variety of models, using the JAGS software in R. We show how to construct both the population model and the observation model needed for each dataset. Participants will learn how to fit population models to real-world data, via case studies that include data on counts, productivity, mark-recapture, dead-recoveries, and radio-tracking. There is also an emphasis on both model-checking and model comparison to aid model development and refinement.

DATES: September 8 - December 20, 2026

FORMAT: Fully online, learn-at-your-own-pace

PRICE: From 450students/unemployed;550

employed Early bird discount (saves at least 75)whenyouregisterbyAugust9

DETAILS & REGISTRATION: <https://www.centerforwildlifestudies.org/courses/p/integrated-population-models> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Retrieving Genomic Data From Ensembl July28-29

Hello EVOLDIR members

Are you looking to streamline how you access and analyze large-scale genomic datasets for your research? Retrieving Genomic Data From Ensembl is a 2-day seminar livestreaming July 28-29, led by Jorge Batista da Rocha (European Bioinformatics Institute (EMBL-EBI)) and Aleena Mushtaq-Stolworthy (European Bioinformatics Institute (EMBL-EBI)). Researchers in evolutionary biology and genetics can leverage the newly redesigned Ensembl Data Platform to streamline the extraction of high-quality genomic datasets. This seminar provides hands-on training to help you navigate the updated interface, prioritize variants, and integrate comparative genomic data directly into your analytical pipelines. By mastering these retrieval tools, you can efficiently incorporate diverse eukaryotic and prokaryotic genomes to advance your evolutionary research.

Sign up today (<https://instats.org/seminar/retrieving-genomic-data-from-ensembl>) 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 RNAseqTranscriptomics Nov11-20

Dear colleagues, Transmitting Science is offering a new edition of the course "Bioinformatic tools for RNA-seq and transcriptomic data analyses". Registration and more information: <https://www.transmittingscience.com/courses/genetics-and-genomics/bioinformatic-tools-for-rna-seq-and-transcriptomic-data-analyses/> Course Overview: This introductory course provides practical training in the analysis of transcriptomic data generated by RNA sequencing (RNA-seq) using next-generation sequencing (NGS) technologies. Participants will learn how to use bioinformatics workflows to process, analyse, and interpret sequencing data. The course covers essential steps including Linux fundamentals, quality control and pre-processing of sequencing files, handling sequence alignment data, and complete RNA-seq analysis pipelines. Topics include read mapping, transcript assembly, quantification, differential expression analysis, and downstream biological interpretation. A dedicated section on small RNA sequencing introduces specialised workflows, including miRNA analysis and target prediction approaches. For more information or questions, please contact us at courses@transmittingscience.com Best wishes, Haris – Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

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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Online Single Cell Data Analysis

Hello EVOLDIR members

Enhance your research capabilities by mastering advanced computational workflows for high-dimensional genomic datasets. Single Cell Data Analysis 2.0 led by Nikolay Oskolkov (Lund University) is now available as an on-demand streaming seminar. This on-demand seminar provides evolutionary biologists and geneticists with the computational skills needed to analyze cellular heterogeneity at a granular scale. Participants will learn to implement robust single-cell RNA sequencing workflows using R and Python libraries to resolve complex genomic variations. By mastering these state-of-the-art analytical pipelines, researchers can directly investigate evolutionary processes and genetic diversity within heterogeneous cell populations.

Access this seminar (<https://instats.org/seminar/single-cell-data-analysis-20-1>) at your own pace and please share this with colleagues and students who might benefit!

