
E v o l D i r

September 1, 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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BogotaColombia HennigXLIII WilliHennigSociety Nov9-13 Workshop and Award Deadlines Aug31

XLIII ANNUAL MEETING OF THE WILLI HENNIG SOCIETY 9-13 November 2026 Universidad Nacional de Colombia, Bogota, Colombia Chair: Dr. Dimitri Forero

The Willi Hennig Society invites the evolutionary biology community to its XLIII Annual Meeting. The meeting covers phylogenetic theory, methods, and empirical systematics across all groups of organisms. Three workshops run alongside it, and the Society funds student and early-career participation through travel awards. Two deadlines fall on 31 August 2026.

WORKSHOPS (pre-registration closes 31 August 2026)

Each workshop costs USD 100 and admits up to 30 participants.

Workshop 1: Phylogenetic Analysis and Use of TNT (6-8 November 2026). Instructors: Pablo Goloboff (Unidad Ejecutora Lillo, FML-CONICET, Argentina) and Michael Pittman (The Chinese University of Hong Kong).

Workshop 2: Phylogenomics: From Genome-Scale Data to Evolutionary Inference (14-16 November 2026). Instructors: Cinthy Lorena Jimenez Silva (University of Auckland, New Zealand), Jordan Douglas (Australian National University, Australia), and Ambrosio Torres (Museum fur Naturkunde, Berlin, Germany).

Workshop 3: Phylogenetic Biogeography with PhyGeo (14-16 November 2026, online). Instructor: J. Salvador Arias (Instituto de Biologia Subtropical, CONICET-

UNaM, Argentina).

Workshops 2 and 3 share the same dates, so each participant may take only one of them.

Pre-register here: https://www.google.com/url?q=https://forms.gle/3kkXKUHcuDpvJVdG8&source=gmail&ust*86655557613000&sa=E Applicants then receive payment instructions by email, and payment confirms the place.

TRAVEL AND CHILD CARE AWARDS (applications close 31 August 2026)

The Society supports students and postdoctoral researchers who present at the meeting, and awards are also available for early-career researchers. The awards provide USD 800 for participants traveling within South America and USD 1,500 for those traveling from outside South America. Child Care Meeting Awards are also available.

A complete application includes a CV, a travel budget that justifies the proposed expenses, and the title and an outline of the work to be presented (500 words maximum). Student and postdoctoral applicants must arrange for their principal advisor to certify their current status. An application for the Child Care Meeting Award also needs a summary of the need for childcare support and the associated expenses. Priority goes to students who present their work and also participate in one of the workshops.

Apply here: https://www.google.com/url?q=https://forms.gle/4udgy3Nj1Z9rQqvZA&source=gmail&ust*86655557613000&sa=E Award details: https://www.google.com/url?q=https://cladistics.org/awards/&source=gmail&ust*86655557613000&sa=E

REGISTRATION AND ABSTRACTS

Registration and abstract submission open soon. Watch https://www.google.com/url?q=https://cladistics.org/meetings/&source=gmail&ust*86655557613000&sa=E for those announcements.

CONTACT

Local organizers (Universidad Nacional de Colombia):
hennigXLIIII_bog@unal.edu.co

Willi Hennig Society: hennig.society@gmail.com

Website: <https://www.google.com/url?q=https://cladistics.org/&source=gmail&ust`86655557613000&sa=E> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

ber 6th. Checkout is on the 7th. All events take place at Granlibakken Lodge in Tahoe City, California. Bookings are made through Granlibakken, click the link for details - <https://www.theaga.org/agatwentytwenty> [six](https://www.theaga.org/agatwentytwenty) Your reservation through Granlibakken includes all room, board, conference fees, and registration fees to the event. Please contact theaga@theaga.org with questions.

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California Conference AGA2026

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

Registration for the 2026 American Genetic Association Symposium: "Polygenic Adaptation in a Changing World" hosted by AGA President Michael Nachman is open until October 4th, however no refunds can be issued after September 1st. "We now have good examples of the genetic basis of adaptation for many simple traits. However, most evolutionary change involves complex traits, and our understanding of their evolution remains rudimentary. This symposium will promote a broad, synthetic discussion of adaptive evolution for complex traits, bringing together theoreticians and empiricists working on diverse organisms" View available abstracts here: https://drive.google.com/file/d/12S-Pg6-xTkSsTCiJ_tG1Q9tNSExzKVOZ/view?usp=sharing Keynote Speaker Rasmus Nielsen, U California, Berkeley Invited Speakers Rachael Bay, UC Davis Graham Coop, UC Davis Jeff Good, University of Montana Thomas Juenger, University of Texas Joanna Kelley, UC Santa Cruz John Kelly, University of Kansas Sarah Kocher, UC Berkeley Julia Kreiner, University of Chicago Katie Lotterhos, Northeastern University Bret Payseur, University of Wisconsin Dmitri Petrov, Stanford University Paul Schmidt, University of Pennsylvania Molly Schumer, Stanford University Guy Sella, Columbia University Jenny Tung, Max Planck Institute Leipzig Trisha Wittkopp, University of Michigan Samuel Yeaman, University of Calgary Jianzhi Zhang, University of Michigan AGA Symposia are small, friendly meetings that provide excellent opportunities for relaxed interaction with speakers and attendees. All attendees must be AGA members - join us now! <https://www.theaga.org/members> The event runs from mid-day October 4th to the evening of Octo-

Online ESEB PolyAdaptSTN August27

You are cordially invited to attend the upcoming ONLINE seminar of the Special Topic Network Polygenic Adaptation (STN-PolyAdapt) funded by the European Society for Evolutionary Biology which will take place on 27th August, 2026, 3 pm CET.

Our speaker for this seminar is Dr. Lisandro Milocco from Stockholm University, DDLs Fellow.

Title: A Dynamical Approach to the Genotype-Phenotype Map for Evolutionary Prediction

Meeting details: Date: August 27, 2026 Time: 3 PM CET Zoom link to join the seminar: <https://eu02web.zoom-x.de/j/67456493876?pwd=407EG2m0JiAjt8lHmPMv3FKDzy5ntT.1> Meeting ID: 674 5649 3876 Passcode: 820136

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

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

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

SEPEEG2026 Auburn U Oct23-25

Registration deadline reminder: SEPEEG 2026 closes September 1st. SEPEEG (Southeastern Population Ecology and Evolutionary Genetics) is a long-running annual meeting bringing together students, postdocs, and faculty from across the Southeast to discuss research on ecology, population biology, evolution, and genetics in a casual, single-session format. The 53rd meeting will be hosted by Auburn University this fall. Venue: Alabama 4-H Center, Columbiana, AL Dates: October 23-25, 2026 Registration deadline: September 1, 2026 Registration: https://secure.touchnet.net/C20021_ustores/web/store_main.jsp?STOREID=459 Conference website: <https://webhome.auburn.edu/~lss0021/sepeeg26/> We are excited to announce a full program with 64 research presentations including two keynote speakers, four sessions of oral presentations, and 31 poster presentations. The full schedule is available at <http://aub.ie/program>. Dorm lodging is \$225 and includes two nights accommodations (bed linens and towels provided), all meals on Saturday, Sunday breakfast, and a Sunday box lunch. The Alabama 4-H Center is a beautiful lakeside facility with free time built into the afternoon program to enjoy the grounds. Please forward this message to potentially interested colleagues, students, and lab groups. See y'all in Alabama!

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TheLinneanSociety London PlasmoGen26 6November2026

Dear all, We are delighted to invite you to Plasmo-Gen26, a free student-led one-day symposium bringing together population geneticists and malaria researchers to explore the current and future landscape of malaria research. Date: 6 November 2026, 09:00-17:00 Venue: The Linnean Society of London, Burlington House, Piccadilly, London W1J 0BF Funded by the Genetics Society, the day will include talks from students and invited speakers, group discussions/games, and refreshments throughout the day, including a small breakfast, lunch, and coffee breaks. In the evening, a dinner will be organised at a nearby restaurant (at attendees' own cost). Topics will include: - How Ancestral Recombination Graphs (ARGs) are changing inference and relatedness estimation

- Demographic inference from Plasmodium genomes
- Detecting signals of selection
- And more!

Register to attend and/or submit an abstract to present a talk: <https://bit.ly/4harilz> Key dates - Abstract submission deadline: 25 September 2026, 23:59

- Selected talks announced: 9 October 2026
- Registration deadline: 23 October 2026, 23:59

If you have caring responsibilities and would like to attend, the Genetics Society may be able to support you through their Carer's Award (up to GBP60 per day): <https://genetics.org.uk/grants/carers-award/> We hope to see you there! Best wishes, Janeesh Bansal (Imperial College London) . j.bansal@ic.ac.uk Fernanda Miron (Queen Mary University of London) . m.f.mirontoruno@qmul.ac.uk

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AuburnU PhDAssistantship Genomics ForestEcology

PhD assistantship in genomics and disease ecology

I am looking to fill a fully funded PhD assistantship in the College of Forestry, Wildlife, and Environment at Auburn University, beginning January 2027. Research in the Willoughby lab broadly examines how genetic and genomic variation shapes the persistence, evolution, and health of wild populations. Our work combines whole-genome sequencing, bioinformatics, experiments, and quantitative modeling to address questions in conservation genetics, evolutionary biology, and disease ecology. Additional information about our research and lab group is available on the Willoughby Lab website (<https://willoughbylab.auburn.edu>).

The student will contribute to a newly funded project investigating brown-spot needle blight, an emerging threat to loblolly pine forests and timber production in the southeastern United States. This project continues a large interdisciplinary effort to characterize the fungi associated with the disease and understand its effects on pine growth and forest ecology. The student's research will examine how genomic characteristics of pine-associated fungi, their responses to environmental stress, and fungal community composition contribute to variation in disease severity. The research will likely combine whole-genome sequencing, controlled experiments, RNA sequencing, and predictive modeling. The student will gain experience in fungal culturing, comparative genomics, bioinformatics, gene-expression

analysis, and the integration of genomic, environmental, and ecological data. The precise emphasis of the dissertation can be shaped around the student's interests within the broader goals of the funded project.

The project is part of a large, interdisciplinary collaboration involving forest pathologists, geneticists, spatial scientists, extension specialists, graduate and undergraduate students, and scientists from Auburn University and the U.S. Forest Service. The ability and willingness to communicate across disciplines will therefore be important. The student should be interested in learning both laboratory and computational approaches and in connecting fundamental biological questions with an applied forest-health problem. Previous experience with molecular laboratory methods, fungal biology, genomics, bioinformatics, statistics, or programming is desirable, but applicants are not expected to arrive with experience in all—or even most—of these areas. Please do not self-select yourself out of applying. There are many ways to acquire the skills needed for a successful graduate experience, and the position is designed to provide training across laboratory, computational, and quantitative components of the research. More important qualifications include intellectual curiosity, persistence, a willingness to learn unfamiliar methods, clear communication, and the ability to work both independently and as part of a collaborative team.

Auburn University is a very high research activity institution located in a mid-sized community in east-central Alabama. Auburn and neighboring Opelika offer a relatively low cost of living, restaurants, farmers markets, community events, and the Gogue Performing Arts Center. The nearby Kreher Preserve and Nature Center, Chewacla State Park, Tuskegee National Forest, and other public lands provide year-round opportunities for

outdoor recreation. Graduate students in the College of Forestry, Wildlife, and Environment receive a competitive stipend, tuition remission, and opportunities for professional development.

I will interview prospective students before they submit a formal application to Auburn's graduate program. Interested candidates should email Dr. Janna Willoughby at jwilloughby@auburn.edu with: 1) a brief description of their background and research interests; 2) an explanation of why this project interests them; and a PDF of their CV.

Informal inquiries are welcome. Applications will be evaluated on a rolling basis and interviews are likely to occur no later than October 1, 2026.

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AustraliaAdelaideU AntarcticSeabirds AncientDNA

PhD or MPhil Position: Ancient DNA of Antarctic Seabirds The Australian Centre for Ancient DNA at Adelaide University, South Australia in collaboration with the Australian Antarctic Division, Tasmania is seeking a PhD or MPhil student to investigate long-term ecosystem change in Antarctica using ancient environmental DNA preserved in seabird excreta deposits. This project aims to reconstruct Antarctic coastal ecosystem dynamics over thousands of years using ancient environmental DNA and ecological modelling. It will investigate long-term changes in biodiversity, seabird populations, food webs, and disease dynamics, and use these insights to forecast ecosystem responses to future climate change. The successful candidate will join a collaborative team of geneticists and ecologists with strong links to the Australian Antarctic Division. The position is fully funded and is open to both Australian and international candidates. Applicants should have a BSc (Honours) or Master's degree (GPA ≥5) in a relevant field such as ecology, genetics, bioinformatics, marine science, environmental science, zoology, or conservation biology. Experience in molecular laboratory work is desirable, as are bioinformatic skills, strong communication and the ability to work effectively in a team. Applicants must have a genuine interest in Antarctic conservation. The supervisory team includes Dr Theresa Cole, Prof. Damien Fordham, Assoc. Prof. Bastien Llamas (Adelaide University), and

Dr Louise Emmerson (Australian Antarctic Division). Please contact theresa.cole@adelaide.edu.au regarding the project and role. To apply, please visit "<https://adelaide.edu.au/research/research-degrees/research-projects/>" and search for SRTSR0178 Applications close 30 September 2026.

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AustraliaAdelaideU CaveInvertebrate environmentalDNA

PhD or MPhil Position: Cave invertebrate environmental DNA The Invertebrates Systematics Group at Adelaide University is seeking a PhD or MPhil student to investigate cave biodiversity in the Nullarbor using environmental DNA and population genomics. The research will develop new approaches for detecting cave-dwelling invertebrates and reveal patterns of connectivity and dispersal among populations, helping to improve our understanding and conservation of subterranean ecosystems. The successful candidate will join a collaborative team of geneticists, taxonomists, and ecologists with strong links to industry, government, and conservation partners. The position is fully funded and is open to both Australian and international candidates. Applicants should have a BSc (Honours) or Master's degree (GPA ≥5) in a relevant field such as ecology, genetics, bioinformatics, environmental science, zoology, conservation biology, or a related discipline. Experience in molecular laboratory techniques is desirable, as are strong communication skills and the ability to work effectively as part of a team. The supervisory team includes Dr Jess Marsh, Prof. Steven Cooper, and Dr Theresa Cole (Adelaide University). Please contact jess.marsh@adelaide.edu.au regarding the project and role. please visit "<https://adelaide.edu.au/research/research-degrees/research-projects/>" and search for SRTSR0551 Applications close 30 September 2026.

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BC-CAS Czechia ButterflyGenomicsHighElevations

PhD Position: Genomics of butterflies at high elevations (Please, feel free to distribute to all potential candidates) Closing date: September 11, 2026

We are seeking a motivated PhD student to join our international team at the Biology Centre of the Czech Academy of Sciences. You will be part of an exciting research project aimed at understanding the evolution and adaptation of butterflies flying at high elevations. The goal of the PhD work is to infer signatures of selection in Pierini white butterflies in the tropical Andes, and to study population structure and differentiation along elevational gradients.

You will have the opportunity to generate new genome assemblies and whole-genome resequencing for butterflies that are only found at 1,500-4,000 m in the Andes. The focus of the research is on *Phulia* and *Leptophobia*, two rapidly diversifying genera with high-elevation specialists of independent origins.

You will benefit from international networking, hands-on training and research mobility, working within a collaborative and multidisciplinary team.

Priority will be given to candidates who have co-authored at least one scientific publication (submitted or accepted). Experience with population genetics, bioinformatics and/or comparative genomics is advantageous for this position.

Required qualifications: - Master's degree in biology or related fields (awarded before start). - Good communication skills in English. - Independence and documented research productivity.

Funding and Environment: The position is fully funded through a combination of research grant salary and student stipend. The PhD program (4 years) is based at the Faculty of Science, University of South Bohemia (<https://www.prf.jcu.cz/en>).

The research facility at the Biology Centre CAS (<https://www.entu.cas.cz/en/>) is in Ceske Budejovice, a charming historical city in the south of the country, within easy reach of Prague and Vienna. Our working environment (Department of Ecology, Institute of Entomology) is highly diverse and international.

How to apply: Send your application in English to

pavel.matos@entu.cas.cz, consisting of one single PDF containing the following: - Cover letter, outlining your motivation, how your background and skills fit the project, and your potential plans within the research focus of this position (max. 2 pages). - CV, including contact details of at least two referees familiar with your work.

The deadline for applications is September 11, 2026. The top ranked candidates will be selected for an interview in English. The start date is expected in autumn 2026 (Czechia).

For further information, please do not hesitate to contact me.

Dr. Pavel Matos-Maravi Biology Centre, Czech Academy of Sciences Branisovska 31, 37005, Ceske Budejovice, Czechia Email: pavel.matos@entu.cas.cz Web: <https://pavelmatos.wordpress.com/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

ClemsonU SeasonalPlasticityGenetics

The Van der Burg lab is currently seeking 1-2 applicants for the 2027 application cycle! We work on the evolution, genetics and physiology of seasonal plasticity in butterflies and moths. Current projects include: (1) Investigating how seasonal signaling differences are regulated at the molecular level in butterflies, and (2) how winter diapause is regulated at the molecular level in moths. Specific projects will be tailored to individual students.

We are particularly interested in students with a background in Ecology and Evolution, with a strong interest in integrative research, including genetics, physiology and bioinformatics. Experience working with insects is preferred, but not required.

For more information on the specific research projects and recent publications, please visit <https://www.vanderburglab.com/research>. Currently, funding is available through TA-ships, with several GRA funding applications pending.

Clemson University is an R1 research institute located in beautiful upstate South Carolina. Students will join through the Department of Biological Sciences on Clemson's main campus.

If you are interested or have any questions, please reach out to me directly via email at karinv@clemson.edu.

PhD applications are due on December 1st, 2026. GRE test scores are not required and there is no application fee.

–

Karin R. L. van der Burg, PhD she/her/hers Assistant Professor Biological Sciences Clemson University

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Germany HeidelbergU Dep of Biodiversity and Plant Systematics

We offer a PhD position within an ambitious plant research environment:

Exploring the concept of disparity as an evolutionary principle of plant robustness

The Cluster of Excellence GreenRobust (<https://greenrobust.de/>) invites applications for a PhD position in the Department of Biodiversity and Plant Systematics at the Center for Organismal Studies (COS), Heidelberg University.

The emergence of form and function as a result of the genetic make-up of a plant has to rely on newly generated genetic diversity on which evolution can act on, and which may result in new and even diversified functions and species diversification. On a macroevolutionary scale chromosome and in particular genome duplications are among the most prominent processes leading to the divergent evolution of orthologue and paralogue genes, and which provides respective genetic diversity that ultimately define variation from the molecular to the morphological level. Genetic/Genomic and respective functional diversity will be used to explore the concepts of diversity and disparity beyond morphological form and function and explore the principles of this idea on genomic/genetic level across the Brassicaceae family (Walden et al., 2020; Nature Communications: 10.1038/s41467-020-17605-7). The successful candidate will join the research group of Marcus Koch and will closely collaborate with Nora Walden. The project combines evolutionary genomics with conceptual research on phenotypic variation along the phylogenetic space and across different levels of complexity of trait and characters (morphology, traits, and genetic diversity).

The overarching goal of our joint project, REVALUATION, is to re-evaluate ambiguous ligand-receptor interactions in an evolutionary framework and apply concepts of diversity and disparity. Plants rely on pattern recognition receptors (PRRs) to detect invading pathogens, with leucine-rich repeat receptor-like proteins (LRR-RLPs) representing one of the most diverse receptor families. The Medina-Puche/Gust groups at the ZMBP in Tübingen explore how genome evolution drives the diversification of these plant immune receptors and their capacity to recognize diverse pathogen-derived molecules, using the Arabidopsis receptor RLP30 and the Nicotiana receptor RE02 as model systems (Yang et al., 2023, Nature Communications; Yang et al., 2025, Nature Biotechnology). Our partners in Tübingen focus on molecular and functional biology to discover novel Brassicaceae immune receptors and unravel the molecular principles governing ligand recognition and downstream signalling in RLP30/RE02-like receptors.

Main Task, qualification and skills:

We are seeking an enthusiastic and highly motivated graduate with an excellent Master's degree in Biology, Biochemistry, or a related discipline. The ideal candidate - Has a strong interest and thorough understanding of plant evolutionary biology and genomics - Is proficient in English, has excellent writing skills - Has hands-on experience in plant evolutionary biology and bioinformatics and statistical data analysis skills (ideally using R)

The successful applicant will benefit from:

- A stimulating, collaborative, and supportive international research environment.
- Integration into the interdisciplinary GreenRobust research network (Heidelberg, Tübingen, Stuttgart).
- Access to state-of-the-art research infrastructure and facilities.
- Opportunities for scientific and professional development through mentoring and career training.

The position is available from November 2026 and is funded for three years (65Heidelberg and our partner project location Tübingen is a vibrant university town offering an exceptional quality of life in a beautiful historic setting. Heidelberg University is committed to equal opportunities and diversity. We particularly encourage applications from qualified women. Applicants with severe disabilities will be given preferential consideration in cases of equal qualification, in accordance with German law.

Please submit your application as a single PDF file containing: - a non-AI letter of motivation, all relevant certificates - a summary of your previous research experience

rience - a curriculum vitae - the contact details of two academic referees

Applications should be sent as one single PDF latest by 9th October 2026 via email to Prof. Dr. Marcus Koch (marcus.koch@cos.uni-heidelberg.de) and Dr. Nora Walden (nora.walden@cos.uni-heidelberg.de). Screening of applications will begin on 10th October 2026 and continue until the position is filled. Please be prepared for an online meeting via ZOOM.

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up

at <https://evoldir.net/brian/evoldir/evoldir.html>

Kiel Germany Antimicrobial resistance evolution

Kiel, Germany - PhD position on Antimicrobial resistance evolution

Application deadline: 23. August 2026.

The PhD position is for 3,5 years with a possible extension for another 6 months. It is based in the Schulenburg group (<https://evoecogen-kiel.de/>) at Kiel University in Northern Germany. The PhD project aims at understanding how evolutionary principles can be harnessed to constrain bacterial adaptation to antimicrobial drugs. The specific focus is on the influence of mutation rates for resistance against different antimicrobials and associated evolutionary trade-offs, such as collateral sensitivity, on resistance evolution. As model pathogen, we will focus on UTI *E. coli* and/or lung-infecting *Pseudomonas aeruginosa*. As a general reference, check out the group's publications on AMR evolution, as listed on our webpage (<https://evoecogen-kiel.de/publications>). The position will be integrated within the graduate school on Translational Evolutionary Research (<https://transevo.de/>), providing numerous opportunities for exchange with colleagues working on related topics.

Your profile: Master of Science or equivalent; Master thesis or equivalent in the field of Evolutionary Biology or Microbiology; Competences and experiences in experimental as well as molecular laboratory work with

microorganisms; Knowledge in the field of statistics or bioinformatics; English language skills at level C1

Beneficial: Competences and experience in experimental research on antimicrobial resistance; Competences and experience in performance of evolution experiments; Competences and experience in genome analysis and in genetic manipulation of mikroorganisms; Publication(s) from earlier research work

For enquiries regarding the position and research topic please contact Prof. Dr. Hinrich Schulenburg: hschulenburg@zoologie.uni-kiel.de

Please apply via the following link: <https://www.uni-kiel.de/personal/de/stellen/extern/wiss/doktorand-in-am-zoologischen-institut-ag-schulenburg> Applications should be submitted as a single PDF. Applications should include: (1) A letter of motivation (max. 2 pages, Arial 11, line spacing 1.15). In your motivation letter, please explain how your background fits the required profile and how your research interests align with the group research focus. (2) Curriculum vitae. (3) Master certificate (or current grades transcript in case of ongoing studies)

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PhD HeidelbergU Evolutionary Genomics

Center for Molecular Biology (ZMBH), Heidelberg University, Germany A PhD position (3 years, with possible extension) is available immediately in the evolutionary genomics group of Henrik Kaessmann at Heidelberg University. Applications will be reviewed on a rolling basis until the position is filled. We are seeking a highly qualified, motivated, and enthusiastic candidate with a keen interest in evolutionary questions and a passion and aptitude for experimental molecular/genomics work, computational/bioinformatics analyses, or both. Projects in our lab usually combine experimental and computational components, with the relative emphasis tailored to the specific project and the candidate's interests and expertise. Our lab investigates a broad range of questions related to the origins and molecular evolution of organs in mammals and other vertebrates and the underlying genomic changes, with a particular focus on the evolution of gene expression and its regulatory basis (see home.kaessmannlab.org and zmbh.uni-

heidelberg.de/kaessmann for more information). As part of this research, we have generated extensive comparative genomics datasets (e.g., single-cell RNA-seq and ATAC-seq) across species, based on samples from our unique organ collections, and analyzed them using state-of-the-art bioinformatics approaches, increasingly incorporating AI and deep learning (see, e.g., Sarpoulos et al., Science 2026). This work has provided insights into the origins and functional evolution of protein-coding genes, alternative splicing, long noncoding RNAs, microRNAs, and sex chromosomes across organs and species, as well as their phenotypic implications. We currently offer a range of possible projects addressing the evolution of gene expression and its regulatory basis across expression layers, organs, and species in mammals and other vertebrates. These projects will combine the generation of unique new datasets using cutting-edge experimental approaches (e.g., long-read spatial transcriptomics) across diverse organs, from the brain to the gonads, with state-of-the-art computational and deep-learning approaches. Projects may also include detailed molecular and functional characterization of particularly exciting candidate evolutionary changes using organoid and mouse models, CRISPR-based approaches, and synthetic genomics, supported by the expertise and infrastructure of our local Center for Synthetic Genomics (www.syn-gen.de). Specific projects will be developed together with the successful candidates based on their individual interests, expertise, and skills. In our lab, we place great importance on a collaborative, supportive, and positive team spirit. Many of our projects are driven by small, closely interacting teams of experimental and computational researchers who combine complementary expertise and work together enthusiastically. We also greatly value the diverse cultural and international backgrounds of our lab members, which contribute to an open and enriching research environment. The working language of our institute is English, and its members form a highly international community. The ZMBH is located in Heidelberg, a picturesque and vibrant international city on the Neckar River and at the edge of the Odenwald forest. Heidelberg offers an exceptionally stimulating and collaborative research environment, with the European Molecular Biology Laboratory (EMBL), German Cancer Research Center (DKFZ), Heidelberg Institute for Theoretical Studies (HITS), and Max Planck Institute for Medical Research located in close proximity to the University. For more information about our group and the institute more generally, please visit our website at the ZMBH (<http://www.zmbh.uni-heidelberg.de/Kaessmann/>). Please submit a CV, a statement of research interests, and the names and contact details of three references to Henrik Kaessmann

(h.kaessmann@zmbh.uni-heidelberg.de).

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TexasTechU Insect Microbe Genomics

The Manthey research group in the Department of Biological Sciences at Texas Tech University is recruiting 1-2 PhD students to work on funded genomics projects beginning Fall 2027. Funding for accepted students is generally an \$30k annual salary through combined grant and departmental funding.

We currently have openings for funded projects related to genomics of carpenter ants and their microbial symbionts. Graduate students would be encouraged to develop their own projects under these broad themes. For more information about these lines of research and our lab more generally, please visit: mantheylab.org.

Interested individuals should email a CV/resume to Dr. Joseph Manthey (jdmanthey@gmail.com or joseph.manthey@ttu.edu), as well as an informal statement of how your interests overlap with the research projects in the lab.

The Department of Biological Sciences has a strong and dynamic group of scientists with a focus in ecology and evolutionary biology. The department has strengths in multiple areas of genomics, bioinformatics, and specialized disciplines of ecology and evolutionary biology. The departmental website can be found here: <http://www.depts.ttu.edu/biology/> Deadline for applications Our department has a deadline of January 1 for applicants applying to start the following fall. Please find all application details here: <http://www.depts.ttu.edu/biology/academics/graduate/prospective-students/> All qualified applicants are encouraged to contact me with their statement of interest. While academic scores have a role in admissions, motivation and enthusiasm for genomics and research experience are highly valued.

Joseph D. Manthey, Ph.D. Associate Professor, Biological Sciences Texas Tech University Email: jdmanthey@gmail.com — joseph.manthey@ttu.edu <https://mantheylab.org/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UArkansas 2PhD Eco-Evo-Devo

Description

The Levis Lab (<https://levisna.wixsite.com/nicholasalevis>) at the University of Arkansas is recruiting two PhD students to join our group beginning Spring or Fall 2027. Our lab studies how developmental mechanisms, environmental variation, and evolutionary processes interact to produce phenotypic diversity. The students will develop independent dissertation projects within one of two research areas:

1. Eco-evo-devo of spadefoot toad physiology

This project will investigate how physiological systems enable, constrain, and evolve alongside environmentally induced developmental variation. Spadefoot tadpoles provide a powerful system for studying how diet, competition, and ecological conditions influence alternative trophic phenotypes.

2. Sexual selection and polyphenism in shark-tooth nematodes

This project will examine how sexual selection interacts with environmentally responsive development in *Pristionchus* nematodes. These animals produce alternative feeding morphs with distinct ecological functions, creating an unusually tractable system for connecting developmental mechanisms with mating competition, reproductive fitness, and genetic manipulation.

Desired qualifications

Students with interests in evolutionary biology, developmental biology, physiology, animal behavior, genetics, or ecology are encouraged to apply. Previous experience with these organisms is not required. We are particularly interested in applicants who are intellectually curious, comfortable working across biological scales, and interested in developing theoretically motivated experimental research. Experience with data analysis in R is a plus.

Funding mechanism

Students in the Levis Lab are generally supported as teaching assistants in the Biological Sciences Department. Eligible students are encouraged to apply for the Distinguished Doctoral Fellowship (DDF) and Doctoral Academy Fellowship (DAF) (<https://graduate-students.uark.edu/cost-and-funding/>) through UArk. The DDF adds an \$22,000 per year for four years, and

the DAF adds \$12,000 per year for four years to a student's base salary. Note that GRE scores are required to apply for DDF and DAF. The deadlines for nomination are September 30, 2026 (DDF) and October 7, 2026 (DAF) for a January 2027 start and December 11, 2026 (DDF) and February 4, 2027 (DAF) for August 2027 start.

To inquire, please visit the lab website and prepare a copy of your -CV, -a brief description of research interests and motivation for applying, -unofficial transcript(s) and other relevant test scores

Please email materials to nlevis@uark.edu with the subject line: "Prospective PhD student: Spadefoot Physiology" or "Prospective PhD student: Sexual Selection" Applications will be reviewed on a rolling basis beginning immediately

Additional information about the graduate program and application process is available here:

Department of Biological Sciences: <https://biology.uark.edu/> University of Arkansas Biology Graduate Program Guidelines: <https://biology.uark.edu/academics/graduate/> University of Arkansas Ecology, Evolution, and Organismal Biology: <https://eeob.uark.edu/> Please share with students who may be interested! Contact Nicholas Levis nlevis@uark.edu

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UCork FishConsGenomics

PHD POSITION: CONSERVATION GENOMICS OF WRASSE FISH

The Fish Evolutionary Ecology group at University College Cork, in collaboration with the Marine Institute, is offering a PhD position to work on the ecological genomics and conservation biology of wrasse in Ireland.

Wrasse play a vital ecological role in coastal ecosystems and are exploited as cleaner fish in salmon aquaculture. Yet, knowledge gaps persist regarding their population structure, adaptive capacity, and genetic health—gaps that this project aims to fill using cutting-edge genomic tools. This four-year PhD project will deliver the first comprehensive genomic assessment of wrasse in Irish waters, addressing urgent conservation and management needs. The proposed focus is on Ballan wrasse (*Labrus bergylta*), a species that is declining in Ireland

and for which both wild-caught and farm-reared individuals are increasingly used in aquaculture. There is scope to also look at other wrasse species such Corkwing or Goldsinny.

The aim is to use a sequencing approach (e.g. lcWGS) to interrogate genome-wide patterns of neutral and adaptive genetic diversity within and across populations along the Irish coastline and ecological/anthropogenic drivers.

The PhD student will join a vibrant and dynamic team of geneticists and ecologists working on fish and other taxa, with strong links to government agencies, industry, and NGOs. The student will spend time at both University College Cork (the School of Biological Earth and Environmental Science) and the Marine Institute (near Galway City). Both institutes are located close to medium to large size cities, on the doorstep of some of the most beautiful coastline in Europe.

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

The position is funded for 4 years and the preferred start date is 1 Oct 2026 (but a Jan 2027 start also possible). The primary supervisor will be Dr Tom Reed (UCC), and the secondary supervisor Dr Ilaria Coscia (Marine Institute). Please write to Dr Tom Reed (treed@ucc.ie) if you have further questions about the project or position.

University College Cork is committed to equity and diversity and actively promotes equal opportunities. To apply for this position, please send a letter of motivation and CV, together with contact details of two references and your certificates as a single pdf (<10 MB) to treed@ucc.ie with the subject "Application: Your Name [PhD Wrasse Genomics]".

The deadline for applications is Sep 6, 2026, or until the position is filled. Interviews to be held shortly thereafter, online.

Associate Prof. Dr Tom Reed University College Cork Evolutionary Ecology of Fish and other taxa DEPARTMENT: <https://www.ucc.ie/en/bees> /SUPERVISORS: <https://research.ucc.ie/en/p>

[ersons/thomas-reed/ie.linkedin.com/in/ilaria-coscia-5136382a](https://www.linkedin.com/in/ilaria-coscia-5136382a) Thomas Reed treed@ucc.ie; Ilaria Coscia ilaria.coscia@marine.ie

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UHHohenheim PhD single-cell evo-devo of orchid flowers

PhD Position: Single-cell evo-devo of orchid flowers (Please feel free to distribute to all potential candidates)

*** Key info *** Applications until: 2 October 2026 or until the position is filled Preferred starting date: 1 January 2027 Location: University of Hohenheim, Stuttgart, Germany Detailed job posting: <https://rb.gy/k1t44g> *** Description *** We are seeking a highly motivated PhD student (f/m/d) with a keen interest in evolutionary developmental biology of flowers and a solid knowledge of genomics and bioinformatics. The successful candidate will be part of a project to identify key genes underlying the developmental genetic basis of pollinator-relevant floral traits, such as shape, colour and scent, at single-cell resolution. The project will compare flowers of 3 closely related species of sexually deceptive Ophrys orchids at different developmental stages, using state-of-the-art single-nucleus RNA-Seq approaches to pinpoint regulatory networks and their species differences. Candidate gene validation will use RNA in situ hybridisation techniques. For information on the study system, see e.g. Sedeek & al. (2014, Mol. Ecol.) or Russo & al. (2024, Nat. Comm.).

*** Main tasks *** - Initial field work (Puglia, Italy) for plant sample collection - Library preparation and analysis of single-nucleus RNA-Seq data - Data integration and computational analysis to infer gene regulatory networks - Validation of candidate gene expression by fluorescent RNA in situ hybridisation - Publication of the findings in high-quality peer-reviewed journals - Presentation of results in scientific meetings and seminars - Interaction with MSc students working on morphogenetic modelling, proteomics and flower 3D shape data

*** Your profile *** Qualifications and skills: - Completed master's degree (or equivalent; min. 240 ECTS as (under)graduate) in biology or a related discipline, allowing the enrolment as a doctoral student - Thorough understanding of genomics, plant developmental and evolutionary biology - Good bioinformatics and statistical data analysis skills (ideally using R) - Molecu-

lar lab experience to facilitate RNA in situ techniques, isolation of nuclei and library preparation - Good communication skills and proficiency in oral and written English. German or Italian skills are a plus

The ideal candidate should be highly motivated and able to articulate her/his motivation for this project clearly in the cover letter. S/he should be intellectually rigorous, well organised, scientifically independent and resilient, with a thorough understanding of evolutionary biology, development, genomics and molecular biology, and would ideally have a strong interest in floral development and orchid pollination.

*** Salary and Benefits *** Salary and conditions of this 3-year position are according to public service positions in Germany (TV-L E13; 65

*** Working environment *** The University of Hohenheim is an innovative and international research university in the south of Stuttgart. The pleasant campus is close to the airport and hosts a well-equipped research infrastructure, a baroque palace and rambling parks. The successful candidate will work in a young, active and interdisciplinary environment and be part of the Cluster of Excellence GreenRobust, working at the Universities of Hohenheim (Dept. of Plant Evolutionary Biology) and Tübingen (Timmermans lab).

*** How to apply *** Your application should consist of a non-AI letter of motivation (1-2 pages), CV and (if applicable) publication list, certificates, and the names and e-mail addresses of three academic referees. The letter of motivation should detail why you are personally interested in the project, why you find it relevant and why you think you are well-suited to undertake it. Please submit your application as a single PDF to Prof. Philipp Schlüter via admin190b at uni-hohenheim.de. Any requests for further information should also be directed to this address. Screening of applications will begin on 2 October 2026 and continue until the position is filled.

The University of Hohenheim seeks to increase the proportion of women in research and teaching and strongly encourages qualified female scientists to apply. With equal qualifications, preference will be given to candidates with disabilities.

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UK Glasgow UStrathclyde Statistical complexity in the evolution of biological networks

PhD Studentship: Statistical Complexity in the Evolution of Biological Networks Advancing network science to understand the organisation, function and evolution of biological systems We are seeking an ambitious PhD student to develop a new generation of approaches for understanding the structure and evolution of biological networks. Biological systems are extraordinarily complex. Protein-protein interaction networks, gene regulatory networks, metabolic networks and other molecular interaction systems contain enormous numbers of components and interactions, and their organisation is both far from random and far from regular. Their networks exhibit hierarchy (a few nodes with many connections and many nodes with few), homophily (nodes which are more "similar" are more likely to connect), modularity and other forms of structure that emerge from the underlying biological processes governing how components interact. But only recently have methods been proposed to measure network complexity directly and parsimoniously. So, how statistically complex are biological networks? What mechanisms generate this complexity? And, critically, how is this network complexity related to biological function and evolutionary history? This PhD will address these questions by bringing together computational and evolutionary biology with network science and statistical physics. The project is aligned with SPNDL a Scottish Enterprise High Growth Spin-Out project developing an app for cross-species protein-protein interaction network visualisation. It is expected there will be significant interaction with this project, allowing the student access to a cutting-edge technology for studying and analysing PPI networks while providing new analytics that can add to the platforms utility. Research themes The project will be organised around three closely connected themes.

1. The statistical complexity of protein-protein interaction networks and other biological systems The first goal will be to establish how statistical complexity manifests itself in biological networks across species and taxonomical categories, with an initial focus on protein-protein interaction (PPI) networks. You will extend and apply normalised measures of statistical complexity to large-scale PPI networks (e.g. via STRING and related databases) across species, tissues, and condi-

tions. 2. The roles of "popularity" and "similarity" in explaining statistical complexity Popularity (degree heterogeneity/node fitness) and similarity (latent geometric/functional proximity) have each been proposed as drivers of real-world network structure, and their combination has been shown to generate complexity levels matching real networks better than either alone. This theme will test and refine popularity-similarity generative models specifically for biological data, asking which combinations of hierarchy and geometry – and which link-formation mechanisms (e.g. common-neighbour/triadic-closure-like growth) – best explain the complex structure of biological networks, and what this implies about the hidden "similarity spaces" (functional, co-expression-based, structural) organising protein interactions. This could ultimately lead to models that explain why biological networks have the structures that they do, rather than simply describing those structures after the fact. 3. Evolutionary evidence linking statistical complexity and functional heterogeneity Moving from structure to consequence: does higher statistical complexity confer greater resilience, evolvability, or functional diversification? Building on evidence that gene-expression-based (rather than random or purely degree-based) attachment mechanisms enhance the resilience of PPI networks as new proteins are added, this theme will investigate whether statistically complex network architectures are evolutionarily favoured- comparing network growth models against real evolutionary data across species, and asking whether complexity itself is a signature (or driver) of functional heterogeneity and adaptive capacity. Possible questions here include: - Does network complexity increase, decrease or reorganise during evolution? - Are more statistically complex networks associated with greater functional diversity? - Are highly heterogeneous networks more evolvable, more robust, or both? - Do conserved and rapidly evolving proteins occupy systematically different positions in the complexity landscape?

A particularly exciting possibility is to investigate whether statistical complexity provides a quantitative bridge between network structure and biological function: rather than viewing complexity as merely a mathematical property of a network, can we show that it reflects the functional heterogeneity and evolutionary history of the biological system?

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at <https://evoldir.net/brian/evoldir/evoldir.html>

UNebraska-Lincoln Comparative Evolutionary Genomics

The Zhang Lab at the University of Nebraska-Lincoln (School of Biological Sciences & Nebraska Center for Virology) invites applications for a fully funded PhD student position in comparative evolutionary genomics. Our lab investigates the genomic architecture, evolutionary dynamics, and environmental/ecological drivers of major phenotypic and immunological shifts across animal lineages. We are seeking a highly motivated PhD candidate to join two interdisciplinary research projects: 1. Cellular Predation, Motility, and the Cambrian Explosion Investigating how ancient cellular predator-prey dynamics, failed phagocytosis, and stress-induced genomic instability generated the structural and regulatory substrates underlying early metazoan architectural diversification and body-plan evolution. 2. Evolution of Sexual Reproduction and Genome Architecture Exploring the evolutionary pressures, chromosomal dynamics, and genomic transitions involved in the origination and maintenance of sexual reproduction.

Key Qualifications: Bachelor's or Master's degree in Biology, Genomics, Evolutionary Biology, Bioinformatics, Computational Biology, or a related discipline. Strong interest in evolutionary genomics, phylogenomics, comparative genomics, or the origin of complex metazoan traits. What We Offer: Full Financial Support: Graduate stipend, tuition waiver, and health insurance. Cutting-Edge Research Environment: Access to state-of-the-art computational resources, high-performance computing clusters, and the vibrant research community of the School of Biological Sciences and the Nebraska Center for Virology. How to Apply: Interested candidates should send an email to Dr. Luwen Zhang at lzhang2@unl.edu or lzhang2@nebraska.edu with the subject line "PhD Application - Evolutionary Genomics" including: - A cover letter detailing your research interests, background, and alignment with the lab's work. - A current Curriculum Vitae (CV). - Contact information for 2-3 academic references.

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U Pittsburgh PhD UrbanEcoEvo Hummingbirds

The Alaasam Lab at the University of Pittsburgh is hiring two Ph.D. students for the 2027 Fall semester. We are an integrative biology lab interested in the behavioral, physiological, and genetic mechanisms that hummingbirds are using to cope with urbanization. We are open to students with broad interests within the realm of 'urban ecology and evolution', including physiology, energetics, movement ecology, behavior, genetics/genomics, functional morphology, community-sourced data, GIS, bioacoustics, etc. Students may work on diverse projects involving any combination of field, laboratory, and computational work. Our group also prioritizes community engagement and strives to apply what we learn to promote conservation and environmental justice. More info about our research & lab philosophies can be found here (<http://www.valentina-alaasam.com>).

Ph.D. students will enroll in the Ecology and Evolution graduate program (<https://www.biology.pitt.edu/graduate/e-e-program>) within the larger Biology Department. Positions are fully funded for 5 years (with one term of required teaching for), during which students will receive a competitive stipend (\$38,000), tuition waiver, and health benefits. No GRE or TOEFL exams required.

Prospective students should contact Dr. Valentina Alaasam (valentina.alaasam@gmail.com) with a brief summary of interests, CV, and the contact info for 2-3 references. Interviews will begin in early October and remain rolling until the positions are filled. Official applications to the University of Pittsburgh are December 1, 2026.

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USA OklahomaU PhD Opportunities in Host-Microbiome Interactions

PhD Opportunities in Host-Microbiome Interactions

Caesar Lab School of Biological Sciences The University of Oklahoma Norman, Oklahoma, USA

The Caesar Lab investigates how host-associated microbiomes assemble, function, and evolve. Using eusocial bees as a model system, we develop an eco-evolutionary framework to understand the processes shaping host-microbe interactions. We are particularly interested in how host trait evolution, microbial interactions, and host association shape microbiome dynamics and the evolution of microbial symbionts. To investigate these processes, we combine fieldwork, multi-omics, bioinformatics, and microbial assays conducted both in vitro and in vivo.

We are particularly interested in recruiting students excited about:

1. Computational and quantitative approaches:

- Microbiome data analysis
- Bioinformatics and comparative genomics
- Statistics and ecological modeling
- Phylogenomics
- Programming (R, Bash, Python)

2. Experimental approaches:

- Microbiology and microbial ecology
- Molecular biology
- Culturing and characterization of microbial isolates
- Experimental design and host-microbe-microbe interaction assays

Prior experience is not required; curiosity, quantitative thinking, and enthusiasm for learning are highly valued!

Lab highlights: - Access to OU's OSCER high-performance computing resources - International fieldwork opportunities - Microbial culture collection from social bees

Interested applicants are encouraged to contact Dr. Lilian Caesar (caesarl@ou.edu) before applying to discuss research interests and potential projects. Please in-

clude a brief description of your research interests, your CV, and contact information for references. Application deadline: December 1, 2026 For more information: <https://www.ou.edu/cas/biological-scienceshttps://liliancaesar.com> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

USA UMissouriStLouis PhD in AntherBiology EvoDevo

Are you fascinated by the diversity of plants and their reproductive structures? Is your goal a career in academia, biotechnology, agriculture, or government agencies in the most botanically focused city in the world? The Marchant Lab at the University of Missouri - St. Louis and is recruiting PhD students to start Fall 2027. We are particularly interested in students with a background in plant biology, cellular biology, developmental biology, evolution, bioinformatics, or conservation; however, highly self-motivated students with a passion for botany and science are welcome to get in touch. Who we are: The Marchant Lab (<https://www.marchantlab.com/>) is an innovative and collaborative research group at the forefront of both applied and basic plant sciences. We use single-cell RNA-sequencing (scRNA-seq), comparative genetics/genomics, and digitized herbarium specimens to investigate questions in plant reproductive biology, development, ecology, and evolution using both model and non-model plant systems. We are particularly interested in the biology and evolution of anthers. In the lab you will pursue a primary project plus there are ample opportunities for collaborative projects within the lab and with diverse cooperators. The lab atmosphere is supportive, inquisitive, and committed to providing each student with the most effective training cognizant with individual goals. Where we are: We are based in the Biology Department at the University of Missouri - St. Louis (UMSL). With its world-class universities (UMSL, Washington University, St. Louis University), research institutions (Donald Danforth Plant Science Center, Missouri Botanical Garden), and agricultural companies (Bayer, Pivot Bio, Yield Lab), St. Louis has the highest concentration of plant science PhDs in the world and is an ideal setting for anyone interested in plant biology. St. Louis is one of the most livable cities in the US and was recently ranked the top city to start a career in. If you are interested in joining the

lab, email Dr. Marchant (dm9vh@ums1.edu) your CV and a brief statement on your background and research interests. Applications for the UMSL Biology PhD program are due by December 15th and applications for the Masters program are considered on a rolling basis. Teaching and/or research assistantships are guaranteed for PhD students for five years. The Marchant Lab welcomes international graduate students; however, please get in touch well before the December deadline as your applications must also go through the International Students Office.

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USA UofColorado Museum Invertebrate MS

The University of Colorado Boulder's Museum and Field Studies Graduate (MFS) Program (<https://www.colorado.edu/cumuseum/graduate-program/about-program>) is recruiting a Master's student for the Invertebrate Zoology section. The goal of the MFS program is to produce high quality museum professionals. Our students go on to become collections managers, curators, researchers, museum educators etc., with considerable hands-on training and the theory of museology to build successful careers in museums and other institutions throughout the world. The program combines rigorous training in museology and scientific research in invertebrate zoology, evolution, and symbiosis.

The position will be fully funded through a Graduate Assistant position in the Invertebrate Zoology section. Working 20 hours per week at the collections, the selected student will earn a stipend, tuition remission, and formal education and training in specimen care, data management, and collection organization as well as research experience. Collections projects could include pitfall trap invertebrate identification, cataloging incoming collections, ethanol remediation, mollusk inventory, and other various tasks.

Applicants must have basic knowledge or interest in non-insect invertebrate taxa and willingness to complete either a research thesis or project as required by the program. For inquiry, please submit your CV and a brief cover letter to the Curator of Invertebrate Zoology, Dr. Jingchun Li at Jingchun.Li@colorado.edu

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USA UOklahoma Host-MicrobiomeInteractionsPhD

PhD Opportunities in Host-Microbiome Interactions

Caesar Lab School of Biological Sciences The University of Oklahoma Norman, Oklahoma, USA

The Caesar Lab investigates how host-associated microbiomes assemble, function, and evolve. Using eusocial bees as a model system, we develop an eco-evolutionary framework to understand the processes shaping host-microbe interactions. We are particularly interested in how host trait evolution, microbial interactions, and host association shape microbiome dynamics and the evolution of microbial symbionts. To investigate these processes, we combine fieldwork, multi-omics, bioinformatics, and microbial assays conducted both in vitro and in vivo.