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

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Online SingleCellRNA-seq June23-25

We still have space available in our upcoming Single Cell RNA-seq workshop (virtual but live instruction - June 23-25). This hands-on workshop is designed for researchers interested in analyzing and interpreting single-cell RNA-seq data. Participants will gain practical experience understanding experimental design considerations for single-cell RNA-seq experiments, converting raw sequencing data into count or expression matrices, assessing dataset quality, clustering cells (UMAP, t-SNE), identifying cluster-specific markers and annotating cell types, integrating datasets across conditions, and performing trajectory analysis to study cell differentiation. Learn more & register here: [cbcsupport@helpspotmail.com](https://bioinformatics.uconn.edu/cbc-workshops/WHEN:Virtual(MSTeams)-recordingsdistributedWHEN:10:00AM-2:00PMESTCOST:SeewebsiteforregistrationdetailsRegistrationisfirstcome,firstserved.No prior bioinformatics experience needed! Questions? E-mail: <a href=)

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Online SpatialOmics 14-16September

Dear all, We are pleased to announce the Physalia online course: Spatial Omics Data Analysis: ¿From Raw Data to AI Insights

Dates: 14-16 September

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

Spatial omics technologies are transforming how we study tissue organization, cell interactions, and gene regulation in space. This course provides a complete, practical workflow—from raw data to advanced analysis and AI-driven insights.

Participants will learn how to work with modern SpatialData-centric workflows and integrate multiple

data modalities, including transcripts, cells, and images.

You will learn how to: - Perform preprocessing and quality control of spatial omics data - Analyze spatial structure, cell-cell interactions, and gene-level patterns - Apply spatial statistics and neighborhood-based analyses - Understand and critically evaluate AI-based approaches in spatial biology The course combines lectures, hands-on tutorials, and guided discussions, with a strong focus on reproducibility and real-world applications.

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 SpeciesDistributionModeling Sept8-Dec20

Looking to build your skills in species modeling? Check out the online course "Species Distributing Modeling" from Center for Wildlife Studies (<https://www.centerforwildlifestudies.org/>) this fall.

DESCRIPTION: The long list of approaches to determining the boundaries of a species' distribution can be split into three broad categories: presence-only, presence-absence, and presence-background models. This class will focus on contrasting the assumptions and modeling goals of each modeling framework, providing a solid foundation for applying these techniques to a broad range of applications. We emphasize the importance of selecting the appropriate modeling techniques to fit, evaluate, and extrapolate modeling outputs. We will demonstrate how a suite of R packages can be utilized to perform the analyses required at various stages of a modeling exercise. For each module in this course, we will work on a case study to illustrate the main stages of a modeling exercise, which will guide you to advance in your final project (for those working on one).

DATES: September 8 - December 20, 2026

FORMAT: Fully online, learn-at-your-own-pace

PRICE: From 450students/unemployed;550 employed Early bird discount (saves at least 75)whenyouregisterbyAugust9

DETAILS & REGISTRATION: <https://www.centerforwildlifestudies.org/courses/p/species-distribution-modeling> Emily J. Uhrig, PhD Director of Education Center for Wildlife Studies

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Online SpeciesDistributionModelsInR 14-18September

Dear all,

We are pleased to announce the 10th edition of the online course "Species Distribution and Ecological Niche Modelling in R", taking place from 14-18 September.

For more information and registration, please visit: <https://www.physalia-courses.org/courses-workshops/course45/>

During this hands-on course, participants will learn the theory and practice of Species Distribution Models (SDMs) and Ecological Niche Models (ENMs), from fundamental concepts to real-world applications. Using reproducible workflows in R, participants will build, validate, and apply models based on species occurrence data of their choice.

Topics include:

- o Fundamental concepts and theory behind SDMs and ENMs
- o Data preparation and model building in R
- o Model evaluation and validation
- o Understanding model assumptions, strengths, and limitations
- o Predicting and projecting species distributions across space and time
- o Best practices for reproducible ecological modelling

Previous experience with R is recommended, although all scripts will be provided and explained in detail.

Related courses:

- 1) Species distribution models with BART - ONLINE, 1-3 July <https://www.physalia-courses.org/courses-workshops/barts/>
- 2) Landscape Genomics - ONLINE, 13-17 July <https://www.physalia-courses.org/courses-workshops>

/course17

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

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UGoettingen Germany AI Engineer ImageAnalysis PlantDiseases

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

Engineer for AI-based image analysis and optical sensing of plant diseases 80Starting 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.

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 condi-

tions, 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, doctoral 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/OBF/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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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
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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 L^AT_EX 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 L^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.