We are particularly interested in recruiting students excited about:

1. Computational and quantitative approaches:

- Microbiome data analysis
- Bioinformatics and comparative genomics
- Statistics and ecological modeling
- Phylogenomics
- Programming (R, Bash, Python)

2. Experimental approaches:

- Microbiology and microbial ecology
- Molecular biology
- Culturing and characterization of microbial isolates
- Experimental design and host-microbe-microbe interaction assays

Prior experience is not required; curiosity, quantitative thinking, and enthusiasm for learning are highly valued!

Lab highlights: Access to OU's OSCER high-performance computing resources International field-work opportunities Microbial culture collection from social bees

Interested applicants are encouraged to contact Dr. Lilian Caesar (caesarl@ou.edu) before applying to discuss research interests and potential projects. Please include a brief description of your research interests, your

CV, and contact information for references. Application deadline: December 1, 2026 For more information: <https://www.ou.edu/cas/biological-scienceshttps://liliancaesar.com> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UWesternAustralia SeadragonConservationGenomics

Seadragon conservation in Southern Australia (genomics) Doctor of Philosophy

Description Seadragons are iconic temperate Australian fish that face increasing threats based on urbanization and climate change. Progress in population genetics has seen gradual improvements in the resolution of our knowledge of seadragon population structure. This type of information is critical for underpinning any risk analyses for on-the-ground actions ie translocations or captive breeding programs, as well as extinction risk.

The project supported here will be further developed with the recruited student's interest and skills. We envision the project to be centered around the genomics of seadragons using Whole Genome Sequencing data (to be generated through in kind funding recently allocated to the project by the Threatened Species Initiative and Bioplatforms Australia). The project will directly contribute to seadragon conservation efforts and will endeavour to deliver data products. It will also engage with communities and conservation groups and co-design work where possible.

Keywords Whole Genome resequencing Conservation Genetics Great Southern Reef

Opportunity status Open Open date 01 Jun 2026 Close date 11 Sep 2026 Research area Biological Sciences

Eligibility UWA eligibility requirements for PhD candidates Citizenship status Domestic International Enrolment status Future student Specific requirement Desired Skills - strong scientific writing skills - effective communication style - self-motivated - experience with analysis of genomic or other large data (e.g. bash, R, python) - experience in extraction of high molecular weight DNA

How to apply Please email Nerida Wilson a copy of your CV, degree certificates, transcripts and cover letter detailing your relevant expertise and motivation for this

PhD project.

Application assessment will begin on 11 Sep and continue until the position is filled.

Contact Nerida Wilson - nerida.wilson@uwa.edu.au

Scholarship details Scholarship type Stipend scholarship Scholarship value AUD \$38,110 (2026 rate) Availability Application assessment will begin on 11 Sep and continue until the position is filled.

School School of Biological Sciences Course type Doctorates

<https://researchdegrees.uwa.edu.au/scholarships/1x9y7w/seadragon-conservation-in-southern-australia-genomics> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

UWesternAustralia SeadragonEcology

Seadragon conservation in Southern Australia (ecology)
Doctor of Philosophy

Description Seadragons are iconic temperate Australian fish that face increasing threats based on urbanization and climate change. Ongoing knowledge gaps mean that specific management actions cannot be proposed or assessed accurately. The commencement of individual-level monitoring through the initiative SeadragonSearch has contributed to addressing some of these knowledge gaps to date. The combination of widescale citizen science involvement, with cutting edge Artificial Intelligence tools, means that useful ecological data is being amassed in a way previously not thought possible.

The project supported here will be further developed with the recruited student's interest and skills. We envision the project to be centered around the ecology of seadragons using data directly from the SeadragonSearch database, and may incorporate eDNA surveys as well. The project will directly contribute to seadragon conservation efforts and will endeavor to deliver data with specific applications in mind. It will also engage with communities and conservation groups and co-design work where possible.

Keywords Population ecology Conservation eDNA Great Southern Reef

Opportunity status Open Open date 01 Jun 2026 Close date 11 Sep 2026 Research area Biological Sciences

Eligibility UWA eligibility requirements for PhD candidates Citizenship status Domestic International Enrolment status Future student Specific requirement

Desired skills - strong scientific writing skills - effective communication style - self-motivated - familiarity with population ecology principles - GIS and spatial data analysis - experience with eDNA assays

How to apply Please email Nerida Wilson a copy of your CV, degree certificates, transcripts and cover letter detailing your relevant expertise and motivation for this PhD project.

Application assessment will begin 11 Sep and continue until the position is filled.

Contact Nerida Wilson nerida.wilson@uwa.edu.au

Scholarship details Scholarship type Stipend scholarship Scholarship value AUD \$38,110 (2026 rate) Availability Application assessment will begin on 11 Sep and continue until the position is filled.

School School of Biological Sciences Course type Doctorates

<https://researchdegrees.uwa.edu.au/scholarships/1x9y7v/seadragon-conservation-in-southern-australia-ecology> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Vigo Spain Institute of Marine Research OLDMUSSEL

Fully funded PhD position (4-years) OLDMUSSEL: Analysis of the long-term adaptation of bivalves to environmental change using ancient remains

We are looking for a pre-doctoral researcher to work on an interdisciplinary project which will integrate archaeology, genomics, and ecology, to understand how aquatic populations adapt to long-term climate change and intense human fishing pressures, with mussel and oysters as study species and the Galician estuaries as a natural laboratory. The PhD will be based at the Institute of Marine Research (IIM-CSIC) in Vigo (Spain) supervised by researchers from the ACUABIOTEC Lab (Prof Sofia Consuegra) and the Immunology and Genomics group (Prof Antonio Figueras & Dr Magali

Rey) and will run in close collaboration with the OLD-SALMO project (<https://oldsalmo.csic.es>) and their multidisciplinary team. The PhD candidate will be registered at the University of Vigo, with a designated academic tutor.

Key objectives and tasks include: - Establishing a 5,000-10,000 year genetic baseline by conducting museum and field sampling trips to prehistoric shell pits across the North of the Iberian Peninsula. - Developing and optimising novel protocols to extract and validate ancient DNA from historical samples. - Modelling temporal changes in genomic diversity, quantifying genetic erosion, and analysing morphological traits (size and age) to link past evolutionary shifts with historical climate events. - Investigating cutting-edge bivalve long-term genetics, including complex open pangenome architectures and immune system gene expansions. The project includes close collaboration with the University of Cantabria's Department of Prehistory for archaeological support. Fieldwork, molecular tasks, and

phenotypic analyses will be supported by the OLD-SALMO and the Immunology and Genomics project teams. Core training will cover molecular wet-lab techniques, bioinformatics, aquatic population omics, mollusc ecology, molecular evolution, image analysis, and advanced statistics. Requisites: Undergraduate and Masters degree in molecular ecology, population genomics, Evolutionary biology or similar and knowledge of R, Python or similar. Ideally, but not necessarily, experience working with degraded DNA (ancient or environmental) and aquatic environments.

To apply for this position, please send a CV and letter of intention to Prof Sofia Consuegra, sconsuegra@iim.csic.es or Magali Rey mrey@iim.csic.es. Deadline for applications is the 25 of August 2026 and interviews will take place the 31st of August- 1st of September via zoom.

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**Assistant Professor
Evolutionary Biology U Nevada
Las Vegas**

The University of Nevada, Las Vegas invites applications for Assistant Professor in Evolutionary Biology, School of Life Sciences [R0153361]. Starting in Fall 2027

ROLE of the POSITION The School of Life Sciences at the University of Nevada, Las Vegas invites applications for a tenure-track Assistant Professor in Evolutionary Biology. The ideal candidate will establish an integrative research program that investigates the processes and drivers of adaptation using modern experimental, genomic, and/or computational approaches, including adaptation to extreme or rapidly changing environments. We are particularly interested in researchers exploring a mechanistic understanding of how non-genetic processes, such as epigenetic regulation, interface with genetic variation to effect phenotypic variation and adaptation. The candidate will be expected to integrate their research program with the mission of the School of Life Sciences and to collaborate with existing faculty across multiple areas of expertise, including local adaptation and speciation; host-microbiome and plant-pest coevolution; and organismal physiology in extreme environments. Additional collaborative opportunities exist in the Department of Chemistry and Biochemistry. The University's location in the Mojave Desert also offers opportunities to study adaptation in a natural extreme-environment system, though research need not be tied to any particular study system or environment. The successful applicant is expected to establish a rigorous research program supported by extramural funding, generate peer-reviewed scholarship, mentor and advise graduate students, teach effectively at the undergraduate and graduate levels (focus on evolutionary biology, epigenetics, molecular ecology, or mechanisms of adaptation) and engage in service activities. For further information and to apply, click here: https://nshe.wd1.myworkdayjobs.com/UNLV-External/job/UNLV1-Main-Campus-Las-Vegas/Assistant-Professor-in-Evolutionary-Biology--School-of-Life-Sciences--R0153361-_R0153361 (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

**AU CharlesStuartU Gulbali
Institute Senior Research Fellow
Molecular Ecology Molecular
Diagnostics**

JOB: Senior Research Fellow in Molecular Ecology / Molecular Diagnostics

Position: Senior Research Fellow (equivalent to research-only associate professor) **Hiring Organization:** Gulbali Institute, Charles Sturt University **Job Location:** Albury-Wodonga, Australia **Application Due Date:** August 27, 2026

We're hiring for a senior-level five year research-only fellowship position. It's listed as "molecular diagnostics", but is really molecular ecology or -omics very broadly defined. Salary is \$167,348 to \$184,243 AUD plus 17

<https://external-jobs.csu.edu.au/cw/en/job/499082/associate-professor-of-molecular-diagnostics> Full Time, Fixed Term (5 years from appointment) Level D - \$167,348 to \$184,243 pa (plus 17

Join Charles Sturt University's Gulbali Institute and lead the development of a nationally recognised molecular diagnostics research program addressing some of Australia's most significant agricultural, environmental and biosecurity challenges. This is a rare opportunity to establish and grow a cutting-edge capability applying molecular ecology, environmental DNA (eDNA) and emerging molecular technologies to deliver practical outcomes for communities, industry and government.

Working within a collaborative, multidisciplinary research environment, you'll secure competitive research funding, build strategic partnerships and mentor the next generation of researchers. Backed by significant investment in purpose-built molecular laboratories and research infrastructure, you'll help shape the future of applied molecular diagnostics while strengthening the University's reputation as a leader in regional and globally relevant research. Success in this role will be reflected in the lasting research capability, partnerships and environmental impact you create.

About you: You are an ambitious and collaborative research leader who is driven to build a nationally recognised research program with lasting environmental and societal impact.

You have a proven ability to attract competitive research funding and develop sustainable partnerships across government, industry and the research sector.

You thrive on building and mentoring high-performing, inclusive research teams, creating opportunities for the next generation of researchers to succeed.

You are passionate about translating molecular science into practical solutions that inform environmental policy, biosecurity and natural resource management.

You bring a strong track record of scientific excellence and are motivated to grow Charles Sturt University's reputation as a leader in applied molecular diagnostics through innovation, collaboration and research impact.

About us: We are a university of the land and people of our regions. True to the character of regional Australia we have gumption, we have soul and we collaborate with others. We develop holistic, far-sighted people who help their communities grow and flourish.

The Wiradjuri phrase *yindyamarra winhanganha* means the wisdom of respectfully knowing how to live well in a world worth living in. This phrase represents who we are at Charles Sturt University - our ethos. It comes from traditional Indigenous Australian knowledge, but it also speaks to the mission of universities - to develop and spread wisdom to make the world a better place.

Harnessing technology, we thrive as a distributed yet connected community, welcoming and engaging with people across Australia and the world.

Visit our website to learn about our great range of employee benefits.

This position is open to Australian Citizens and Permanent Residents; or applicants who hold a current valid work visa commensurate with this position.

Additional information is available in the position description or by contacting:

Professor Lee Baumgartner — Executive Director, Gullbali Institute — lbaumgartner@csu.edu.au

Closing Date: 11pm AEDT, 27 August 2026

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Aus Monash U Lectureship Ecology-Evolutionary Biology

The School of Biological Sciences at Monash University seeks to appoint a Lecturer or Senior Lecturer in Ecology or Evolutionary Biology.

We welcome applicants who work in the substantive areas of Ecology or Evolutionary Biology, and those who take interdisciplinary approaches combining Ecology or Evolutionary Biology with, for example, physiology or genetics/genomics. We are particularly interested in applicants who work with study systems that compliment those already in the School and applicants who undertake field and/or experimental research. The successful applicant will be expected to contribute to teaching in the broad area of data science, for example BIO2010 Data Science for Biologists and BIO3100 Advanced Methods in Field Ecology, as well as subjects relevant to their discipline area.

<https://careers.pageuppeople.com/513/cw/en/job/679705/lecturer-senior-lecturer-in-ecology-or-evolutionary-biology> Location: Clayton campus, Melbourne Employment Type: Full-time Continuing appointment Remuneration: \$123,138 - \$146,228 pa Level B / \$150,841 - \$173,931 pa Level C (plus 17

Applications Close: Monday 21 September 2026, 11:55pm AEST

To Apply please include in your application a CV and four documents that together address the selection criteria: - Cover letter - Equity, Diversity and Inclusion Statement (no more than 1 page, addresses KSC 2) - Research statement (no more than 2 pages, addresses KSC 3) - Teaching statement (no more than 1 page, addresses KSC 4) Longlisted applicants will be asked to provide a short (approximately 20 minute) teaching video on a topic chosen by the selection committee.

For instructions on how to apply, please refer to <https://www.monash.edu/jobs/how-to-apply/applying-for-the-job>. Enquiries: Professor Craig White, Head of School, School of Biological Sciences, Craig.White@monash.edu

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CaliforniaDeptOfWaterResources MolecularEcologist

The California Department of Water Resources is hiring for a permanent Molecular Ecologist (Environmental Scientist). View the advert here: <https://calcareers.ca.gov/CalHrPublic/Jobs/JobPosting.aspx?JobControlId=529889> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Job AssistantProfessor Plant-BioticInteractions TexasTechUniversity

Assistant Professor of Plant-Biotic Interactions Position Number: 45795BR

Closing Date: September 21, 2026

Applicants must apply at: <https://tinyurl.com/y4e95jm6> to position number 45795BR

Position Description The Department of Biological Sciences in the College of Arts and Sciences at Texas Tech University (TTU) invites applications for a full-time 9-month tenure-track Assistant Professor position to begin September 1, 2027. We seek a candidate with expertise in the study of plant-biotic interactions, broadly defined. The successful candidate will be provided a competitive start-up package to develop their research program and will be expected to attract external funding for research related to plant-biotic interactions. Potential areas of specialization include, but are not limited to:

Plant-soil microbe (e.g., fungal, bacterial, virus) interactions Plant-pollinator interactions Plant-herbivore interactions

The candidate's research may span any area of biology, from cell biology and genetics to ecology and evolutionary biology. Preference will be given to applicants who employ integrative approaches that bridge multiple levels of biological organization and methodologies. A research focus that includes fundamental biological

research will be considered an asset.

The successful candidate will be expected to contribute to undergraduate and graduate education by developing and teaching courses that align with their expertise and departmental needs, and by mentoring undergraduate students, graduate students, and postdocs.

The successful candidate will benefit from collaborative opportunities within Biology, complementing our expertise in the ecology, evolution, physiology, and genetics of plants as well as our expertise in genomics, entomology, and plant-microbial systems. Depending on the candidate's expertise, they could interface with several other departments and centers on campus, including Plant and Soil Science, Natural Resources Management, the E.L. Reed Herbarium, and the Museum at TTU.

All prospective employees are encouraged to visit Work at Texas Tech to learn more about becoming a part of our campus community.

About the University

Founded in 1923, Texas Tech University began with a mission to serve the needs of West Texas, but its impact has always reached far beyond. Today, Texas Tech, located in Lubbock (pop. 300,000+), is home to a vibrant community of more than 42,000 students. Texas Tech's 1,800-acre campus showcases Spanish Renaissance architecture and is home to one of the country's largest public art collections. Its 13 colleges include a prestigious School of Law and a distinguished School of Veterinary Medicine. These programs equip students with the skills and knowledge needed to excel in their respective fields. Built on the values of West Texas – hard work, grit and authenticity – the university graduates students who are deeply engaged in service to their communities and well-positioned to succeed in the world. Texas Tech is committed to achieving research and scholarly accomplishments that compare favorably to the member institutions of the Association of American Universities (AAU). For more than 100 years, Texas Tech has been a premier destination for those seeking a world-class education and a unique, personalized experience as a member of the Red Raider family.

About the College

The College of Arts & Sciences is composed of 15 departments, offering a wide variety of courses and programs in the humanities, social and behavioral sciences, mathematics, physical sciences, and natural sciences. The College has more than 10,000 students enrolled representing more than a quarter of the overall Texas Tech University student population while maintaining a 22:1 student to faculty ratio.

About the Department/School/Area

The Department of Biological Sciences (<https://www.depts.ttu.edu/biology/>) is a community of faculty, students, and staff committed to teaching and training students, producing innovative research that advances basic and applied sciences, and engaging with the public. As one of the largest programs within the College of Arts and Sciences, we offer three undergraduate degrees to more than 1800 students, and three MS degrees and a doctoral degree to approximately 125 graduate student trainees. Our 42 faculty conduct cutting-edge research across all levels of biology, spanning from how we as individuals learn and teach about biology to the cells, systems, and organisms that make up our global biosphere. We serve students through online and face-to-face learning and research opportunities.

Major/Essential Functions

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at <https://evoldir.net/brian/evoldir/evoldir.html>

Job ResearchAssociateI RegulationOfEndosymbiosis U Miami

The Wilson Lab seeks a Research Associate for an NSF-funded project testing the hypothesis that mTORC1 acts as a master regulator of the aphid/Buchnera endosymbiosis. Aphids house Buchnera in specialized bacteriocytes and must coordinate bacterial population growth with their own development and reproduction across generations. We are asking whether a conserved nutrient-sensing pathway is the mechanism that makes that coordination possible – a question at the intersection of cell biology and the evolution of symbiosis that has not been addressed directly in any insect system.

This is a laboratory-based position carried out as part of a collaborative research team. The Research Associate will contribute to experiments across the project, with a central focus on microinjection and microdissection of aphids, and will share responsibility for maintaining the lab's aphid colonies and host plants, which requires reliable attention on a regular schedule, including some weekends.

This position is well suited for someone preparing for graduate school or developing a technical research career.

Required qualifications B.S. in biology, biochemistry, microbiology, or a related life science at time of hire At least one year of undergraduate research experience in a laboratory setting, or equivalent Careful, consistent bench technique and accurate record-keeping The ability to work with limited day-to-day supervision as part of a multidisciplinary team

Desirable, but not expected Standard molecular biology methods (nucleic acid extraction, PCR, gel electrophoresis) Light or fluorescence microscopy Rearing or handling of insects or other invertebrates Basic quantitative skills

Prior work on insects or symbiosis is not expected. What matters is curiosity about how endosymbioses are regulated and a willingness to work in a system where some of the tools are still being built.

The successful candidate will join the Wilson Lab within the Host-Microbe Interactions (HoMI) Laboratory, part of the Symbiosis@UM cluster in the Department of Biology, on the Coral Gables Campus of the University of Miami.

What the position offers The Research Associate will receive hands-on training in confocal microscopy, digital droplet PCR, and the microinjection and microdissection of insects, contribute to publications as a co-author, and work alongside undergraduate researchers in the lab. Candidates intending to pursue graduate training will be supported with mentoring and letters of recommendation. The University of Miami provides institutional access to career development resources for all employees.

Terms The appointment is for one year, renewable for a total of up to two years, contingent on satisfactory performance and continued availability of funds. Anticipated start date September 1, 2026, or as soon as possible thereafter.

To apply Please submit a CV and a cover letter describing your fit for the position and your career goals, including the names and contact information for two referees. A full list of Wilson Lab publications is available on Google Scholar under Alex C C Wilson. <https://careers.miami.edu/us/en/job/R100100314/Research-Associate-1-Biology> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Smith College Northampton MA Assistant Professor of Biological Sciences Genetics-Genomics

Assistant Professor of Biological Sciences - Genetics/Genomics, Smith College

Description Smith College is seeking to fill a tenure-track position as Assistant Professor of Biological Sciences beginning July 1, 2027. The selected candidate will develop innovative courses and an independent research program in the Genetics, Evolution, and Molecular Biology track. We encourage applications from colleagues working with human, model, or novel systems, who are interested in basic or applied questions, and whose methods are not exclusively computational. The successful candidate will meaningfully incorporate undergraduates in research which combines molecular biology with experimental, field and/or computational approaches. A PhD by the time of appointment, and a commitment to inclusive undergraduate education are essential. Candidates with postdoctoral experience, a record of research publications, and evidence of teaching and/or pedagogical training are preferred. Teaching responsibilities will include participation in the teaching of BIO 230 (Genetics, Genomics, and Evolution), as well as intermediate/advanced offerings in the candidate's area of expertise. We seek applicants whose research interests complement and broaden the existing expertise in the Department of Biological Sciences. Candidates from groups underrepresented in the Biological Sciences are encouraged to apply. In addition to a competitive benefits package, pay for newly-hired assistant professors with a terminal degree beginning the first year of the tenure clock in Fall 2027 is typically between \$92,000-96,000. Salary decisions are dependent on several factors, including but not limited to teaching and work experience beyond the terminal degree, as well as market, disciplinary, and internal peer equity factors. Located in Northampton, MA, Smith College is the largest women's college in the country and is dedicated to excellence in teaching and research across the liberal arts. A faculty of outstanding scholars interact with students in small classes, as advisors, and through student-faculty research projects. Smith College offers opportunities to foster faculty success at every career stage, such as those listed here. State-of-the-art resources at Smith include the Centers for Molecular Biology, Microscopy & Imaging, and

Mass Spectrometry, along with the MacLeish Field Station, Botanic Garden, an accredited animal care facility (with mammalian, amphibian, zebrafish systems in place), and access to high performance computational resources through Unity. The new faculty member will have opportunities to collaborate with Smith College's programs in Biochemistry, Neuroscience, Exercise and Sport Studies, Environmental Science and Policy, Engineering, Computer Sciences, and Statistics and Data Sciences. In addition, the Smith belongs to a multi-institutional Consortium which provides a rich intellectual and cultural life for faculty and students, as well as opportunities for collaborative research and mentoring of graduate students through our M.Sc. in Biological Sciences program, and of doctoral students through our affiliation with the University of Massachusetts at Amherst. As set forth in our mission and values, Smith College is committed to promoting a culture of equity and inclusion among students, staff and faculty. The College will not discriminate in employment on the basis of age, race, color, ethnicity, national origin, creed, religion, sex, sexual orientation, gender identity, gender expression, pregnancy, genetic information, age, veteran status, physical or mental disability, or any other classification protected by law. Smith College is an equal opportunity employer and complies with all state and federal laws that prohibit discrimination. Application Instructions Submit application to <https://apply.interfolio.com/190342> Applications consist of a cover letter, curriculum vitae, a teaching statement (2 pg maximum), a research statement (3 pg maximum), an inclusion statement (2 pg maximum) and the full contact information of three confidential references. Candidates who advance may be asked for additional materials. Please direct any questions about the position or the application process to Lisa Mangiamiele (lmangiamiele@smith.edu). Review begins August 28, 2026.

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UC-Berkeley Tenure track faculty in genetics genomics evolution and development

Position overview Position title: Assistant Professor - Genetics, Genomics, Evolution, and Development - Molecular & Cell Biology Salary range: The current salary range for this position is \$84,100 - \$132,900 (9-month academic year salary), however, off-scale salary and other components of pay, which would yield compensation that is higher than this range, are offered to meet competitive conditions. Anticipated start: July 1, 2027 Application Window Open date: July 27, 2026 Next review date: Monday, Oct 19, 2026 at 11:59pm (Pacific Time) Apply by this date to ensure full consideration by the committee. Final date: Monday, Oct 19, 2026 at 11:59pm (Pacific Time) Applications will continue to be accepted until this date. The Department of Molecular and Cell Biology (MCB) at the University of California, Berkeley invites applications for a tenure-track faculty position in the Genetics, Genomics, Evolution, and Development (GGED) Division, at the Assistant Professor level. Position description We broadly seek applicants studying fundamental aspects of genetics, genomics, evolution, and/or developmental biology. We welcome candidates working across model systems and approaches, from molecular, cellular, and quantitative genetics to genomic technologies, comparative and evolutionary biology, and the mechanisms governing developmental patterning and organismal form. We are particularly interested in scientists whose work opens new conceptual or technical directions for the division and who will complement and extend our existing strengths. This position would have the opportunity (if desired) to interact with the Innovative Genomics Institute, the Advanced BioImaging Center, the Developmental and Regenerative Biology group, and the Center for Computational Biology at the University of California, Berkeley.

Faculty at the assistant rank in our department demonstrate excellence, originality, and productivity in research, the strong potential to obtain external funding, a capacity for excellence in teaching and mentoring of undergraduates, graduate students, and post-docs, and a commitment to service consistent with Berkeley's principles of community. Applicants are encouraged to visit Molecular and Cell Biology (<https://mcb.berkeley.edu/>) to learn more about the de-

partment and our mission. Our department is committed to addressing the family needs of faculty, including dual career couples and single parents. We are also interested in candidates who have had non-traditional career paths or who have taken time off for family reasons, or who have achieved excellence in careers outside academia. For information about potential relocation to Berkeley, or career needs of accompanying partners and spouses, please visit: New Senate Faculty — Office for Faculty Equity & Welfare (<http://ofew.berkeley.edu/new-faculty>)

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UC Davis Plant Evolutionary Biology

The Dept. of Evolution and Ecology at UC Davis is hiring an Asst. Prof in Plant Evolution. The search is broad – we're interested in everything from evo-devo and macroevolution to evolutionary ecology, pop/quant gen, and anything in between.

Please share broadly and encourage talented folks to apply!

<https://recruit.ucdavis.edu/JPF07777> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UChicago Ecology Evolution Department Research Support Position

Dear colleagues,

Julia Kreiner and I are looking to fill a research support position in our lab groups in the Ecology & Evolution Department at UChicago. The position is full-time (in-person, salaried, benefits) but the work load is split 50/50 between our two lab groups. We share a large wet lab space and office space across our research groups, creating a dynamic and interactive work environment with colleagues bringing diverse perspectives and interests in plant ecology, evolution, genetics, and genomics.

For this position, we are seeking applicants with experience with wet lab techniques in plant genetics and genomics, including standard and high-molecular weight DNA extraction and library preparation. Full details and instructions to apply can be found on Workday: https://uchicago.wd5.myworkdayjobs.com/External/job/Chicago-IL/Research--Analyst_JR34674. The minimum experience required is a BS or equivalent (ideally with some work experience), but we are open to hiring at the MS or PhD level if the fit is right; salary will be commensurate with experience and training.

More information about the research groups can be found on our lab websites: <https://carleylab.uchicago.edu>/<https://kreinerlab.com/>. The posting will be open for at least a couple of weeks, and we aim to have the position filled for fall. Please feel free to pass this opportunity along to anyone in your networks that you think may be interested! Prospective applicants are welcome to email me with questions before applying if they wish (1carley@uchicago.edu).

Best, Lauren Carley

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UMaine Technician-Research Assistant in Arabidopsis chromosome biology

The Tan lab at the School of Biology and Ecology, UMaine, Orono (ME) is currently searching for a motivated technician/research assistant to join our NSF/DBT-funded plant minichromosome project team. Please apply by September 15th, 2026 for full consideration. Link below to job ad and to apply: ##### https://fa-ewca-saasfaprod1.fa.ocs.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1/job/3029/?utm_medium=jobshare&utm_source=External+Job+Share (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UMass Amherst AssistantProf EvolutionaryBiology

Job Summary The Department of Biology at the University of Massachusetts Amherst invites applications for a full-time, tenure-track position in the area of Evolutionary Biology. We are seeking talented applicants qualified for an assistant professor position. Under exceptional circumstances, highly qualified candidates at other ranks may receive consideration. The successful candidate will be expected to establish a vibrant, externally funded research program, effectively teach and mentor undergraduate and graduate students, and contribute to service in support of the department and college. The successful candidate will also have a demonstrated understanding of the strength that is brought to science through diversity, equity, inclusivity, and accessibility. The Department of Biology is committed to building a vibrant and inclusive academic community that reflects and advances the university's strategic priorities.

We seek to hire an Evolutionary Biologist who studies the mechanisms, patterns, and/or processes that underlie the origins and maintenance of biological diversity. We are particularly interested in applications from candidates who employ quantitative techniques such as genomics, phylogenetics, advanced imaging, modeling, and/or machine learning to answer fundamental questions related to the mechanisms that drive adaptation at any taxonomic scale, from deep time to how species respond to rapid/extreme environmental change. We especially encourage applications from individuals who will complement existing departmental strengths in organismic evolutionary biology. The Biology Department provides a collaborative and broad research environment, with faculty whose research spans all levels of biological organization. This position will join a cohort of recent departmental hires in developmental cell biology, plant biology, neurobiology, and genetics. Faculty members in the biology department train graduate students through one or more interdepartmental graduate programs in Organismic and Evolutionary Biology, Molecular and Cellular Biology, Plant Biology, and Neuroscience and Behavior.

About UMass Amherst The flagship of the Commonwealth, the University of Massachusetts Amherst is a nationally ranked public land-grant research university

that seeks to expand educational access, fuel innovation, inspire creativity, and share and use its knowledge for the common good. Founded in 1863, UMass Amherst sits on nearly 1,450-acres in scenic Western Massachusetts and boasts state-of-the-art facilities for teaching, research, scholarship, and creative activity. The institution advances a diverse, equitable, and inclusive community where everyone feels connected and valued—and thrives. UMass Amherst offers a full range of undergraduate, graduate and professional degrees across 10 schools and colleges, and 100 undergraduate majors. We believe every member of our university community can contribute to our ongoing success by striving for the highest level of excellence as we seek breakthrough solutions to mounting environmental, social, economic, and technological challenges in our world.

Requirements Candidates must have a Ph.D. or equivalent in Biology or a related field with relevant post-doctoral experience. We are seeking talented applicants qualified for an assistant professor position.

Salary Information The University expects to pay within an approximate range between \$79,350 and \$124,349 for this position. Please note: The low end of this range is based on the minimum salary for the rank included in the collective bargaining agreement between the University and the Massachusetts Society of Professors, UMass Amherst/MTA/NEA. The high-end of the pay range reflects an increase above the median salaries at this rank within the department for faculty who may have multiple years of faculty experience. The specific pay for this position will be determined by the University based on consideration of all relevant factors, including faculty rank and required relevant certifications, when and if it decides to extend an offer of employment.

Additional Information This position could begin as soon as September 1, 2027. Questions pertaining to this position can be directed to the search committee chair, Dr. Craig Albertson at EvoBioSearch@umass.edu.

Application Instructions Along with the application, please submit a (1) cover letter; (2) curriculum vita; (3) statement of research interest; (4) teaching philosophy; and (5) contact information for three professional references. Please see the link below to submit your application. <https://careers.umass.edu/jobs/assistant-professor-evolutionary-biology-amherst-massachusetts-united-states>

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UNewMexico ResearchTech EvolutionaryGenomics

The Evolutionary Genomics lab in the Department of Anthropology at the University of New Mexico (<https://anthropology.unm.edu/research/research-labs/lab/evolutionary-genomics-and-reproduction-lab.html>) is searching for a research technician and laboratory coordinator to support research and day-to-day laboratory operations. Our lab uses genomic approaches and cell culture models to study the evolution of reproduction and aging in humans and non-human primates. The successful applicant will contribute to both laboratory operations and ongoing research projects, with responsibilities spanning molecular genomics, cell culture, data analysis, literature-based research, and laboratory organization. This position is well suited for a recent graduate seeking research experience prior to graduate school, although applicants with additional experience are encouraged to apply. This position has funding for 2 years, with the possibility to extend based on funding availability.

KEY RESPONSIBILITIES Laboratory Research Perform routine molecular biology and genomics procedures, including DNA/RNA extraction, nucleic acid quality assessment, PCR, and library preparation for sequencing. Perform and maintain mammalian cell cultures, including routine passaging, media preparation, cryopreservation, and assessment of cell viability and growth. Maintain accurate and organized records of experiments, samples, protocols, and laboratory materials. Maintain laboratory equipment and monitor routine equipment performance and maintenance needs. Research and Data Analysis Contribute to ongoing research projects in evolutionary genomics, reproduction, and aging. Perform literature searches, data mining, and organization of research information. Conduct basic data processing and statistical analyses using R or other analytical software. Contribute to preparation of figures, tables, presentations, manuscripts, and other research materials. Laboratory Operations and Organization Order, receive, and appropriately store laboratory supplies and biological materials. Manage laboratory inventory and organize laboratory supplies, samples, and reagents. Assist with laboratory safety, training, documentation, and compliance requirements.

The Evolutionary Genomics Lab provides a collabora-

tive and supportive research environment designed to foster learning, professional growth, and the development of new research skills. The successful applicant will have opportunities to contribute meaningfully to ongoing research projects and earn authorship on resulting peer-reviewed publications. For more information and to apply, please visit the official posting on UNMjobs: [https://unm.csod.com/ux/ats/careersite/18/home/requisition/37777?c=unm&cfdd\[0\]\[id\]=255&cfdd\[0\]\[options\]\[0\]=1916](https://unm.csod.com/ux/ats/careersite/18/home/requisition/37777?c=unm&cfdd[0][id]=255&cfdd[0][options][0]=1916)

The position could start anytime between October - December 2026. Applications will be considered on a rolling basis, but should be submitted by 30 September for full consideration.

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USA Bloomington IndianaU Department of Biology Research Associate position

Research Associate position in the Department of Biology at Indiana University, Bloomington (USA) The Moyle Lab at Indiana University, Bloomington is seeking a Research Associate/Lab manager to join our group. Our lab in Evolution, Ecology, and Behavior investigates the genetic and evolutionary processes that shape speciation and adaptation. The main goal for this position is to conduct research investigating ecological, functional, and genetic variation associated with fruit color transitions, to understand mechanisms of repeated evolution of this important and diverse trait. The ideal candidate would have 2 or more years of experience in a research setting, or a Master's degree that includes research experience. Information about responsibilities, qualifications, and compensation can be found at the link: <https://indiana.peopleadmin.com/postings/33973>. For questions, please feel free to email Leonie Moyle (lmoyle@iu.edu). Applications will be reviewed as they are received and continue until the position is filled.

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USA ColoradoCollege Assistant Professor of Organismal Biology-Ecology

The Department of Organismal Biology & Ecology at Colorado College invites applications for a tenure-track Assistant Professor of Organismal Biology & Ecology with specialization in animal biology and ecology, to begin in Fall 2027.

<https://jobs.coloradocollege.edu/jobs/assistant-professor-of-organismal-biology-ecology-on-campus-colorado-united-states>
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USA ColoradoCollege organismal biologist focused on animals and ecology

The Department of Organismal Biology & Ecology at Colorado College invites applications for a tenure-track Assistant Professor of Organismal Biology & Ecology with specialization in animal biology and ecology, to begin in Fall 2027.

Preferred Qualifications Undergraduate teaching experience, mentoring undergraduate research experience, and a commitment to diversity, equity, inclusion, and antiracism in biology are also priorities. Application Instructions - Application Deadline - last day to submit an application: 09-16-2026 - References will be contacted to upload a letter of recommendation when a candidate accepts a Zoom/Phone interview - Inquiries about the position may be sent to the OBE Department Chair, Dr. Rachel Jabaily at rjabaily@coloradocollege.edu. All application materials should be posted by September 16 at 11:55 pm MDT. You must meet the minimum qualifications to be considered for this position. Required Documents 1) a cover letter highlighting relevant professional background; 2) a teaching statement that outlines your approach to undergraduate teaching and includes examples from your teaching that demonstrate your commitment to inclusive peda-

gogy; 3) a research statement that includes your approach to engaging undergraduate students in research (3 pages maximum); 4) curriculum vitae; 5) undergraduate and 6) graduate transcripts (unofficial copies and screenshots are suitable for applications; the successful candidate will be required to send official transcripts); and 7) contact information for at least three references who can submit a confidential letter of recommendation; however, only the references of short-listed candidates will be asked to expeditiously submit a letter.

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USA U of the South Assistant Professor Integrative Biology

The Department of Biology at the University of the South (commonly known as Sewanee) seeks applications for an Assistant Professor in Integrative Biology. We seek a dynamic scholar who studies animals at multiple biological scales and whose research will meaningfully involve and engage undergraduates. We are especially interested in candidates who can contribute to courses in anatomy, physiology, organismal biology, ecology, or genetics. A PhD is required and post-doctoral experience preferred. The Sewanee Biology Department is a collaborative community committed to excellence in undergraduate education, mentorship, and research. Faculty teach small classes, involve students directly in scholarship, and benefit from opportunities for interdisciplinary collaboration across the sciences. Located on the Cumberland Plateau, the 13,000 acre campus encompasses some of the most biodiverse forests in the eastern United States while well-equipped lab facilities support a broad range of molecular, organismal, ecological, and environmental research. The Biology Department spans Molecular Biology and Genetics, Integrative Biology, and Ecology and Biodiversity while contributing to interdisciplinary majors in Biochemistry, Neuroscience, and Environment and Sustainability and a thriving pre-health program. Faculty typically teach 5 classes per year with lab sections counting towards that total. Attributes of a Successful Candidate A PhD is required and post-doctoral experience preferred. Supplemental Information For preliminary review, applicants must submit the following documents: (1) 2-page cover letter describing your experiences and approaches to teaching and research (2) curriculum vitae (3) 1-2 page teaching statement describing your ap-

proach to inclusive education at the undergraduate level (4) 2-3 page research statement describing (a) your past and current work, (b) your research plans for the next 5 years as appropriate for an undergraduate-only institution, and (c) how you anticipate integrating undergraduates in your research (5) contact information for 3 references Applications should be submitted here: <https://www.schooljobs.com/careers/sewanee/jobs/5449661/assistant-professor-in-integrative-biology?pagetype=job0pportunitiesJobsReview> will begin on October 1, 2026 and continue until the position is filled. Please contact Dr. Matt Schrader (msschrad@sewanee.edu) with any questions. Matt Schrader (he/him) Associate Professor and Chair Department of Biology University of the South 735 University Avenue Sewanee, TN 37383-1000

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USA Utah Natural History Museum Director of Science

Organization: Natural History Museum of Utah Job Title: Director of Science Job Summary: The Natural History Museum of Utah (NHMU) seeks an accomplished scientist and leader to serve as Director of Science. This is an opportunity to lead the science team at NHMU, the largest natural and cultural history museum in the intermountain west. Founded in 1963 as the state of Utah's natural history museum and part of the University of Utah in Salt Lake City, NHMU has grown into a distinguished scientific and cultural institution with the mission to illuminate the natural world and the place of humans within it.

NHMU's collections and research team includes research curators (most of whom are jointly appointed faculty and represent six academic departments and four colleges across the University of Utah); collections managers and lab managers; registrars; digitization staff; postdoctoral, graduate and undergraduate researchers and interns; and volunteers. NHMU's natural and cultural history collections comprise more than two million objects, with notable strengths in Paleontology, Archaeology, Ethnography, and Biology of the west. NHMU also manages the Range Creek Field Station, which was established to facilitate scientific investigation and preservation of Range Creek Canyon's rich archaeological record.

Reporting to the NHMU's Executive Director, the Director of Science will provide strategic leadership for the Collections & Research (C&R) Department. This senior leadership role provides strategic direction for the museum's research programs, collections stewardship, and field activities, ensuring alignment with institutional mission, public engagement, and scholarship in natural and cultural history. The Director of Science works with stakeholders to support, guide, and advocate for the Museum's collections and research enterprise and provides managerial and mentoring leadership for C&R staff.

The Director of Science will support and collaborate on philanthropic and external agency funding efforts and represent the C&R Department as part of the Museum's senior leadership team, reporting to the Executive Director. The Director will work with internal and external stakeholders to strategically amplify NHMU's scientific reputation and relevance.

Job Responsibilities :

Strategic Leadership & Vision - Provide long-term, strategic leadership for the Department, ensuring excellence in research and collections stewardship. - Collaborate with the C&R Department and Museum leadership to develop and implement scientific priorities that align with NHMU's mission, institutional strategic plan, and the broader University of Utah research enterprise. - Champion interdisciplinary, collaborative, and inclusive scientific practices across the Museum.

Collections & Research Oversight - Support research programs, collections management, and collection growth across the natural and cultural science disciplines represented at NHMU. - Support the development, preservation, documentation, digitization, and accessibility of collections according to best professional practices, ethical standards, and applicable regulations. - Support NAGPRA-related consultation and repatriation. - Support and encourage impactful research, scholarship, and dissemination, including peer-reviewed publications, exhibitions, digital resources, and public programs.

Management & Staff Leadership - Provide effective managerial leadership for the C&R team. - Foster a collegial, respectful, and inclusive departmental culture that values mentorship, professional development, and collaboration. - Oversee departmental planning, goal setting, performance evaluation, and resource allocation.

Funding & External Partnerships - Assist and collaborate in identifying and pursuing external funding opportunities for research and collections projects, includ-

ing grants, donations, and partnerships. - Work closely with the Department, Museum leadership, and philanthropy staff on proposal development, donor engagement, and stewardship of funded projects. - Cultivate relationships with the University of Utah's Office of the Vice President for Research, funding agencies, peer institutions, Tribal partners, community organizations, and professional networks.

Museum & University Leadership - Represent the Department as a member of NHMU's Department Heads leadership team, contributing to institution-wide planning, policy development, and strategic decision-making. - Collaborate with the C&R Department and other Department Heads to integrate research and collections into exhibitions, education, public programs, and community engagement initiatives. - Serve as an advocate for the C&R Department within NHMU, the University of Utah, and the broader museum and scientific community.

Required Qualifications: - Ph.D. in a scientific discipline relevant to NHMU.

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UWisconsinMadison PopulationGenomics

The research group of John Pool at the University of Wisconsin - Madison invites applications for a 1 year lab tech position. The Pool Lab has a strong focus on population genomics and the genetics of adaptive evolution (especially with regard to local adaptation), and it supports an emerging emphasis on the genetics of early stage reproductive isolation. Most of the lab's projects leverage the natural diversity and experimental power of *Drosophila melanogaster*, while other projects are driven by population genetic simulations, methods, or data resources. The major research focus of this position is distinct - it emphasizes looking at variation within common laboratory strains of *Drosophila melanogaster*. We have evidence that different labs' copies of these strains are very different at the genetic level, which threatens the reproducibility of *Drosophila* research. Thus, it's critically important for the research

going on in thousands of *Drosophila* labs that we sort out what variation exists within these nominal strains and identify uncontaminated versions of them that the whole fly research community can work with going forward. The position in question will coordinate the receipt and handling of fly stocks from labs around the world, and will lead studies of phenotype-level variation among these sub-strains (in part by mentoring undergraduate researchers). The hired individual will also help with other research projects in the lab as they're able to, and they will help with various lab support tasks. 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. We're hoping to find someone available to start within the next few months. Please see this page for further details and to apply (open just until 8/20): <https://jobs.wisc.edu/jobs/research-specialist-madison-wisconsin-united-states-e6485805-54ee-4e6a-b65c-b6cdc1c93b97> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UWisconsinMadison TechDrosophilaVariation

The research group of John Pool at the University of Wisconsin - Madison invites applications for a 1 year lab tech position. The Pool Lab has a strong focus on population genomics and the genetics of adaptive evolution (especially with regard to local adaptation), and it supports an emerging emphasis on the genetics of early stage reproductive isolation. Most of the lab's projects leverage the natural diversity and experimental power of *Drosophila melanogaster*, while other projects are driven by population genetic simulations, methods, or data resources. The major research focus of this position is distinct - it emphasizes looking at variation within common laboratory strains of *Drosophila melanogaster*. We have evidence that different labs' copies of these strains are very different at the genetic level, which threatens the reproducibility of *Drosophila* research. Thus, it's critically important for the research

going on in thousands of *Drosophila* labs that we sort out what variation exists within these nominal strains and identify uncontaminated versions of them that the whole fly research community can work with going forward. The position in question will coordinate the receipt and handling of fly stocks from labs around the world, and will lead studies of phenotype-level variation among these sub-strains (in part by mentoring undergraduate researchers). The hired individual will also help with other research projects in the lab as they're able to, and they will help with various lab support tasks. 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. We're hoping to find someone available to start within the next few months. Please see this page for further details and to apply (open just until 8/20): <https://jobs.wisc.edu/jobs/research-specialist-madison-wisconsin-united-states-e6485805-54ee-4e6a-b65c-b6cdc1c93b97> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

WashingtonUnivStLouis All Professor ranks Rules of Life AI

This AI oriented search is open to evolutionary biologists with an AI angle to their research.

Cluster hire in AI for Modeling the Physical World and Living Systems Washington University in St. Louis - Danforth Campus: School of Arts & Sciences Location St. Louis, MO Open Date Aug 14, 2026 Description Washington University in St. Louis invites applications for multiple tenure-track faculty positions at the rank of Assistant, Associate, or Full Professor for a +AI cluster search spanning the departments of Biology, Chemistry, Philosophy, Physics, Psychological & Brain Sciences, and Statistics & Data Science. Faculty recruited through this process will join a vibrant cohort of faculty recruited in an earlier Rules of Life search undertaken to promote transdisciplinary collaboration and dialogue to explore fundamental questions regarding living systems and the physical world. Life operates across a

diversity of scales, from molecular-scale processes shaping cellular function to the delicate dynamic balance of our biosphere as a whole. System-level properties and processes are affected by interactions operating at all scales and between scales. Understanding these interconnected systems requires an interconnected and multidisciplinary research community. From AI-driven advances in protein structure and dynamics, to advanced imaging methods enabled by quantum sensing, to imaging and modeling the human brain and behavior, to developing entirely new mathematical and computational frameworks to achieve insight from complex data, transformative advances in life sciences will require the integrated efforts of scientists and scholars working across disciplinary boundaries. Moreover, these advances will be accelerated through the combination of artificial intelligence and machine learning with other experimental and computational approaches. Finally, advances in science and technology raise foundational questions about the nature of artificial and natural intelligence, and how they relate to conscious experience and human values. We anticipate multiple hires to expand upon a successful Rules of Life cluster search and to create a robust hub of science researchers and philosophers using diverse yet interconnected methods to advance life sciences from molecular to ecological scales while also considering the relationship between AI and humanity. Preference will be given to applicants whose research combines AI-driven inquiry with experimental, computational, or data-science methods, and who demonstrate synergy with current areas of strength at Washington University. Joint applications exhibiting a high degree of potential for research collaboration will also be considered. For more information about this search, the application portal, specific AI-related themes and contacts for search-related questions, visit <https://insideartsci.washu.edu/rules-of-life>

lifeDuties will include conducting research, teaching, advising students, and participating in departmental governance and university service. WashU aims to create an environment that encourages and supports wide-ranging exploration at the frontier of discovery by embracing diverse perspectives from individuals of all identities and backgrounds. We promote higher education and rigorous research as a fundamental component of an open, vibrant society. We strive to enhance the lives and livelihoods not only of our students, patients, and employees but also of the people of the greater St. Louis community and beyond. We do so by addressing scientific, social, economic, medical, and other challenges in the local, national, and international realms. Each year Washington University publishes a Safety and Security brochure that details what to do and whom to contact in an emergency. This report also publishes the federally required annual security and fire safety reports, containing campus crime and fire statistics as well as key university policies and procedures. You may access the Safety and Security brochure at <https://police.wustl.edu/clery-reports-logs/>. Qualifications Candidates should have a Ph.D. in Biology, Chemistry, Data Science, Philosophy, Physics, Psychology, Statistics, or a closely related field. Candidates for the rank of Associate or Full Professor should have an outstanding academic record of research, publication, teaching, and service commensurate with tenure at this rank. Application Instructions For fullest consideration, applications should be submitted by October 1, though review will continue until available positions are filled.

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American Genetics Association Researcher Community Engagement Award

Research Community Engagement Award (RCE)

Submission Deadline 31 Aug 2026 Awards Announced
30 Sept 2026

The American Genetic Association grants RCE Awards
to AGA members for engaging with local communities.

Overview

Building meaningful relationships between scientists and the communities connected to their research is essential for trust, ethical research practice, and long-term collaboration. Research shows that distrust in science often stems from perceived institutional authority and inaccessible expertise (Yearly, 2000). In biodiversity genomics and related fields, strong partnerships with local and Indigenous communities are now recognized as critical—but are rarely provided dedicated funding sources through traditional research grants.

The Award for Researcher Community Engagement is a pilot program from the AGA to support the relational work that enables responsible science and development of trust in the broader scientific enterprise. Funding covers activities that strengthen trust, foster communication, and encourage more co-created understanding between researchers and the communities where they work, do research, plan to do research, or come from. We are particularly interested in proposals that will engage rural, under-resourced urban communities, Indigenous communities, or communities that do not have a long history of engagement with scientists.

Purpose

To provide financial support for community engagement activities that fall outside typical research funding, including extended stays, cultural participation, gift-giving (cash gifts not allowed), and other relationship-building expenses.

Eligible Applicants

AGA members at any career stage working in biological, ecological, or genomic sciences who demonstrate a commitment to ethical, culturally respectful engage-

ment with a specific community.

Award Details

Funding Amount: Applicants may request up to \$2,000 to be encumbered within 12 months of the award.

Apply here: <https://www.theaga.org/rce-awards-form> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Awards American Genetics Association

Awards Available: Deadline 31 Aug The Humane Genomics Education Award and the Research Community Engagement Award from the American Genetics Association Call for Educators, Creators, and Community Leaders: The Humane Genomics Education Award Are you passionate about making genomics accessible, ethical, and understandable for everyone? The American Genetic Association (AGA) is seeking innovative thinkers, educators, and community leaders for the Humane Genomics Education (HGE) Award. This award recognizes and supports individuals and teams who are breaking down barriers in science education and fostering conversations about the ethical, humane, and societal impacts of genomic technology. Potential grant-supported activities could include, but are not limited to, curriculum and course development, continuing education for instructors, development of educational resources, travel to workshops, and support for guest speakers. The Humane Genomics Education Award is a pilot program from the AGA to support educational activities and initiatives that improve genetics education and promote 'Humane Genomics'. 'Humane genomics education' is an approach to teaching modern genetics and genome science that improves understanding of genetics, decreases students acceptance of non-scientific notions of genetic essentialism, and reduces racial bias by dismantling persistent misconceptions about race and genetics. For more information and to apply, please go to: <https://www.theaga.org/hge-awards-form> Submission Deadline: 31 August 2026. Awards Announced: 30 September 2026

The American Genetic Association grants RCE Awards to AGA members for engaging with local communi-

ties Building meaningful relationships between scientists and the communities connected to their research is essential for trust, ethical research practice, and long-term collaboration. Research shows that distrust in science often stems from perceived institutional authority and inaccessible expertise (Yearly, 2000). In biodiversity genomics and related fields, strong partnerships with local and Indigenous communities are now recognized as critical—but are rarely provided dedicated funding sources through traditional research grants. The Award for Researcher Community Engagement is a pilot program from the AGA to support the relational work that enables responsible science and development of trust in the broader scientific enterprise. Funding covers activities that strengthen trust, foster communication, and encourage more co-created understanding between researchers and the communities where they work, do research, plan to do research, or come from. We are particularly interested in proposals that will engage rural, under-resourced urban communities, Indigenous communities, or communities that do not have a long history of engagement with scientists. For more information and to apply, please go to: <https://www.theaga.org/rce-awards-form> Submission Deadline: 31 August 2026. Awards Announced: 30 September 2026

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BES Cross-Journal Special Issue-70 years of ecological genetics-Call for Papers

70 years of ecological genetics: Past, present, and future <https://besjournals.onlinelibrary.wiley.com/hub/call-for-papers/70yrs-of-ecological-genetics> Journals: Journal of Applied Ecology (<https://besjournals.onlinelibrary.wiley.com/journal/13652664>), Journal of Animal Ecology (<https://besjournals.onlinelibrary.wiley.com/journal/13652656>), Methods in Ecology and Evolution (<https://besjournals.onlinelibrary.wiley.com/journal/2041210X>)

Guest editors: - Dr Tin Hang (Henry) Hung (University of Oxford, UK) - Professor Paul Ashton (Edge Hill University, UK) - Dr Rebecca Whitla (University College Dublin, Ireland) Since the Ecological Genetics Group first gathered in 1956, the field has undergone a pro-

found transformation. What began as phenotypic observation in natural populations has evolved into an era of high-throughput sequencing and environmental omics that was once barely imaginable. Yet, across seven decades of rapid methodological evolution, the core objective of ecological genetics has remained unchanged and increasingly urgent: understanding the mechanisms by which organisms persist, adapt, or fail in the face of an anthropogenic global change. This cross-journal Special Feature marks the 70th anniversary of the discipline by synthesizing its foundational history with the cutting-edge developments now bridging fundamental inquiry to global application. We highlight research across the full continuum of ecological genetics, emphasizing how genetic and genomic insights inform broader ecological processes, conservation management, and environmental policy. We particularly welcome empirical, theoretical, and perspective submissions addressing the following themes, but are open to any broader topics of ecological genetics: - Synthesis and reflections of ecological genetics: Reviews and perspectives tracing the evolution of core theories from traditional fieldwork to modern omics, identifying the prioritized questions that will define the field's next chapter. - Lessons from long-term ecological genetic studies: Submissions utilizing rare, multi-decadal datasets to provide the essential temporal context needed to understand local adaptation, genetic diversity, and population persistence over time. - Genomics in policy and management: Applied research demonstrating how high-resolution genetic data informs conservation strategies and biodiversity policy, including critical frameworks for data sovereignty and equitable genomic governance. - Next-generation monitoring: Organized in collaboration with the UK DNA Working Group, this theme features emerging genetic and computational tools, emphasizing bidirectional knowledge exchange to ensure novel monitoring techniques are practically applicable for large-scale assessments. - Genetics of adaptation and resilience under global change: Empirical and theoretical work investigating the genetic mechanisms underlying species' survival or decline when exposed to rapid environmental stressors. All proposals will be assessed by the Special Feature Editors to be invited to submit to the Special Feature. For papers that are invited to submit, they will undergo identical rigorous peer review as all papers submitted to the journals and invitation to submit does not guarantee eventual acceptance. For accepted papers, they will be published in their respective journal when they are ready and also added to this page. You can read more about the British Ecological Society's special feature process here. If you have any queries, please contact admin@journalofappliedecology.org.

To submit a proposal to this Special Feature, please fill out this form. The call for proposals will close on the 5th November 2026 at 3pm GMT

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BMC Biology RepetitiveDNA Call for Papers

BMC Biology is currently welcoming original research submissions for an upcoming article Collection: "Repetitive DNA across the tree of life: structure, function, and evolution".

This Collection highlights the roles of transposable elements, satellite repeats, duplications, and other repetitive sequences in genome architecture, regulation, and evolutionary innovation.

Topics include, but are not limited to:

- Origins, diversity, turnover, and horizontal transfer of repetitive DNA - Repeat-driven genome-size change, chromosome evolution, speciation, and adaptation - Centromeres, telomeres, heterochromatin, sex chromosomes, and accessory chromosomes - Regulatory innovation, exaptation, domestication, non-coding RNAs, and 3D genome organization - Host-repeat conflict, repeat activity and silencing, and small-RNA- or chromatin-mediated control - Repeat variation in populations and pangenomes, structural variation, and somatic mosaicism - Roles in development, environmental responses, aging, genome instability, health, and disease - Methods for assembling, annotating, quantifying, visualizing, validating, and functionally testing repetitive sequences

Submission Deadline: May 21, 2027 (flexible upon request)

Submission Process: Select the Collection name from the dropdown menu during submission and note your interest in your cover letter.

Policies: Standard BMC Biology editorial criteria, peer review, and APCs apply (with standard waiver policies).

For submission guidelines and full details, please visit the BMC Biology Collection Page: <https://link.springer.com/collections/ecfgbhibgd> Feel free to reach out directly if you have any questions.

Kind regards

Jullien Flynn, Fabrizio Ghiselli, Oleg Simakov. Jullien Flynn, Fabrizio Ghiselli, Oleg Simakov.

ESEB Call Policy and Evolutionary Biology Funds 30Sep2026

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

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Evolutionary Applications Special Issue Host-Microbe Dependency and Adaptive Change

Evolutionary Applications – Special Issue Call for Authors and Guest Editors: Emerging Trends in Host-Microbe Dependency and Adaptive Change for Conservation and Management (expected to launch in October 2026)

We would like to invite contributions for an upcoming Special Issue in Evolutionary Applications focused on "Emerging Trends in Host-Microbe Dependency and Adaptive Change for Conservation and Management."

ABOUT THE SPECIAL ISSUE: This Special Issue will explore how evolutionary interactions between hosts and their associated microbiomes influence adaptation, resilience, and applied conservation outcomes in wild and captive populations. We welcome empirical, theoretical, and methodological advances, as well as syntheses, reviews, and perspectives.

Submissions should apply an evolutionary framework, possess clear relevance to conservation or management, and appeal to the broad readership of Evolutionary Applications.

Potential topics include (but are not limited to): - Microbiome-mediated adaptation and eco-evolutionary dynamics - Hologenomic and co-evolutionary approaches in wildlife conservation - Microbial responses and host resilience under environmental change - Host health, immunity, and host-microbe co-adaptation - Conservation interventions and microbiome management in captive or production populations

CALL FOR GUEST EDITORS: We are actively seeking researchers interested in joining our guest editorial team. This is an excellent opportunity to gain editorial experience, contribute to an emerging area at the intersection of evolutionary biology and conservation, and help assemble an influential collection. We strongly encourage applications from both established and early-career/emerging researchers.

HOW TO CONTRIBUTE / CONTACT: The Special Issue is expected to launch in October 2026. If you are interested in contributing as an author or joining the guest editorial team, please contact us directly.

Contact: Sishuo Wang, sishuowang@hotmail.ca;

Jingdi Li, judy.li@ubc.ca Best, Sishuo & Jingdi

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Free Online Bee Identification Key for North America

We are pleased to report that The Bee Genera of North and Central America (Hymenoptera: Apoidea): Second Edition is now freely available online. This is a fully revised version of the 1994 publication with updated taxonomy, keys, notes on the genera, illustrations, and habitus photos of all 173 genera of bees in North and Central America. There are some nice features in the electronic version, including hyperlinks connecting keys to notes to illustrations, which will facilitate usage.

The PDF is available on the Smithsonian Institution's Scholarly Press website and can be viewed and downloaded here: <https://doi.org/10.5479/si.9781944466909.hc> DOI: 10.5479/si.9781944466909.hc

Please share this with colleagues and anyone interested in identifying bees of North and Central America!

Bryan Danforth, Sean G. Brady, Karolyn Darrow, Silas Bossert, Eduardo A.B. Almeida, Jason Gibbs, John L. Neff, Terry Griswold, Laurence Packer

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SMBE 2027 IDEA Proposals by Oct 05 2026

Society for Molecular Biology and Evolution

2027 IDEA Call for Proposals

Deadline October 05, 2026

SMBE, through the IDEA (Inclusion, Diversity, Equity and Access) task force, aims to address systemic racism, sexism, colonialism and other exclusion in our SMBE society. With this in mind, a budget of up to \$25,000 per year, as well as a fund for Local Leadership in Science (up to \$10k) and Outreach (up to \$10k) will be dedicated to initiatives that help reduce inequities

in molecular biology and evolution research. The task force would therefore like to invite members of SMBE to propose initiatives that would take place in the year 2027.

The proposal should help address IDEA, local leadership in science, or outreach related to research in the field of molecular biology and evolution. In addition, the projects that directly benefit more SMBE members are more encouraged. The projects that could potentially be sustainable beyond the funded year are also more encouraged. We welcome proposals that request the full or only a portion of the budget (budget justification needed). We will promote diversity of awardees in the funding decision. Examples of proposed activities include, but are not limited to, workshops, symposia, training opportunities, stand-alone featured talks, or inequity data collection in particular groups, countries, or regions (to name a few). If you are interested in knowing what projects have been previously funded, please visit SMBE IDEA tab of the SMBE website (<https://www.smbe.org/idea-initiatives-funded-projects/>).

How to apply:

<https://docs.google.com/forms/d/e/1FAIpQLSftmzJc-EkyuSNfKdWxxRck4p-EORyfhQ3Vj4pVUPmvk0FJxg/viewform> Applicants should use this link to the form to submit your initial description of proposals. You will find more detailed information in the form.

Application Timeline (All deadlines are 5pm local time):

5th of October (Mon) - Submit your initial description.
30th of October (Fri) - Be notified on whether your project is selected for full submission.
23rd of November (Mon) - Submit your full project plan if selected.
11th of December (Fri) - Be notified of the final funding decision.

If you have any questions, please reach out to us at smbe.idea@gmail.com.

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UCambridge Department Zoology
Cichlid Eco-Evo-Devo Group
Technician post

A Research Laboratory Technician post is available in the Cichlid Eco-Evo-Devo Group directed by Dr Emilia Santos in the Department of Zoology at the University of Cambridge.

The successful candidate will work on PredictingSPOTS, an ERC Consolidator Grant investigating the genomic and developmental basis of colour pattern diversification and convergence in East African cichlid fishes. The project uses egg-spots - a sexually selected pigmentation pattern found on the anal fins of male cichlids - as a tractable model to understand how morphological innovation arises and evolves, combining GWAS and QTL mapping, spatial and single-cell transcriptomics, CRISPR/Cas9 genome editing, and data-driven mathematical modelling.

The principal aim of this post is to support genome editing in cichlid fishes and genomic library preparation for next-generation sequencing. The postholder will design and execute CRISPR/Cas9 (and other) genome editing strategies, generating and characterising mutant and transgenic cichlid lines to investigate gene function in vivo. The role also covers aspects of genomic library preparation, including the development and implementation of scalable single-nuclei multimodal approaches such as sci-seq (DOI: 10.1038/s41596-022-00752-0) and SHARE-seq (DOI: 10.1016/j.cell.2020.09.056). We have extensive in-house experience with genome editing in cichlids (e.g., DOI: 10.1098/rsos.220077 and DOI: 10.1098/rsob.230257), so while developmental genetics experience is desirable, it is not essential to apply. Experience with molecular biology and genomic library preparation methods is essential.

The successful candidate will join the Cichlid Eco-Evo-Devo lab, a team of nine members, including PhD students and postdocs and will work closely with other technicians and team members from the wider DAB Skylab, which includes the groups of Prof. Stephen Montgomery and Prof. Chris Jiggins. Candidates will need to be reliable, proactive, and able to work autonomously within guidelines, while also being strong team players able to train and support others in the lab.

For more information, please refer to this link: <https://www.cam.ac.uk/jobs/research-laboratory-technician-fixed-term-pf50326> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

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AMNH Chapman Postdoctoral Fellowship

Postdoctoral Fellowship – American Museum of Natural History – Department of Ornithology

The DeRaad Lab at the American Museum of Natural History (AMNH) is recruiting a postdoctoral fellow to investigate the evolutionary genomics of birds. Fellows will be expected to utilize and contribute to the exceptional American Museum of Natural History ornithology collection. Supported research topics could include population genetics, conservation genetics, and

speciation, with projects grounded in museum ornithology. The postdoctoral fellow will be encouraged to develop independent research ideas, while also getting the opportunity to plug into existing projects as desired. The AMNH is a vibrant and supportive environment where the postdoctoral fellow will get to interact with an active research community. The postdoctoral fellow will also have access to a multitude of professional development opportunities offered by AMNH and nearby universities (Columbia, CUNY, NYU, etc.).

The annual salary will be \$73,316 plus benefits. This is a full-time position with a 2 year appointment length and the possibility of further extension pending satisfactory work reviews.

Responsibilities: The postdoc will generate and lead

data analysis for both short read and long read genomic sequence data. Relevant experience could include working in a molecular lab extracting DNA and preparing DNA libraries for sequencing. Additionally, a qualified candidate must have experience designing and implementing bioinformatic pipelines for assembling genomes, variant calling, and performing population genetic / phylogenetic analyses. Familiarity working with avian museum specimens and handling degraded DNA (either in the lab or in silico) is a plus.

Required qualifications: Ph.D. or equivalent in evolutionary biology, computational biology, or related fields and demonstrated record of productivity and publications. Experience with processing and analyzing genomic data, computer programming (e.g., python; R), genomics, molecular evolution, and avian biology.

Contact and Application: To apply, please send a cover letter explaining your qualifications and interest in the position (one page), a complete CV, and the contact information for two references, by email as a single pdf file to Devon DeRaad (devonderaad@gmail.com) with the title "Chapman Postdoc Fellowship". Evaluation of the applications will begin September 7th, 2026 and continue until the position is filled, with a desired start-date July-August 2027.

The American Museum of Natural History is an Equal Opportunity/Affirmative Action Employer. The Museum does not discriminate with respect to employment, or admission or access to Museum facilities, programs or activities on the basis of race, creed, color, religion, age, disability, marital status, partnership status, gender, sex, sexual orientation, gender identity, gender expression, genetic information, pregnancy, alienage or citizenship status, current or former participation in the uniformed services, status as a veteran, or national or ethnic origin, or on account of any other basis prohibited by applicable City, State, or Federal law. Additional protections are afforded in employment based on arrest or conviction record, status as a victim of domestic violence, stalking and sex offenses, unemployment status, and credit history, in each case to the extent provided by law. If special accommodations are needed in applying for a position, please call the Office of Human Resources.

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Austria Vetmeduni Vienna Drosophila postdoc

Postdoc: Understanding polygenic adaptation with genomic time series data from *Drosophila* populations evolving in a novel environment.

Our laboratory runs more than 15 replicated experimental evolution studies across three *Drosophila* species, spanning more than 400 generations of adaptation in different environments. The successful candidate will characterize the genomic response of the evolved populations, drawing on available genomic time-series data (Pool-seq and haplotype data). Molecular phenotypes can also be generated to aid in interpreting these results. The postholder will have considerable latitude in prioritizing the research focus among the available data. The position starts on 1.10.26, though a later start date is negotiable, and is funded for up to two years (if starting 1.10.). Successful candidates will have the opportunity to take over flies and data of the ongoing evolution experiments – an excellent springboard toward an independent position. The position is based at the Institut für Populationsgenetik, Vetmeduni Vienna (<https://www.vetmeduni.ac.at/en/population-genetics>), but embedded in the network of evolutionary biology in Vienna (<https://www.evolvienna.at>) and the FWF funded research priority on Polygenic Adaptation (<https://www.vetmeduni.ac.at/sfb-polygenic-adaptation>). Interested candidates should send their application (CV, short statement of research interests, with connection to the advertised position, contact details for 2 references) to Christian Schlotterer (schlotc@gmail.com).

The search will continue until the position is filled, but for full consideration, applications should be received by September 15.

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Austria Vetmeduni Vienna Phenotypic Drosophila postdoc

Postdoc: phenotypic characterization of *Drosophila* populations evolved in a novel temperature environment

Our laboratory runs more than 15 replicated experimental evolution studies across three *Drosophila* species, spanning more than 400 generations of adaptation. The successful candidate will work alongside two part-time technicians to characterize the phenotypic response of the evolved populations, taking a leading role in selecting which phenotypes to investigate – potentially including molecular phenotypes such as RNA-Seq, scRNA-Seq, metabolomics etc. Genomic time-series data for these populations will also be available. The position starts on 1.10.26, though a later start date is negotiable, and is funded for up to two years (if starting 1.10.). Successful candidates will have the opportunity to take over flies and data of the ongoing evolution experiments – an excellent springboard toward an independent position. The position is based at the Institut für Populationsgenetik, Vetmeduni Vienna (<https://www.vetmeduni.ac.at/en/population-genetics>), but embedded in the network of evolutionary biology in Vienna (<https://www.evolvienna.at>) and the FWF funded research priority on Polygenic Adaptation (<https://www.vetmeduni.ac.at/sfb-polygenic-adaptation>). Interested candidates should send their application (CV, short statement of research interests, with connection to the advertised position, contact details for 2 references) to Christian Schlotterer (schlotc@gmail.com).

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GeorgiaU Quantitative and Computational Disease Ecology

The Sundaram Lab at the University of Georgia has a postdoctoral position open to model global infectious disease patterns and animal hosts. The successful candi-

date will be housed in Athens, GA, within a vibrant research community in the University of Georgia. Our lab specializes in combining computational tools, spatial modeling, and machine learning to understand disease dynamics, forecast epidemics, and quantify zoonotic potential across global scales. The postdoctoral scholar will play a central role in conducting data-intensive research across the full arc of zoonotic spillover and human outbreak events. Responsibilities include co-creating research questions; acquiring and harmonizing large-scale ecological and pathogen datasets; building predictive, spatial, or machine learning models; synthesizing literature; writing manuscripts; and presenting findings to scientific audiences. This position is ideal for researchers passionate about applying ecological and evolutionary principles to infectious disease problems. Prior experience and/or enthusiasm towards data science, computational modeling, and applying quantitative frameworks to pressing ecological and public health challenges is a plus. How to Apply: For full job details and to submit your application, please visit the UGA Jobs portal: University of Georgia — Postdoctoral Research Associate- Sundaram: <https://www.ugajobsearch.com/postings/499394> To learn more about our ongoing projects, visit <https://www.mekalasundaram.com/>. For any preliminary questions, feel free to reach out directly to Dr. Mekala Sundaram at msundara@uga.edu.

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Germany UniMainz Theoretical Evolutionary Ecology

The Theoretical Evolutionary Ecology group, led by Prof. Hanna Kokko, at the Institute of Organismic and Molecular Evolution at the University of Mainz, Germany, invites applications for a 3-year postdoc position starting 1 January 2027 (Salary level TV-L E13, 100). Experience in mathematical modelling in the field of evolutionary ecology (broadly interpreted) is essential; interest in engaging with the empirical side of this field is a plus. Our group consists of people of diverse nationalities and the group communicates in English, which is also the language of teaching. The postdocs in this group all contribute some of their time to teaching BSc and MSc students. Applications must be sent in a single pdf and include: (1) a CV, publication list, and contact details of at least two referees, (2) a motivation

letter stating what the applicant would ideally like to work on (max. 2 pages), (3) a 'journal club task'. We have a weekly journal club, see kokkonuts.org -> 'Journal club' for a list of recently discussed papers. Choose one, and write a max. 3 page document on (a) why this paper piqued your interest and (b) what are the statements and questions you would have said about it in the journal club, had you been able to attend. Applicants should send their pdf to Prof. Hanna Kokko (hkokko@uni-mainz.de) with the subject line "Post-doctoral position in Theoretical Evolutionary Ecology' Your Name". The application review will commence on 25 September 2026. The position will remain open until filled.

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Heidelberg U EvolutionaryGenomics

Center for Molecular Biology (ZMBH), Heidelberg University, Germany A postdoctoral position (3 years, with possible extension) is available immediately in the evolutionary genomics group of Henrik Kaessmann at Heidelberg University. Applications will be reviewed on a rolling basis until the position is filled. We are seeking a highly qualified, motivated, and enthusiastic candidate with a keen interest in evolutionary questions and a strong background and hands-on experience in experimental molecular and genomics approaches. Additional experience in computational/bioinformatics analyses is highly welcome. Projects in our lab usually combine experimental and computational components, with the relative emphasis tailored to the specific project and the candidate's interests and expertise. Our lab investigates a broad range of questions related to the origins and molecular evolution of organs in mammals and other vertebrates and the underlying genomic changes, with a particular focus on the evolution of gene expression and its regulatory basis (see home.kaessmannlab.org and zmbh.uni-heidelberg.de/kaessmann for more information). As part of this research, we have generated extensive comparative genomics datasets (e.g., single-cell RNA-seq and ATAC-seq) across species, based on samples from our unique organ collections, and analyzed them using state-of-the-art bioinformatics approaches, increasingly incorporating AI and deep learning (see, e.g., Sarropoulos et al., Science 2026). This work has provided insights into the origins and functional evolution of

protein-coding genes, alternative splicing, long noncoding RNAs, microRNAs, and sex chromosomes across organs and species, as well as their phenotypic implications. We currently offer a range of possible projects addressing the evolution of gene expression and its regulatory basis across expression layers, organs, and species in mammals and other vertebrates. These projects will combine the generation of unique new datasets using cutting-edge experimental approaches (e.g., long-read spatial transcriptomics) across diverse organs, from the brain to the gonads, with state-of-the-art computational and deep-learning approaches. Projects may also include detailed molecular and functional characterization of particularly exciting candidate evolutionary changes using organoid and mouse models, CRISPR-based approaches, and synthetic genomics, supported by the expertise and infrastructure of our local Center for Synthetic Genomics (www.syn-gen.de). Specific projects will be developed together with the successful candidates based on their individual interests, expertise, and skills. In our lab, we place great importance on a collaborative, supportive, and positive team spirit. Many of our projects are driven by small, closely interacting teams of experimental and computational researchers who combine complementary expertise and work together enthusiastically. We also greatly value the diverse cultural and international backgrounds of our lab members, which contribute to an open and enriching research environment. The working language of our institute is English, and its members form a highly international community. The ZMBH is located in Heidelberg, a picturesque and vibrant international city on the Neckar River and at the edge of the Odenwald forest. Heidelberg offers an exceptionally stimulating and collaborative research environment, with the European Molecular Biology Laboratory (EMBL), German Cancer Research Center (DKFZ), Heidelberg Institute for Theoretical Studies (HITS), and Max Planck Institute for Medical Research located in close proximity to the University. For more information about our group and the institute more generally, please visit our website at the ZMBH (<http://www.zmbh.uni-heidelberg.de/Kaessmann/>). Please submit a CV, a statement of research interests, and the names and contact details of three references to Henrik Kaessmann (h.kaessmann@zmbh.uni-heidelberg.de).

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Kiel Germany Evolution of phenotypic heterogeneity and heteroresistance in bacteria

Kiel, Germany - Postdoc - Evolution of phenotypic heterogeneity and heteroresistance in bacteria

Application deadline: 27. August 2026.

The postdoc position is for 5 years, based in the Schulenburg group (<https://evoecogen-kiel.de/>). The research is part of the ERC project on CrypticBenefits and aims at understanding how antimicrobial heteroresistance and more generally phenotypic heterogeneity evolves in bacteria. As a model, we will focus on the opportunistic bacterial pathogen *Pseudomonas aeruginosa*. The work combines evolution experiments with whole genome sequence analysis, bacterial genetics, and functional analysis. As a general reference, check out the group's publications on AMR evolution, as listed on our webpage (<https://evoecogen-kiel.de/publications>).

Necessary competences and qualifications: PhD in the area of Evolutionary Biology; In-depth knowledge of central concepts of Evolutionary Biology; Competences and experiences in research on the Evolution of microorganisms; Competences and experiences in the field of statistics and bioinformatics; English language skills at level C1

Beneficial competences: Competences and experience in: (i) the planning and performance of evolution experiments; and/or (ii) high-throughput experiments; (iii) genome analysis; (iv) genetic manipulation of microorganisms; (v) advanced statistics (e.g., multivariate statistics, GLMs) and programming (e.g., python, R); (vi) Publication(s) from earlier research work.

For enquiries regarding the position and research topic please contact Prof. Dr. Hinrich Schulenburg: hschulenburg@zoologie.uni-kiel.de

Please apply via the following link: <https://www.uni-kiel.de/personal/de/stellen/extern/wiss/wissenschaftliche-mitarbeiter-in-am-zoologische-n-institut-ag-schulenburg> Applications should be submitted as a single PDF. Applications should include: (1) A letter of motivation (max. 2 pages, Arial 11, line spacing 1.15). In your motivation letter, please explain how your background fits the required profile and how your research interests align with the group research focus. (2) Curriculum vitae. (3) PhD certificate

MichiganStateU EvolutionaryBiology

The Ecology, Evolution, and Behavior (EEB) program at Michigan State University invites applications for a Postdoctoral Fellowship in Ecology, Evolution, and Behavior. The MSU EEB Presidential Postdoctoral Fellowship is a two-year position that includes a generous salary and research stipend. Fellows are fully participating members of EEB. They are expected to develop cutting-edge research programs and innovative community engagement initiatives, and will be mentored by two or more EEB core faculty members. A list of possible faculty mentors can be found here: <https://eeb.msu.edu/people/core-faculty.aspx>. Candidates should contact potential faculty mentors before applying.

The position is two years, subject to review after one year, with an annual salary of \$65,000 plus benefits, as well as a research stipend of \$8,000 per year. Postdocs are expected to be based on MSU's campus and up to \$1,000 of moving expenses may be reimbursed from the research stipend in the first year. We encourage applications from candidates in any early-career stage, from finishing PhD students to current postdoctoral scholars. International candidates are eligible. Applications are due November 1, 2026.

For more information on the MSU Foundation EEB Postdoctoral Fellowship, including detailed application instructions, please see <https://eeb.msu.edu/initiatives/postdoctoral-fellowship/index.aspx>. Michigan State University is an Equal Opportunity/Affirmative Action employer. E-mail any questions to committee co-chairs Dr. Kevin J. Liu (kjl@msu.edu) and Dr. Lars Brudvig (brudvig@msu.edu).

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Montpellier France Transposable elements in date palm

Postdoctoral position in functional and population genomics of transposable elements in date palm

A junior postdoctoral researcher position (2 years since PhD) is open in the DIADE laboratory in Montpellier, France, under the supervision of Yann Bourgeois. You will investigate the population dynamics of transposable elements and their contribution to functional genome annotation in date palm (*Phoenix dactylifera*). More senior candidates are also welcome to apply; however, given the available funding, the position may be limited to 12 months rather than the planned 18 months. The net salary (after all taxes) will be approximately EUR2,000/month for a junior postdoctoral researcher. You can read more about the research done in DIADE here: <https://www.umr-diade.fr/en/> The successful candidate will contribute to the second component of an ANR (French National Research Agency) project (DaTEPalm), which aims to understand how functional constraints and regulatory networks influence the deleterious effects of transposable elements (TEs) and their evolutionary dynamics in date palm. They will work closely with the project leader and contribute to the scientific supervision of the PhD student associated with the project, as well as to the dissemination and valorisation of results through analyses, publications and scientific presentations. The main objective is to integrate population genomic approaches with functional genomic data (gene expression, chromatin accessibility, DNA methylation and regulatory-region annotation) to identify genomic and functional factors predictive of the selective effects of TEs. The project will combine genomic, transcriptomic, epigenetic and regulatory-network data with population-genetic information, using statistical approaches and, where appropriate, machine-learning and deep-learning methods. Activities may include generating and analysing RNA-seq, ATAC-seq and DNA-methylation data, constructing gene regulatory networks, analysing whole-genome resequencing and TE datasets, and applying evolutionary modelling and simulations. Preliminary work describing the population genetics methodological framework that may be employed can be found here: https://yannbourgeois.github.io/assets/html/Blog_post_TE_selection_inference.html https://github.com/YannBourgeois/te_dfe At the start

of the project, more than 40 samples sequenced with Nanopore and covering the extant genetic diversity of date palm should be available, with funding for at least 20 additional samples. The project also benefits from a large cohort of nearly 1,000 palm trees resequenced with Illumina short reads.

The candidate will join the DIADE research unit in Montpellier, France, with access to major French HPC infrastructures and opportunities to collaborate with national and international researchers working on evolutionary genomics. The project may also involve fieldwork in France and potentially the Middle East. The candidate will have considerable flexibility in defining the specific research direction within the broader objectives of the project.

Applicants should hold a PhD in biology, evolutionary biology or bioinformatics and have strong expertise in genomics, transcriptomics, comparative genomics, scripting and computational analyses. Experience with population genomics, long-read sequencing, transposable elements and/or deep learning would be particularly valuable. Autonomy, rigour, adaptability, good communication skills and a collaborative spirit are expected. You can contact the PI, Yann Bourgeois, at yann.bourgeois@ird.fr for informal enquiries.

Applications should be submitted through the dedicated IRD recruitment webpage: https://emploi-irdecrutement.ird.fr/offre-de-emploi/emploi-chercheur-en-genomique-fonctionnelle-et-evolution-des-elements-transposables-f-h-_804.aspx Interviews are expected to take place in the second half of September, with a planned start in early November 2026.

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OklahomaStateU EvolutionBehavioralVariation

The Reichert lab in the Department of Biology at Oklahoma State University is seeking a postdoctoral researcher to work on an NSF funded project on the energetic drivers of individual variation in animal communication behavior. The project focuses on the relationship between metabolic rate and acoustic signaling behavior in gray treefrogs and will involve field recordings of acoustic signals, playback experiments to assess behavioral plasticity, measurement of metabolic rate us-

ing respirometry and investigations of the genetic basis of metabolic and behavioral phenotypes. The postdoc will be expected to lead the data collection on project experiments, develop new projects in line with their interests and the aims of the grant, communicate project results through scientific publications and presentations and contribute to student mentorship. The Reichert lab is dedicated to the professional development of all lab members and there will be opportunities to develop skills in teaching, mentorship and outreach. The lab is also dedicated to a research environment that is supportive of all members. The position can start as early as October 15, 2026, but the start date can be adjusted based on the selected candidate's availability.

The position can be potentially renewed up to 03/31/2029.

For full details and to apply, please see <https://jobs.okstate.edu/jobs/postdoctoral-fellow-in-biology-af9026-stillwater-oklahoma-united-states> Contact Michael Reichert with any questions: michael.reichert@okstate.edu and see <https://reichertlab.com/> for more information about our work.

Michael Reichert Associate Professor Department of Integrative Biology Oklahoma State University

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Paris Evolutionary-Immuno-Genomics

Postdoctoral position in human evolutionary genomics / immunogenomics / functional genomics (Paris, France)

We invite applications for a 24-month postdoctoral position at the interface of human evolutionary genomics, immunogenomics and functional genomics. The position is part of the IMMUNARCH project, funded by Universite Paris Cite until January 2029, and will start no later than 31 January 2027. The postdoctoral researcher will investigate the evolutionary history of archaic genetic variation associated with immune function. The project will combine ancient genomes, population genetic analyses, and functional genomic data to identify and characterize archaic variants with potential effects on immune phenotypes and reconstruct their evolutionary histories. Available functional datasets include results from massively parallel reporter

assays (MPRAs), chromatin accessibility (ATAC-seq), and gene expression (RNA-seq) experiments across different immune cell types and experimental conditions.

Research activities - Integrate ancient and present-day genomic data with functional genomic datasets to identify archaic variants with potential regulatory effects on immune phenotypes - Analyze ancient genomes to reconstruct the evolutionary histories and allele frequency trajectories of functionally relevant archaic variants - Investigate and compare evolutionary signals across immune pathways, cell types, and pathogen-response categories - Contribute actively to manuscript preparation and the presentation of results at international conferences
Required profile - PhD in evolutionary genomics, functional genomics, bioinformatics, or a related field - Strong background in functional genomics, performing associated experiments (MPRA, ATAC-seq, RNA-seq), and analysis of the corresponding large-scale genomic datasets - Strong computational skills and experience with scientific programming, particularly related to the analysis of ancient genomes - Excellent written and spoken English - At least one first-author publication (published or in press) - Ability to work independently and collaboratively in an international research environment Experience with cell culture and organoid systems would be an advantage.

Environment The position will be based jointly at the Institut Jacques Monod (IJM) and the Institut Pasteur, both located in the heart of Paris, in a dynamic, international research environment with computing infrastructure adapted for large-scale genomic analyses. The postdoctoral researcher will be jointly supervised by Dr. Stephane Peyregne, head of the paleogenomics group at the IJM, and Prof. Lluís Quintana-Murci, head of the Human Evolutionary Genetics Unit at the Institut Pasteur. The Peyregne group uses ancient genomes to investigate human evolutionary history and its relevance to human biology and health. The Quintana-Murci group investigates the evolutionary history and functional diversity of the human immune system. Together, the two groups provide complementary expertise in paleogenomics, population genetics, human evolutionary genomics, immunogenomics, and functional genomics.

Remuneration and benefits Salary starts from approximately EUR2,500 per month after taxation, depending on experience, according to French public research scales. Health insurance costs for the candidate and their family are included in the taxation (https://www.cleiss.fr/docs/regimes/regime_france/an_1.html). Foreign nationalities can benefit from government support for housing and children's education depending on their income. French school fees are free or low.

Applications Applications can be addressed to Stephane Peyregne (stephane.peyregne@ijm.fr) and Lluís Quintana-Murci (lluis.quintana-murci@pasteur.fr). Please send a CV, a brief statement of research interests, as well as contact information for 2-3 referees. Review of applications will begin immediately and continue until the position is filled.

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Paris EvolutionaryImmunoGenomics

Postdoctoral position in human evolutionary genomics / immunogenomics / functional genomics (Paris, France)

We invite applications for a 24-month postdoctoral position at the interface of human evolutionary genomics, immunogenomics and functional genomics. The position is part of the IMMUNARCH project, funded by Université Paris Cité until January 2029, and will start no later than 31 January 2027. The postdoctoral researcher will investigate the evolutionary history of archaic genetic variation associated with immune function. The project will combine ancient genomes, population genetic analyses, and functional genomic data to identify and characterize archaic variants with potential effects on immune phenotypes and reconstruct their evolutionary histories. Available functional datasets include results from massively parallel reporter assays (MPRAs), chromatin accessibility (ATAC-seq), and gene expression (RNA-seq) experiments across different immune cell types and experimental conditions.

Research activities - Integrate ancient and present-day genomic data with functional genomic datasets to identify archaic variants with potential regulatory effects on immune phenotypes - Analyze ancient genomes to reconstruct the evolutionary histories and allele frequency trajectories of functionally relevant archaic variants - Investigate and compare evolutionary signals across immune pathways, cell types, and pathogen-response categories - Contribute actively to manuscript preparation and the presentation of results at international conferences

Required profile - PhD in evolutionary genomics, functional genomics, bioinformatics, or a related field - Strong background in functional genomics, performing associated experiments (MPRA, ATAC-seq, RNA-seq), and analysis of the corresponding large-scale genomic

datasets - Strong computational skills and experience with scientific programming, particularly related to the analysis of ancient genomes - Excellent written and spoken English - At least one first-author publication (published or in press) - Ability to work independently and collaboratively in an international research environment Experience with cell culture and organoid systems would be an advantage.

Environment The position will be based jointly at the Institut Jacques Monod (IJM) and the Institut Pasteur, both located in the heart of Paris, in a dynamic, international research environment with computing infrastructure adapted for large-scale genomic analyses. The postdoctoral researcher will be jointly supervised by Dr. Stephane Peyregne, head of the paleogenomics group at the IJM, and Prof. Lluís Quintana-Murci, head of the Human Evolutionary Genetics Unit at the Institut Pasteur. The Peyregne group uses ancient genomes to investigate human evolutionary history and its relevance to human biology and health. The Quintana-Murci group investigates the evolutionary history and functional diversity of the human immune system. Together, the two groups provide complementary expertise in paleogenomics, population genetics, human evolutionary genomics, immunogenomics, and functional genomics.

Remuneration and benefits Salary starts from approximately EUR2,500 per month after taxation, depending on experience, according to French public research scales. Health insurance costs for the candidate and their family are included in the taxation (https://www.cleiss.fr/docs/regimes/regime_france/an_1.html). Foreign nationalities can benefit from government support for housing and children's education depending on their income. French school fees are free or low.

Applications Applications can be addressed to Stephane Peyregne (stephane.peyregne@ijm.fr) and Lluís Quintana-Murci (lluis.quintana-murci@pasteur.fr). Please send a CV, a brief statement of research interests, as well as contact information for 2-3 referees. Review of applications will begin immediately and continue until the position is filled.

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Postdoc KansasU PlantBiodiversity

Plant Biodiversity Postdoctoral Researcher The University of Kansas (KU), Biodiversity Institute & Natural History Museum (BI/NHM) invites applications for a two-year, full-time, postdoctoral researcher position in plant biodiversity, situated in the Botany Division and R.L. McGregor Herbarium (<https://biodiversity.ku.edu/botany>). There is potential for renewal of the appointment based on funding developments. Applicants will be expected to conduct herbarium- and specimen-based, innovative research in plant biodiversity, including systematics, evolution, and genomics, and integrative AI applications. Potential complementary research foci include regional floristics, ecology, biodiversity data science, and conservation. The successful candidate will develop an active, collaborative research program as evidenced by peer-reviewed publications, research proposals, herbarium collection advancement, and outreach activities through the herbarium and the BI/NHM.

Additional information and instructions to apply: <https://sjobs.brassring.com/TGnewUI/Search/home/HomeWithPreLoad?partnerid=25752&siteid=5541&PageType=JobDetails&jobid=5233743> Inquiries are encouraged: nico.franz@ku.edu Application review date: September 21, 2026

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Postdoc RegulationOfEndosymbiosis U Miami

The Wilson Lab seeks a Postdoctoral Associate for an NSF-funded project testing the hypothesis that mTORC1 acts as a master regulator of the aphid/Buchnera endosymbiosis. Aphids house Buchnera in specialized bacteriocytes and must coordinate bacterial population growth with their own development and reproduction across generations. We are asking whether a conserved nutrient-sensing pathway is the mechanism that makes that coordination possible – a

question at the intersection of cell biology and the evolution that has not been addressed directly in any insect system.

The position is primarily laboratory-based, with a substantial computational component, and will be carried out as part of a collaborative research team.

Required qualifications Ph.D. in cell biology, developmental biology, evolutionary biology or a related field at time of hire Hands-on experience with confocal microscopy Competence in applied statistics A record of peer-reviewed publication The ability to advance a project with limited day-to-day supervision, and to work productively in a multidisciplinary group

Desirable, but not expected Experience analyzing high-throughput sequencing data Microdissection and microinjection of insects RNA-seq from small or dissected tissue samples Insect performance and life-history assays

Candidates from any relevant background are encouraged to apply, whether or not they have previously worked on insects or symbiosis. What matters is curiosity about how endosymbioses are regulated and a willingness to work in a system where some of the tools are still being built. The successful candidate will join the Wilson Lab within the Host-Microbe Interactions (HoMI) Laboratory, which is part of the Symbiosis@UM cluster within the Department of Biology, on the Coral Gables Campus of the University of Miami.

What the position offers The Postdoctoral Associate will contribute to publications as first author, have the opportunity to co-mentor undergraduate researchers, and receive support for conference travel. Candidates who wish to pursue independent fellowship funding are encouraged to do so and will be supported with mentoring plans, letters, and feedback on drafts. The University of Miami provides institutional access to career development resources for postdoctoral scholars.

Terms The appointment is for one year, renewable annually for up to three years, contingent on satisfactory performance and continued availability of funds. Start as soon as September 1, 2026.

To apply Please submit a CV and a cover letter, including the names of three referees. In the cover letter, describe your fit for the position and name one specific question about this system that you would want to answer, and how you would approach it. A full list of Wilson Lab publications is available on Google Scholar under Alex C C Wilson. <https://career.s.miami.edu/us/en/job/R100100315/Post-Doctoral-Associate-Biology> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

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Postdoc SyracuseU Drosophila Reproduction

The Dorus and Pitnick labs invite applications for a highly motivated Postdoctoral Researcher to join a dynamic and interdisciplinary research program focused on *Drosophila* reproduction and the evolution of molecular female determinants of sperm function and fertility. The position is supported by an NIH award in collaboration with Dr. Mariana Wolfner at Cornell University that runs through 2031. After mating, sperm participate in diverse interactions with the female reproductive tract that contribute to fertility. The molecular basis and evolution of these interactions are not well understood. The successful candidate will lead an integrative research program that aims to characterize female-derived proteins that participate in spatiotemporally regulated interactions with sperm and contribute to sperm motility, viability and fertilization competency. This research will provide unique training and expertise in evolutionary genetics and genomics, metabolomics, and male and female reproductive biology. This position also offers exceptional opportunities for scientific independence, cross-disciplinary collaboration, and preparation for a career in academia or advanced research. Please feel free to get in touch with questions: sdorus@syr.edu and sspitnic@syr.edu For full details and to submit applications: <https://www.sujobopps.com/postings/113878> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net)

PostDoc UCaliforniaLosAngeles ConservationScience

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

Deadline Approaching

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

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

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

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

wetland ecology) Note: TNC has been a particularly active partner and co-funder in recent years, and we encourage applicants interested in working with TNC mentors to consult: <https://tnc.box.com/shared/static/mprnsvure3vmf29xgpnrn00wl3t5me9l.pdf> Natural History Museum of Los Angeles County: Jann Vendetti (mollusk ecology and evolution; species natural history)

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

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

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

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

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

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

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

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

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

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

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at <https://evoldir.net/brian/evoldir/evoldir.html>

Postdoc U Maryland Epigenetics and social stress in bats

The Wilkinson lab at the University of Maryland, College Park, is hiring a postdoc to join an ongoing NIH-funded project titled "Social stress, epigenetic and immune function across the bat lifespans." This project aims to determine if age, reproductive effort or social stress influence immune function and response across the lifespans of males and females from five different species of bats. The postdoc will be responsible for analyzing RNA and DNA methylation sequence data and will assist with sample collection from wild and captive bats. The postdoc will help plan, conduct, and publish research, contribute to the professional development of undergraduate and graduate students, and assist with data dissemination. Candidates should have a strong background in bioinformatics, genomics and evolutionary biology. A track record of excellent written and verbal communication, and the ability to work well with others is required. Prior experience with analysis of DNA methylation is desirable. Interested candidates should apply through the University of Maryland job portal (https://umd.wd1.myworkdayjobs.com/UMCP/job/University-of-Maryland-College-Park/Post-Doctoral-Associate_JR104749). Please feel free to email (wilkinso@umd.edu), with "Post-doctoral position" in the subject line, before applying to ask questions. This is a one-year appointment with potential for renewal for an additional year. Best Consideration Date: 9/18/2026

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Slovakia Research Position in Forest Genomics

Research Position in Forest Genomics - Slovakia The Institute of Forest Ecology of the Slovak Academy of Sciences (SAS), Zvolen, Slovakia, is seeking a motivated researcher with expertise in genomics and genomic data analysis to join a research project investigating mature

Norway spruce (*Picea abies*) trees that survived severe outbreaks of the European spruce bark beetle (*Ips typographus*). The successful candidate will be involved in genomic analyses aimed at identifying genetic factors associated with tree survival and resistance, including genome-wide association studies (GWAS) and related analyses of genomic datasets. An important component of the project is field research in mountain forests affected by bark beetle outbreaks. We are therefore looking for a researcher who combines strong analytical skills with a proactive attitude towards demanding fieldwork in mountainous terrain. Experience with sampling mature forest trees is highly desirable. Previous experience with sampling from the upper crowns of mature Norway spruce trees, including tree climbing or related techniques, would be a significant advantage. Candidate profile - PhD or equivalent research experience in genomics, population genetics, evolutionary genetics, bioinformatics, or a related field; - demonstrated ability to analyse genomic datasets; - experience with GWAS or related population-genomic approaches; - willingness and physical ability to participate actively in fieldwork in demanding mountainous terrain; - ability to work independently and proactively while contributing effectively to a collaborative research team; - a cooperative approach to scientific writing and preparation of joint publications; - willingness to actively and constructively respond to comments, suggestions and feedback from other team members during manuscript preparation and data analysis; - willingness to contribute proactively to the development of analyses, interpretation of results and preparation of scientific outputs; - experience with mature-tree sampling and particularly upper-canopy sampling is a strong advantage; - experience in forest genetics, forest ecology, or research on conifers is advantageous but not essential. Position Institution: Institute of Forest Ecology, Slovak Academy of Sciences (SAS), Zvolen, Slovakia Duration: 1 September 2026 - 31 August 2030 Gross monthly salary: approximately EUR2,200 The position offers an opportunity to combine forest genomics, evolutionary ecology and challenging field research to address a fundamental question: why do some mature Norway spruce trees survive severe bark beetle outbreaks while surrounding trees die? Applications: [resdinet.eu\[at\]gmail.com](mailto:resdinet.eu[at]gmail.com), please send your CV, Publication list and contact details for two academic referees.

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Sweden Gothenburg Botany PlantScience

Postdoctoral Fellow in Botany (Plant Science) at the University of Gothenburg, Sweden

Reference number PAR 2026/629 Full advertisement, weblink: Goteborgs universitet — Postdoctor in Botany (Plant Science) https://web103.reachmee.com/ext/I005/1035/job?site=7&lang=UK&validator?89bead79bb7258ad55c8d75228e5b7&job_idA235

Subject area description The postdoctoral fellow will work on a Swedish Science Council-funded project using a comprehensive phylogenetic tree of southern African (SA) Asteraceae to evaluate the roles of long-distance dispersal, biome shifts, and environmental change as stimuli of taxonomic and phenotypic diversification. Having undergone a major evolutionary radiation in SA to yield a regional flora comprising ca. 2500 species which has occupied all available environments, from deserts to the alpine zone, Asteraceae offers an ideal system for studying the dynamics of diversification in a continental context. In addition, the physiographic and vegetation diversity of contemporary SA, and a Miocene-Pliocene history involving tectonism and climate change, provide the opportunity to test the agency of contemporary and historical factors as drivers of evolutionary diversification. In addition to the above, the postdoctor will be required to develop an independent research project that makes use of GBG's living collections and/or contributes to GBG's conservation agenda. This project may be systematic, address questions relating to trait evolution and/or geographical distribution, or have an explicit conservation focus (e.g., relating to threat assessment and ex situ conservation practices). There is a possibility to participate in international plant collecting trips. The research will be supervised by Prof G Anthony Verboom (University of Gothenburg and GBG), Dr Nicola Bergh (GBG), and Dr Felix Forest (Royal Botanic Gardens, Kew). The postdoctor will also work closely with a PhD student whose research examines the diversification consequences of intercontinental long-distance dispersal.

Duties - Conduct primary research leading to the publication of at least three papers, two relating to the diversification of SA Asteraceae and one relating to the GBG-based project (see above). Analytical methodologies potentially include bioinformatic processing of

sequence data, phylogenomic analysis, GIS-based spatial analysis, and comparative macroevolutionary analysis. - Attend local and/or international conferences for the purpose of presenting research findings and contribute to fundraising to support such travels. - Deliver seminars and participate in journal clubs and other academic fora at BioEnv and GBG. - Potentially contribute to teaching in BioEnv, up to 10- Organize and run a limited number of training events for GBG scientific and curatorial staff, such as a series of short introductory R workshops (including Rstudio, ggplot, and tidyverse).

Assessment criteria The suitability of applicants will be assessed based on (i) documentary evidence submitted at the time of application, (ii) a short oral presentation given at the time of interview, and (iii) response to interview questions. A subset of applicants will be invited for interview.

Required qualifications for employment: - PhD in evolutionary biology or systematics. - Experience of data management and statistical analysis in R. - Working knowledge of phylogenetic inference and comparative macroevolutionary analysis - Ability to work well both independently and as part of a group. - Organizational skills and ability to co-lead and coordinate a large project which involves processing and analysis of large amounts of data. - Interest in field work. - Excellent English communication skills, both written and spoken.

Desirable qualifications for employment: - Advanced knowledge of plant taxonomy, systematics, and evolution. - Experience of processing and analyzing high-throughput genomic data, spatial data (e.g., SDM), and/or big data (i.e., on an HPC cluster). - Experience of working in a team. - Willingness to mentor undergraduate students. - Driver's license.

Personal qualifications: Given the expectation of independent research development, we require someone who is independent and self-motivated. Since the postdoctoral will be expected to collaborate closely with a PhD student and colleagues at both BioEnv and GBG, we are also looking for someone who is collegial, a good communicator, and capable of working as part of a team.

Employment The employment is temporary, lasting two years, 100

Contact information If you have any questions about the position, please contact: Professor G Anthony Verboom

Sweden UGothenburg Postdoc Plant macroevolution and diversification

Postdoc in Botany (Plant macroevolution and diversification) at the University of Gothenburg, Sweden Application deadline: 2026-09-14

This postdoc is for two years (100

The postdoc will work on a Swedish Science Council-funded project using a comprehensive phylogenetic tree of southern African Asteraceae to evaluate the roles of long-distance dispersal, biome shifts, and environmental change as stimuli of taxonomic and phenotypic diversification. They will also develop a separate research project that makes use of the Gothenburg Botanic Garden's living collections and/or contributes to the garden's conservation agenda. There is a possibility to participate in international plant collecting trips. The research will be supervised by Prof G Anthony Verboom (University of Gothenburg and GBG), Dr Nicola Bergh (GBG), and Dr Felix Forest (Royal Botanic Gardens, Kew).

Required qualifications: - PhD in evolutionary biology or systematics. - Experience of data management and statistical analysis in R. - Working knowledge of phylogenetic inference and comparative macroevolutionary analysis - Ability to work well both independently and as part of a group. - Organizational skills and ability to co-lead and coordinate a large project which involves processing and analysis of large amounts of data. - Interest in field work. - Excellent English communication skills, both written and spoken.

Desirable qualifications: - Advanced knowledge of plant taxonomy, systematics, and evolution. - Experience of processing and analyzing high-throughput genomic data, spatial data (e.g., SDM), and/or big data (i.e., on an HPC cluster). - Experience of working in a team. - Willingness to mentor undergraduate students. - Driver's license.

Personal qualifications: Given the expectation of independent research development, we require someone who is independent and self-motivated. Since the postdoctoral will be expected to collaborate closely with a PhD student and colleagues at both BioEnv and GBG, we are also looking for someone who is collegial, a good communicator, and capable of working as part of a team.

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If you have any questions about the position, please contact: Professor G Anthony Verboom Phone: +46 76 6185923 Email: tony.verboom@bioenv.gu.se Web-page: https://scholar.google.com/citations?user=QT3_z5IAAAAJ&hl=en&oi=ao Please apply via the following link: Goteborgs universitet — Postdoctor in Botany (Plant Science) https://web103.reachmee.com/ext/I005/1035/job?site=7&lang=UK&validator=9b89bead79bb7258ad55c8d75228e5b7&job_id=41235

Applications should be written in English and must include: - A cover letter describing the applicant's motivation for applying and explaining how the applicant meets the selection criteria. - A list of qualifications (CV) - Certificate of PhD exam - Complete list of publications, including submitted and accepted manuscripts (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Switzerland UBasel Phenotypic Plasticity and Selection Analysis

Postdoc fellowship in Phenotypic Plasticity & Selection Analysis (1001 November 2026 or negotiable)

The group of Plant Ecology and Evolution at the University of Basel, Switzerland (<https://duw.unibas.ch/en/ecoevo/>), is looking for a postdoc to lead the analyses and publishing of data collected in a context of plant responses to heat and drought and limits to selection.

Your position You will work on projects investigating plastic responses to climatic challenges and the evolutionary constraints that limit adaptation to extreme climatic conditions. We address these questions using populations and species sampled along elevational gradients, providing a powerful framework for identifying the causes of species' range limits and understanding constraints on the evolution of thermal niches. One available dataset comes from a heat-drought experiment, which enables detailed investigation of the shape of plastic responses along continuous environmental gradients, as well as interactions between climatic factors. A second dataset focuses on the same species and allows you to estimate multivariate selection and predict selection responses across elevational gradients. Together, these datasets offer opportunities to connect environmental variation, phenotypic plasticity, selection, and

evolutionary responses across climatic gradients.

Your profile The fellowship is for applicants who have done a PhD or at least one postdoc in Quantitative Genetics, Phenotypic Plasticity, and/or the Estimation of Selection.

We offer you The initial appointment is for one year. The University of Basel has generous resources for genomic analysis (scientific high- performance computing, data management, training and support). Furthermore, our Department of Environmental Sciences offers a stimulating environment, including a rich spectrum of research activities in life sciences (ecological genomics, population genomics, evolutionary biology, plant ecology, physiology and molecular and cell biology). Finally, Basel is a mid-sized Swiss city, well connected and offering a broad range of cultural and recreational activities.

Application / Contact Motivated applicants should submit (1) a one-page letter that summarizes interests and relevant experience, (2) their CV, (3) copies of PhD and other relevant diploma transcripts, and (4) contact information of two references. We accept only online applications. Applications are welcome until the position is filled and will be reviewed starting September 15, 2026. For more information, contact Yvonne Willi (yvonne.willi@unibas.ch)

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

TempleU Philadelphia Computational-mathematical molecular evolution and comparative genomics

The Liberles Group (<https://sites.temple.edu/liberles/>) is looking for a new postdoctoral scientist to join us, in the areas of computational/mathematical molecular evolution and comparative genomics. We are open to students from various backgrounds who have a passion for studying questions about evolution.

Ongoing research in the group is in areas including models for duplicate gene retention in genomes, in evolutionary systems biology for the context-dependent evolution of genes, and for protein evolution. The exact research topic is open to discussion.

The Liberles Group is based at Temple University in Philadelphia, PA, USA. A strong preference is for a candidate who is willing and able to relocate to Philadelphia. Unfortunately, this is probably most practical for US citizens or researchers of other nationalities who are currently in the United States.

Philadelphia offers a vibrant academic community, noted culinary and cultural opportunities, and a lower cost of living than other major northeastern cities. An ideal start date for the position would be January, 2027, but that is subject to negotiation. Candidates still finishing a Ph.D. with an expected completion in the next year are encouraged to apply. Funding will be guaranteed for a year and extension is possible by mutual agreement and available funding.

Please send your CV, a cover letter describing your interest, and a reprint (or preprint) from your prior work that is most related to theoretical or computational molecular evolution/ comparative or population genomics or phylogenetics (please only send one paper). Apply by email to daliberles@temple.edu

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UCalifornia SantaCruz Evolutionary Theory on Plasticity

Position: Postdoctoral Scholar to Develop Theory on the Evolution of Plasticity

Full details on this position and how to apply are here: https://drive.google.com/file/d/1yiwE90QLE2IZtdPnMDNjD3K_-BLozPcq/view?usp=sharing Description: Professor Suzanne Alonzo, in the Department of Ecology and Evolutionary Biology at the University of California, Santa Cruz (UCSC), invites applications for a Postdoctoral Scholar in Evolutionary Theory on Plasticity. The Postdoctoral Scholar will develop evolutionary theory on transgenerational and phenotypic plasticity in response to parental cues, collaborate with empiricists testing the theory's predictions in the threespine stickleback, and train undergraduate researchers involved in these projects. Applicants must have a doctoral degree in evolution, animal behavior, or a related field and prior experience with mathematical modeling or related quantitative methods. Strong applicants will have prior experience studying sexual selection, parental effects, and/or plasticity. Prior experi-

ence conducting relevant empirical research or collaborating with empiricists to test theory is desired but not required. The Postdoctoral Scholar will join an NSF-funded project that is a collaboration between Professor Suzanne Alonzo's research team and Professor Jennifer Hellman's research team at the Ohio State University. This project also involves training and supervising undergraduate research opportunities and contributing to undergraduate professional development programs at both institutions. Prior experience working with students is therefore also required for this postdoctoral scholar position. Applicants with expertise in developing evolutionary models of plasticity and/or the evolution of reproductive traits are strongly encouraged to apply.

Salary range: Commensurate with qualifications and experience. The posted UC salary scales set the minimum pay based on the individual's Experience Level, which is determined by the number of months of postdoctoral service at any institution. See the salary scale titled Postdoctoral Scholar-Employee/Postdoctoral Scholar-Fellow/Postdoctoral Scholar-Paid Direct - Fiscal Year. A reasonable estimate for this position is \$71,491-\$79,727.

Anticipated start date: Between September 1, 2026 and January 15, 2027.

Application Window: Full consideration will be given to applications completed by September 7, 2026. Applications received after this date will be considered only if the position has not been filled.

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UCambridge UK Cichlid Eco-Evo-Devo Group Department of Zoology Single Nuclei Multiomics

A postdoctoral Research Associate post is available in the Cichlid Eco-Evo-Devo Group directed by Dr Emilia Santos in the Department of Zoology at the University of Cambridge.

The applicant will work on PredictingSPOTS, a recently awarded ERC Consolidator Grant investigating the genomic and developmental basis of colour pattern diversification and convergence in East African cichlid fishes. The project combines genetic mapping, spatial and single-cell transcriptomics, and data-driven mathe-

mathematical modelling to understand how genomic and developmental mechanisms shape trait evolution. The post will focus on egg-spots, a sexually selected pigmentation pattern that has evolved repeatedly and independently across cichlid radiations, offering a tractable system to test whether convergent phenotypes arise through shared or independent developmental paths.

The principal aim for this post is to map the transcriptomic and regulatory basis of egg-spot development and its convergent evolution across a panel of cichlid species, combining spatial transcriptomics and single-nuclei RNA-seq/ATAC-seq with gene regulatory network inference. Strong bioinformatics/computational skills and demonstrable experience analysing high-throughput sequencing data will be essential, as will strong quantitative and statistical reasoning. Experience with spatial transcriptomics, single-nuclei sequencing, or gene regulatory network inference -including machine learning approaches to network or enhancer prediction - is highly desirable, as is a background in evolutionary developmental biology. Candidates will also have the opportunity to test predictions arising from this work using genome editing, in collaboration with the group's Research Laboratory Technician, and to contribute directly to the project's mathematical modelling if interested, though this is not an essential requirement of the role.

The successful candidate will join the Cichlid Eco-Evo-Devo lab, a team of nine members, including PhD students and postdocs and will work closely with the group's mathematical modelling collaborators (Dr. Berta Verd and Dr. Alexandria Volkening). Candidates will need to be highly motivated and develop a good understanding of the nature of the data and the project's scientific aims. Close teamwork and a collaborative spirit will be essential, but team members will be expected to demonstrate scientific independence matching their technical expertise. There will be opportunities to contribute to training new team members and to general project management, as well as to participate in public engagement activities.

For more information, please refer to this link: <https://www.cam.ac.uk/jobs/research-associate-fixed-term-pf50333> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

UGlasgow ReproductiveModeEvolution

University of Glasgow: Postdoctoral researcher in evolutionary genomics

We have a research opportunity at the University of Glasgow in the team of Kathryn Elmer in collaboration with Oscar Gaggiotti (St Andrews), Maureen Bain (Glasgow), Mike Ritchie (St Andrews) and project partners in Slovenia/Germany (Recknagel) and France (de Villemereuil, Le Galliard)

We are seeking a motivated, skilled, creative and enthusiastic postdoctoral researcher for a project on the evolution of oviparous and viviparous reproductive modes, funded by an ambitious NERC Pushing the Frontiers grant.

Our aim is to show how and why transitions between egg-laying and live-bearing evolve. To accomplish this, we will pinpoint the functional traits that matter, determine their genetic basis, and illuminate their evolutionary mechanisms and outcome. This project leverages a distinctly informative oviparous-viviparous common lizard hybrid zone (see e.g. Recknagel et al 2021 *Nature Ecol Evol*, Hunter et al. *Proc B* in press). This project involves a multi-year in situ experiment to track individual fitness and phenotypes across life stages and reshuffle oviparous-viviparous-hybrid genomes through directed genetic crosses. Our research so far has been identifying the genetic basis of i) eco-physiology and reproductive traits and ii) fitness components using genome-wide approaches. In this next step, with that information we will: 1. build fitness landscapes based on the most important genetic variants, and identify if and how these differ between males and females. 2. carry out a simulation study to explore the evolutionary genetic conditions under which the transition between oviparity and viviparity could have taken place, and evaluate the impact of different model parameters (mating, selection, genomic architecture, gene flow) on outcomes.

The PDRA will make a leading contribution to the genomic and evolutionary analysis of empirical data (genomic and phenotypic), selection and fitness landscape analysis, and evolutionary modelling of parity mode evolution (in SLiM or similar). The position is primarily focussed on data analysis and interpretation, with

the on-site experiment and data collection being conducted by the field- and lab-based team members. A very extensive dataset is already in hand. The PDRA will be based in Glasgow and work closely with co-Is in St Andrews, with some travel between sites expected.

Applicants must have a PhD in evolutionary biology, genetics, computational biology, or a closely related field. Prior experience with analyses of genomic data and computational skills are essential and expertise in population genetics is strongly preferred. Previous experience should demonstrate a commitment to research, positive work ethic, computational skills, organisational ability, and publication productivity. A strong track record of evolutionary genomics and/or computational biology is necessary, and on vertebrates (especially squamates) is a benefit. Ability to work well both independently and in a team are a must.

The postdoc will join University of Glasgow's School of Biodiversity, One Health & Veterinary Medicine. Elmer's research group studies the evolution of major adaptive traits by bringing together expertise in evolutionary biology, genomics and gene expression, and organismal biology in environmental context.

The position is for approx 16 months (extensions may be possible). Start date is somewhat flexible; preferably by late 2026. The position is open at grade 6 (early postdoc; research assistant) or grade 7 (experienced postdoc; research associate). See the specific criteria for these grades in the Univ. Glasgow advert for this position.

International applicants may be eligible for a UK work visa sponsored by the University of Glasgow. The University, School and PIs are strongly committed to supporting early career researchers and their professional development. We strive to be a supportive environment and welcome a diversity of applicants!

The University of Glasgow ranks in the world's top 100 universities and recently won the Top University award from the Times Higher Education. The city of Glasgow is lively and cultural, and sits on the doorstep of the great outdoors of the Scottish Highlands, islands, and coast.

The official job description and application requirements are available on the University of Glasgow homepage under current vacancies, <https://www.jobs.gla.ac.uk/job/research-assistant-slash-research-associate-5998778> vacancy reference 205695

We do not expect candidates to meet all criteria under "Knowledge, Qualifications, Skills and Experience", but in your application to the position do please outline how you meet EACH of the essential/desirable criteria listed

in the job advert and any other relevant experience and skills.

****The advertisement closes 16 Sept 2026****

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at <https://evoldir.net/brian/evoldir/evoldir.html>

UGoettingen Germany PlantDiseaseEcoEvo ControlledEnvirExperiments

Postdoc in controlled-environment experiments with fungal pathogens of wheat

Start: 1 February 2027 or shortly after. Application deadline: 11 September 2026 Location: Goettingen, Germany How to apply: one PDF (cover letter, CV, publication list, PhD certificate, two referees) via the university portal. Official advert & application: <https://www.uni-goettingen.de/de/644546.html?details=76559> Contact: alexey.mikaberidze@uni-goettingen.de

A 2.5-year postdoctoral position (E13 TV-L, 100

Using controlled-environment experiments and image-based phenotyping, the postdoc will measure how pathogen fitness / life-history traits – such as infection efficiency, incubation and latent period, lesion expansion, sporulation – vary across the three components of the disease triangle: pathogen genotype, host genotype, and environment. Possible research questions are centered around ecology and evolution of plant-pathogen interactions: how these traits trade off or synergize, how temperature and humidity influence them, and how they can lead to quantitative host resistance. Main pathosystems can be *Zymoseptoria tritici* (septoria tritici blotch), *Puccinia striiformis* (yellow/stripe rust) or *Puccinia triticina* (brown/leaf rust). The successful candidate will frame and lead a distinct project within this framework.

A distinctive strength of our group is that it combines experimental plant pathology and epidemiology with mathematical modeling of disease dynamics. Our large and growing imaging dataset (¿50,000 high-resolution RGB images of diseased wheat leaves) has already underpinned ¿10 peer-reviewed publications. The pheno-

typing data from this project will be published by the postdoc in their own right and will also feed the modeling team to parameterize predictive models of disease dynamics. The Department of Crop Sciences (DNPW) is one of Germany's leading centers for agricultural and crop sciences, and Goettingen is a historic, green and international university town with fast ICE rail links and a high quality of life.

We seek a motivated researcher holding (or close to completing) a PhD in plant pathology, plant sciences, fungal biology, genetics, evolutionary biology, ecology or a related field, with experimental experience on plant diseases and reproducible data analysis (preferably Python). Fluent English required; German not necessary.

Your tasks: - Controlled-environment experimentation: prepare wheat and pathogen material, run inoculation experiments, and optimize conditions to compare isolates, genotypes and environmental regimes. - Optical sensing and image acquisition: collect time-resolved imaging data (RGB as the core approach, with hyperspectral or thermal IR for selected questions), organized reproducibly with metadata. - Data analysis: apply AI image-analysis pipelines to quantify disease development; preprocessing, quality control, trait extraction, statistics and visualization in Python. - Genomic analysis (where relevant): link phenotypic traits to genomic data on the pathogen and/or host, e.g. GWAS, QTL mapping or genomic selection. - Scientific writing and communication: publish in international peer-reviewed journals, present at conferences, and contribute to grant proposals.

What we offer: - A supportive research environment combining experimental plant pathology and epidemiology with mathematical modeling. - State-of-the-art optical sensing (RGB, multi/hyperspectral, thermal IR), greenhouses and growth chambers, and support from technical staff and a dedicated AI-imaging engineer. - Support toward research independence, including mentoring for your own grant and fellowship applications (e.g. DFG, group-leader fellowships). - A collaborative network across Germany and worldwide, and room to shape research directions in a growing lab. - A family-friendly, diverse and international working environment.

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U Goettingen Germany PlantDiseaseEcoEvo MathematicalModeling

Postdoc in mathematical modeling of fungal plant disease dynamics

Start: 1 February 2027 or shortly after. Application deadline: 11 September 2026 Location: Goettingen, Germany How to apply: one PDF (cover letter, CV, publication list, PhD certificate, two referees) via the university portal. Official advert & application: <https://www.uni-goettingen.de/de/644546.html?details=76623> Contact: alexey.mikaberidze@uni-goettingen.de

A 2.5-year postdoctoral position (E13 TV-L, 100

Using mathematical and computational modeling, the postdoc will describe and predict how foliar fungal diseases of wheat develop across scales – from infection, latency, lesion expansion and sporulation on individual leaves to epidemic spread through crop stands and fields over a season. Possible research questions are centered around the ecology and evolution of plant-pathogen interactions: how leaf-scale fitness traits scale up to epidemic velocity, and how pathogens adapt to resistant cultivars and fungicides – how fast their efficacy erodes, and which deployment strategies can slow this adaptation. Modeling approaches span deterministic and stochastic dynamical systems (ODEs, PDEs, integro-differential equations) and spatial models of spore dispersal. Main pathosystems can be *Zymoseptoria tritici* (septoria tritici blotch), *Puccinia striiformis* (yellow/stripe rust) or *Puccinia triticina* (brown/leaf rust). The successful candidate will frame and lead a distinct project within this framework.

A distinctive strength of our group is that it combines mathematical modeling of disease dynamics with experimental plant pathology and epidemiology. Our large and growing imaging dataset (~50,000 high-resolution RGB images of diseased wheat leaves, now expanding to hyperspectral, multispectral, thermal IR and LiDAR) has already underpinned ~10 peer-reviewed publications. This growing wealth of data offers exceptional opportunities to parameterize and validate the models against disease dynamics, in collaboration with experimental researchers within the group. The Department of Crop Sciences (DNPW) is one of Germany's leading

centers for agricultural and crop sciences, and Goettingen is a historic, green and international university town with fast ICE rail links and an excellent quality of life.

We seek a motivated researcher holding (or close to completing) a PhD in theoretical or mathematical biology, applied mathematics, physics or a related quantitative field – or in the biological or agricultural sciences with a strong quantitative and mathematical modeling track record. We expect an excellent command of dynamical-systems modeling (ordinary differential equations and stochastic processes) and solid scientific programming (preferably Python, or C/C++ or R). A genuine interest in plant diseases is essential; the biological grounding is provided by the PI and the experimental team. Fluent English required; German not necessary.

Your tasks: - Formulate clear and interesting biological questions and hypotheses on fungal disease dynamics to guide the modeling research. - Model development and parameterization: build deterministic and stochastic models (ODEs, PDEs, integro-differential equations) and, where relevant, Eulerian/Lagrangian models of spore dispersal; implement, solve and parameterize them using group data or the literature. - Computation and analysis: analyze models analytically and numerically, fit them to the group's image-derived phenotyping data, estimate parameters and quantify uncertainty. - Scientific writing and communication: publish in international peer-reviewed journals, present at conferences, and contribute to grant proposals.

What we offer: - A supportive research environment combining mathematical modeling with experimental plant pathology and epidemiology. - Integration with an experimental team and a large, growing dataset (~50,000 RGB images plus upcoming hyperspectral, multispectral, thermal IR and LiDAR), and support from a dedicated AI-imaging engineer. - Access to high-performance computing for large-scale simulation and inference. - Support toward research independence, including mentoring for your own grant and fellowship applications (e.g. DFG, group leader fellowships). - A collaborative network across Germany and worldwide, and room to shape research directions in a growing lab. - A family-friendly, diverse and international working environment

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U Helsinki Ecological Networks And-Biodiversity Conservation

Postdoctoral Researcher in Ecological Networks and Biodiversity Conservation at the University of Helsinki
Join the University of Helsinki as a Postdoctoral Researcher on the newly funded project ANEW: Arising Novelty in Ecological netWorks: consequences for ecosystem functioning and biodiversity conservation. This is a fully funded 2-year position investigating ecological network novelty and its consequences for biodiversity and ecosystem functioning under global change. The successful candidate will play an important scientific role within the project, combining large-scale ecological datasets, species trait data, ecological network analyses and quantitative modelling. The position will also involve coordinating field surveys of historical seed dispersal networks across Europe, mentoring junior researchers, and contributing to leading collaborative publications. We are looking for a researcher with a background in ecology and experience in quantitative analyses and ecological fieldwork. The position is available from 1 January 2027 or as agreed and will be supervised by Dr Emma-Liina Marjakangas. The project involves collaboration with Prof Heini Kujala (University of Helsinki) and Prof Matthias Schleuning (Senckenberg Biodiversity and Climate Research Centre, Germany). The application deadline is 30 September 2026. Full details and application instructions: <https://jobs.helsinki.fi/job/Helsinki-Postdoctoral-Researcher-in-Ecological-Networks-and-Biodiversity-Conservation/1370769357> For further information about the position, informal enquiries are welcome and may be directed to Dr Emma-Liina Marjakangas at emma.marjakangas@helsinki.fi. Please feel free to distribute the call to potential candidates in your networks.

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UniBern Switzerland Bioinformatics Deadline-extended

Fully funded Bioinformatics Postdoc position (100Genome evolution and population genomics of an allohexaploid fish adaptive radiation)

Supervisor: Dr. Pooja Singh Starting date of position: 01-10-2026

I am seeking to fill a Postdoctoral Researcher position funded for one year, with the possibility of extension for a second year through the Swiss National Science Foundation (SNSF), at the University of Bern, Switzerland. This project is conducted in close collaboration with a team of scientists at Addis Ababa University (Ethiopia). Lake Tana, Ethiopia's largest lake, is a unique biodiversity hotspot and home to the world's last remaining species flock of cyprinid fishes. The genus *Labeobarbus* is hexaploid and underwent a rapid adaptive radiation after Lake Tana filled approximately 15,000 years ago, giving rise to around 17 endemic species. We have recently assembled the first draft hexaploid reference genome for the Lake Tana *Labeobarbus*. In this project, we will reconstruct the evolutionary history and speciation dynamics of this radiation while investigating the roles of polyploidy and hybridisation in adaptation and speciation. The ideal applicant will be a highly motivated and independent bioinformatics researcher interested in understanding the evolutionary dynamics of allopolyploid organisms. Our study system—*Labeobarbus* fishes from Lake Tana—is allohexaploid, presenting exciting computational and evolutionary challenges. The complexity of this reference genome requires someone with strong bioinformatics expertise, excellent problem-solving skills, and a willingness to develop new analytical approaches. The successful candidate will work closely with me, with responsibilities including:

1. Genome and homoeologue annotation of a high-quality genome assembly.
2. Homoeologue-aware phylogenomic reconstruction of the Lake Tana species flock.
3. Collaborating with two PhD students on population genomics and hybridisation analyses.

Requirements Essential - Background in bioinformatics, evolutionary genetics, genomics, or a closely related field. - Extensive experience working in Linux environments and on high-performance computing (HPC) systems. - Strong programming skills in R and/or Python. - Extensive experience analysing

large-scale genomic datasets (HiC, PacBio HiFi and IsoSeq, Illumina Novaseq), and using bioinformatics tools. - Demonstrated ability to solve complex bioinformatics challenges through code development and/or methodological innovation. - Good knowledge of orthology inference, phylogenomics, and associated analytical methods. - Ability to work independently while collaborating effectively and respectfully with colleagues from diverse backgrounds. - Excellent written and spoken English. - Strong organisational, communication, and teamwork skills. Desirable - Experience working with allopolyploid genomes. Application Please submit a single PDF file named: `FirstNameSurname_UBern_Postdoc_2026.pdf` The PDF should contain the following documents in order: 1. Letter of motivation (maximum two pages) describing your research experience, your interest in this position, and how it aligns with your career goals. 2. Curriculum vitae, including a list of publications and other scientific outputs, with a brief description of your contribution to publications directly relevant for this position. 3. Statement of bioinformatics and coding experience (maximum two pages), including links to your GitHub or other code repositories where applicable. Please emphasise any methods or analytical approaches you have developed yourself and highlight any experience working with allopolyploid genomes. 4. Contact details for three referees. 5. PhD and MSc transcripts. Please send your application by email to pooja.singh@unibe.ch with the subject line: "Postdoc application *Labeobarbus*" The application deadline is 11 August 2026 (23:59 GMT+1). Salary Salary will be determined according to the University of Bern salary scheme for postdoctoral researchers. Diversity and Inclusion Diversity, equity, and inclusion are core values of our team. We especially encourage applications from women, people of colour, individuals from the Global South, and others who are underrepresented in bioinformatics and computational biology, particularly those who experience multiple intersecting forms of marginalisation. Further Information For informal inquiries, please contact: Dr. Pooja Singh pooja.singh@unibe.ch More information about my research can be found at: <https://poojasinghebogen.weebly.com> The successful candidate will be based jointly at the Division of Aquatic Ecology & Evolution, University of Bern, and the Department of Fish Ecology & Evolution, Swiss Federal Institute of Aquatic Science and Technology (Eawag).

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UniLincoln UK EvolutionaryEcology Biophysics Insect egg sperm coevolution

This is an externally-funded PDRA position supporting the Leverhulme project "Biophysical and morphological coevolution of egg micropyles and sperm in insects". You will work closely with an international team of researchers across multiple disciplines at the University of Lincoln, UK (<https://graziellaiossa.weebly.com/>) (<https://life-historyresearch.weebly.com/>), in collaboration with the Tulane University, USA.

Duration, start date, salary This is a 3-year position, starting from 01/10/2026 (start date can be flexible). Salary starts at GBP38,784/year.

The project Insect eggs are incredibly intricate and complex structures which are poorly studied when compared to sperm. To fertilise insect eggs, sperm must pass through a tiny pore called a micropyle, which connected to a channel leading inside the egg. Through our previous work on insect egg and sperm, we have shown that sperm and egg micropyles co-evolve.

The aim of this project is to quantify and explore the form and function of insect egg micropyles across insects. The post you would hold sits at the experimental heart of this: fabricating nano-scale physical analogues of egg surfaces and micropylar pores, and imaging live sperm as they move across and through them. These experiments are complemented by evolutionary analysis and mathematical modelling carried out with the wider team.

Role & requirements This is a laboratory-based post and we are looking above all for a strong experimentalist. You will have a PhD (or close to completion) in experimental biophysics, bioengineering, applied physics or a closely allied discipline, with demonstrable hands-on experience of micro- and nanofabrication and of quantitative live-cell imaging. You will fabricate microfluidic devices and develop live imaging protocols to visualise sperm movement over engineered surfaces and through pores. You will also contribute to computational modelling of sperm movement alongside our collaborator Dr Adnan Morshed (Tulane University, USA) and write and run analysis code in R and/or Python. You will have excellent communication skills with the ability to talk to different audiences, as you

will be collaborating with a team of researchers across multiple disciplines both in the UK and overseas.

How to apply Informal enquiries are encouraged, please email Dr Graziella Iossa (glossa@lincoln.ac.uk)

The deadline for application is 10 September 2026. Interviews will be held online on 17 September 2026.

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

Applications must be received online: <https://jobs.lincoln.ac.uk/vacancy.aspx?ref=CHS310A> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net

U Pittsburgh UrbanEvolution Hummingbirds

Location: Pittsburgh, PA, USA (in person) Start date: Fall 2027 (flexible) Duration: 1-3 years (1-year starting contract with potential renewal for an additional 1-2 years) Salary: \$63,580 - \$66,948 + benefits Qualifications: - Ph.D. in ecology, evolutionary biology, genomics, bioinformatics or any related fields - Demonstrated ability to work with genomic datasets - Strong writing skills, publication record and evidence of successful project leadership Dr. Valentina Alaasam in the Department of Biology at the University of Pittsburgh invites applicants for a postdoctoral scholar position to study evolutionary responses of hummingbirds to urbanization. We are an integrative biology lab interested in the behavioral, physiological, and genetic mechanisms that birds use to cope with anthropogenic change, asking questions both within and across populations. The incoming postdoc should be comfortable (and excited about) using a variety of genomic and computational approaches to explore evolutionary questions in areas such as population genomics and demographic inference, landscape genomics, genotype-phenotype association, functional genomics and transcriptomics, comparative genomics, pangenomics, etc. The position involves analyzing existing genetic data, leading publications, molecular lab work, contributing to grant writing, and potentially generating new data in the field (opportunities to work locally in Pittsburgh,

other U.S. cities and/or internationally in Central and South America). The ideal candidate will have a background in genomics and/or evolutionary biology and strong bioinformatic coding skills. Importantly, we are also looking for a someone who will contribute to building a positive, fun, and inclusive lab culture, mentoring undergraduate and graduate students, and contributing to science communication. More info about our research & lab philosophies can be found here: <http://www.valentina-alaasam.com> Dr. Alaasam is committed to supporting postdoctoral professional development by providing opportunities to lead existing projects and publications, contribute to collaborative manuscripts, contribute to grant proposals, pursue their own independent research ideas, mentor students, build relationships with partner organizations, and participate in scientific outreach. The University of Pittsburgh also provides excellent professional development support (<https://www.postdoc.pitt.edu/resources>).

Interested candidates should email Dr. Alaasam (valentina.alaasam@gmail.com) with a brief summary of past experience, ideas for future research directions, a CV, and 2-3 references. Interviews will begin in late October, 2026 and the position will remain open until filled.

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UPotsdam Germany Landscape Ecology

Postdoctoral Researcher (f/m/d) in Landscape Ecology & Biodiversity Science University of Potsdam, Germany — Ref. 345/2026 The Landscape Ecology Group at the University of Potsdam invites applications for a 3-year postdoctoral position (100% We work at the interface of biodiversity science, trait-based and functional ecology, spatial/community ecology, and quantitative modelling, aiming to understand and predict biodiversity patterns across spatial scales. The position offers substantial intellectual freedom to develop an independent research profile. The specific research focus will be developed together with the successful candidate and may connect with ongoing work on biodiversity change, ecological forecasting, spatial ecology, and functional approaches to communities in changing landscapes. The position also includes teaching in the BSc Geoökologie and MSc CLEWS programmes (ap-

proximately one-third of working time). We are looking for candidates with: - PhD in ecology, biodiversity science, environmental science, or a related field - Independent research experience and scientific publications - Teaching experience at BSc and/or MSc level - Strong quantitative skills and experience with reproducible workflows in R and/or Python - Fluency in English Deadline: 18 September 2026 Reference: 345/2026 Full details and application instructions: https://www.uni-potsdam.de/fileadmin/projects/verwaltung/docs/Dezernat3/Ausschreibungen/2_akaPersonal/345_2026_MNF_LandEcol.pdf Informal inquiries are welcome: Prof. Bertrand Fournier – bertrand.fournier@uni-potsdam.de

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Uppsala Sweden-Postdoc in Aquatic Ecosystem Resilience and Climate Adaptation

Uppsala, Sweden - Postdoc in Aquatic Ecosystem Resilience and Climate Adaptation

Application deadline: 17. August 2026.

The postdoc position is for 2 years, based at the Dept. of Aquatic resources at the Swedish University of Agriculture Sciences <https://www.slu.se/en/about-slu/organisation/departments/aquatic-resources/>) with Dr. Ostman (<https://www.slu.se/en/profilepages/o/orjan-ostman/>) as mentor. The position offers opportunities for career development at the interface between ecological research and practical management by combining fundamental ecological and evolutionary research with applied management science to address: i) Which management interventions most effectively increase resilience to climate change in aquatic ecosystems, ii) How do dispersal, ecological interactions and evolutionary adaptation influence the success of climate adaptation measures, and iii) How can evidence synthesis be translated into practical decision support for environmental managers? You will apply systematic reviews, meta-analyses and other evidence synthesis methods to answer these questions. The work includes close collaboration with practitioners to ensure scientifically robust and practically relevant guidance for climate adaptation.

Necessary competences and qualifications: PhD in Biology (Ecology/Evolution), Environmental science or similar discipline.

Beneficial competences: Systematic reviews, meta-analyses or other relevant evidence-synthesising methods should have formed a central part of your thesis or academic career. Experience of research relevant for environmental management, decision support or governance of aquatic resources, and collaborating with practitioners, especially in coastal and marine areas, is an advantage.

For enquiries regarding the position and research topic please contact Dr. Orjan Ostman: orjan.ostman@slu.se

Please apply via the following link: <https://www.slu.se/en/about-slu/work-at-slu/jobs-and-vacancies/postdoktor/> Applications should be written in English and contain 1) a cover letter describing your motivation for the position, your skills and qualifications in relation to the advertised profile, and contact details for two reference persons, 2) a CV documenting your academic career and education with a publication list, and 3) a PhD degree diploma and transcripts of academic records.

Mejl som skickas till SLU blir allman handling. Vi behandlar även dina personuppgifter (<https://www.slu.se/personuppgifter>) när du mejlar oss.

Emails sent to SLU become official documents. We also process your personal data (<https://www.slu.se/en/about-slu/contact-slu/processing-of-personal-data-at-slu/>) when you email us. — När du skickar e-post till SLU så innebär detta att SLU behandlar dina personuppgifter. För att läsa mer om hur detta går till, klicka här (<https://www.slu.se/om-slu/kontakta-slu/personuppgifter/>) E-mailing SLU will result in SLU processing your personal data. For more information on how this is done, click here (<https://www.slu.se/en/about-slu/contact-slu/personal-data/>)

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USA CA Northridge Ecological modeling of plants reproductive niches

The Yoder Lab at CSUN invites applicants for the role of postdoctoral research fellow. The successful applicant will take a collaborating role in a new NSF-funded project (<https://lab.jbyoder.org/2026/06/29/the-yoder-lab-is-building-the-tardis-with-new-support-from-nsf-biodiversity-r-ecology/>) in ecological data science, refining and applying an analysis pipeline, TARDIS, to study plant populations' responses to environmental variation over space and time. They will work with PI Jeremy Yoder and collaborators at Yale University to complete development of a TARDIS package for R, use simulation studies to better understand the pipeline's capabilities, and assist in management of a course-based undergraduate research experience, in which students will build TARDIS models of individual plant species. The full project description is available for download here (<https://drive.google.com/file/d/1AG6y4MFyQCxMQ7UytmtY77YgkVYaH2a/view?usp=sharing>).

The successful applicant will have: - A doctorate with dissertation research in plant ecology, evolutionary biology, or a closely related field, or a planned doctoral dissertation defense and graduation date prior to starting the position; - Demonstrated experience with data science and programming in R, especially working with ecological and/or geospatial data; - Research interests aligned with the project aims and/or the Yoder Lab's research focus (<https://lab.jbyoder.org/projects/>); - Excellent written communication skills and strong familiarity with "classic" and contemporary research on geographical ecology. The most competitive applicant will also have demonstrated experience in one or more of the following: - Species distribution modeling; - Applications of machine learning in ecology; - Empirical or simulation/theory studies of population demography; - Phylogenetic comparative methods; - Developing and publishing R packages. Hybrid work will be possible for many planned project activities, but the postdoc must live within a commutable distance of the CSUN campus at their position start date, and be able to attend meetings in person on campus multiple days per week. The starting date is negotiable, but would ideally be no later than the first quarter of 2027. The project plan and budget provide: - Up to three years

of salary, pending satisfactory progress in the first year, starting at \$71,400/year with benefits and a planned COLA as specified by University policy; - Support for travel to attend conferences and to meet with collaborators at Yale University; - A postdoctoral mentoring plan, in which the postdoctoral fellow will work with PI Yoder to identify and pursue useful professional development opportunities, and to gauge progress towards project aims and their long-term career goals. To apply, please send a CV with complete publications list and a cover letter (two pages, maximum) that clearly explains how you meet the criteria described above to jeremy.yoder@csun.edu. Questions about the project, the postdoctoral position, and the application process may also be directed to this address. Review of applications will continue until a finalist is hired, but for full consideration please submit your materials by Sunday, 6 September, 2026.

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USA WashingtonU Rogers Lab

The Rogers Lab aims to discover genetic solutions that help organisms overcome evolutionary challenges. When organisms are faced with rapid or drastic shifts in selective pressures, how do different sources of genetic variation help them adapt to changing environments? We study the role that complex mutations like duplications, deletions, rearrangements, and TE movement play in evolutionary change. We suggest that complex mutations may function as the "Hopeful Monsters" of the genetic world, offering a key source of evolutionary innovation.

We are searching for postdocs to work in evolutionary genomics of structural variation, gene duplications, and transposable elements. We study these mutations in a variety of organisms including non-model systems with new genetic resources. Existing datasets within the lab can be leveraged for insight regarding how population size influences evolutionary outcomes. We have whole genome data for freshwater mussels, fireflies, elephants, and *Drosophila*. Current funding could support new sequencing for genomes and transcriptomes in other organisms of interest or new analyses could be implemented on public data. Postdocs must be committed to scientific publication.

The ideal postdoctoral candidate will have strong ex-

perience in coding, data analytics, and HPC usage, although experimental lab expertise will be beneficial as well. We hope to find lab members who are excited to address open questions in evolutionary theory that help us better understand how genomes evolve. Members of the lab are expected to contribute to the research community and benefit from local evolutionary genetics working groups, seminar series, and conferences. Established lab members can gain experience in mentorship with undergraduates if desired. Remote positions cannot be considered, so postdocs should expect to work on the GW campus in newly remodeled lab space.

The DC Area offers vibrant social and personal opportunities including museums, live performances, outdoor activities, and a vibrant restaurant scene. Postdocs at GW are eligible for Benefits (https://hr.gwu.edu/postdoc_benefits) including retirement plans, medical, dental, and vision insurance. Compensation will follow NIH pay scales.

Interested candidates should email Rebekah.Rogers@gwu.edu to discuss their research interests and the application process. All hires are subject to HR approval, a background check, and valid work authorization status. Initial appointments will be for 1 year with the option for renewal given positive performance.

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UTexas Austin Evolution Genomics Mitochondria

Postdoc: UTexas.Austin.Evolution.Genomics.Mitochondria

The Havird Lab at the University of Texas at Austin is looking for an enthusiastic and motivated postdoctoral researcher. Our group is generally focused on the evolution, genomics, and physiology of mitochondria. We are especially interested in researchers that will contribute to an ongoing project examining the role of mitochondrial interactions and incompatibilities at species boundaries, but are also open to independent research aligned with interests of the lab. Ongoing projects in the lab examine coevolution between mitochondrial and nuclear genomes, molecular evolution of organellar genomes, the roles of mitochondrial processes in health/disease, and ecophysiology/environmental adaptation. Multiple organismal systems are used in the lab, including microbes, plants, and animals, as well as making use of existing publicly available

genomic datasets. Desirable experience/interests include: - Genomic sequencing/assembly techniques and GWAS-type approaches - Biochemical assays of mitochondrial function and metabolic rate (e.g., seahorse, O2K) - Examining environmental adaptation via molecular and physiological approaches - Broad intellectual interests and enthusiasm for addressing evolutionary questions - Motivation and ideas for seeking independent postdoctoral funding - Mentoring of undergraduate researchers - A desire to foster a positive, fun, and collaborative research environment

Our lab uses large sequencing datasets in many projects, so previous experience in bioinformatics is strongly desired. We are part of the growing Integrative Biology Department at the University of Texas, which has strengths in evolution, genomics, and ecology. Postdocs should therefore expect a large network of colleagues and collaborators across campus. The University of Texas is located in Austin, TX, which is known for its high quality of life, environmental awareness, outdoor culture, live music, and eccentricity. If you are interested in joining the lab or learning more, please email Justin Havird (jhavird@utexas.edu) and provide a statement describing your research interests, career goals, and how you would complement the interests of the lab, along with a current CV ("Boilerplate" correspondence reminiscent of spam will likely be ignored). Timing is flexible, with an anticipated start date sometime in Fall 2026 or Spring 2027. Justin Havird Associate Professor Integrative Biology Dept. (<https://integrativebio.utexas.edu/>) University of Texas <https://sites.utexas.edu/havird/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UWarwick Postdoc in Immune Gene CNVs

We are looking for a postdoc to join our BBSRC/NSF-funded project looking at how gene copy number variation shapes host-microbe interactions.

We welcome applicants from organismal biology, evolutionary ecology, developmental biology, immunology, genomics, or bioinformatics backgrounds. You should

have a strong interest in connecting genomic variation to phenotype and have hands-on 'omics experience in an invertebrate or non-model system. Comfort with both wet-lab and computational work is essential; transgenics experience is a bonus.

This is a two-year position. Application deadline: 6th September 2026. For more details and to apply: <https://warwick-careers.tal.net/vx/lang-en-GB/mobile-0/appcentre-1/brand-4/user-11595/xf-54f73e1b5030/candidate/so/pm/1/pl/3/opp/4669-Research-Fellow-112033-0826/en-GB> Informal enquiries: Ed Smith, ed.g.smith@warwick.ac.uk

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WashingtonStateU Evolutionary Genomics

Postdoctoral Associate in Evolutionary Genomics (term, remote)

Contractual term postdoc to work remotely on whole genome analyses of repeatability of evolution and coevolution in Tasmanian devils and their transmissible cancer, devil facial tumor disease. The successful candidate will be employed by Washington State University and can capitalize on a massive dataset that includes hundreds of whole genomes, transcriptomic and genome-wide SNP capture panels, which are complemented with 25 years of mark-recapture and ecological data in this extremely well-studied natural system. Required are a PhD in Biology, Bioinformatics or related field with very strong bioinformatics, computational skills and an emphasis on evolutionary biology/ genomics. Peer-reviewed publications demonstrating this expertise are also required. Preferred: some postdoctoral experience. Start date: October/November, 2026 (specific date negotiable). Position term: up to 6 months with possible extension depending on funding. Salary: competitive based on experience. Benefits ineligible. Please contact Andrew Storfer (astorfer@wsu.edu) and attach CV for more information.

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Aarhus Denmark PhDcourse eDNA methods in ecology and conservation

Environmental DNA (eDNA) methods in ecology and conservation

Course parameters: Language: English Level of course: PhD course (Masters can participate) Time: 9am-5pm 19th - 23rd October 2026 Capacity limits: 25 Course fee: The course is free of charge for Danish PhD students. PhD students from outside of Denmark will pay a fee of 2000 DKK ECTS credits: 4

Objectives of the course: Environmental DNA (eDNA) is a powerful and rapidly advancing tool in ecological and conservation research. By analysing genetic material collected directly from environmental samples such as water, soil, sediment, and air, eDNA enables non-

invasive biodiversity monitoring, species detection, and ecosystem assessment across a wide range of environments. The aim of this course is to introduce eDNA based techniques to students in ecology and conservation, giving them an overview of the state of the field and a chance to discuss the degree to which eDNA based methods are the appropriate tool to answer their research questions. This PhD school provides an introductory, interdisciplinary overview of eDNA methods and their applications in ecology, conservation biology, and environmental monitoring, with examples spanning freshwater, marine, terrestrial, airborne, and arctic ecosystems.

Key Topics: - Study design and sampling strategies for eDNA - Demonstration of eDNA sampling techniques in the field - water, soil, air! - Overview of Bioinformatics workflows and taxonomic assignment - Applied eDNA for biodiversity monitoring and ecosystem management - Strengths, limitations, and future directions of eDNA approaches

The course will comprise lectures, keynote presentations from leading eDNA researchers, practical (literature-based) group-exercises and presentations.

Learning outcomes and competences: At the end of the course, the student should be able to: - Describe what eDNA is, how it can be used to answer a range of research questions in ecology and conservation and what the main strengths and weaknesses are. - Describe how eDNA methods are used today, both in research and by government and biomonitoring agencies, across aquatic and terrestrial habitats. - Account for the main methods, barcoding genes, reference platforms, primer pairs and PCR and sequencing technologies that can be used to target different groups of organisms. - At the end of the course, students will have a solid understanding of the molecular workflow and the required analysis choices to successfully plan an eDNA based scientific study. - Ability to judge whether a research question can be answered using eDNA techniques. - Critically evaluate published eDNA research.

Prerequisites: None Place: Aarhus University, Riso, Frederiksborgvej 399 4000 Roskilde Denmark

Registration: Please fill out the form: Environmental DNA (eDNA) methods in ecology and conservation: <https://forms.office.com/Pages/ResponsePage.aspx?id=Nh39Ycv-yke319DfA3ChmBBG7vLeBjRCrm012hFSbfVUMkYORU1F0DBRQUFHTEpKMkxQSkpGUEhWUY4u> Deadline for registration is 31st August 2026. Information regarding admission will be sent out no later than Friday 4th September.

If you have any questions, please contact one of our coordinators: Georgina Brennan (g.brennan@ecos.au.dk) Aoife Leonard (aleonard@ecos.au.dk) Adam Kozoi (adamkoziol@ecos.au.dk) Rumakanta Sapkota (rs@envs.au.dk)

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BogotaColombia Phylogenetics Workshops HennigXLIH Nov6-16 Deadline Aug31

PHYLOGENETICS WORKSHOPS AT THE XLIII HENNIG MEETING Bogota, Colombia, and online 6-8 and 14-16 November 2026 Pre-registration closes 31 August 2026

The Willi Hennig Society offers three workshops in connection with its XLIII Annual Meeting (9-13 November 2026, Universidad Nacional de Colombia, Bogota, Colombia). Each workshop costs USD 100 and admits up to 30 participants. Attendance at the meeting is not a requirement.

1. PHYLOGENETIC ANALYSIS AND USE OF TNT: 6-8 November 2026, Bogota. Instructors: Pablo Goloboff (Unidad Ejecutora Lillo, FML-CONICET, Argentina) and Michael Pittman (The Chinese University of Hong Kong).

Tree analysis with TNT, taught by the author of the program. The workshop covers tree searches, support measures, and the analysis of large matrices.

2. PHYLOGENOMICS: FROM GENOME-SCALE DATA TO EVOLUTIONARY INFERENCE: 14-16 November 2026, Bogota. Instructors: Cinthy Lorena Jimenez Silva (University of Auckland, New Zealand), Jordan Douglas (Australian National University, Australia), and Ambrosio Torres (Museum fur Naturkunde, Berlin, Germany).

Analysis of genome-scale data, from assembled sequences to phylogenetic inference.

3. PHYLOGENETIC BIOGEOGRAPHY WITH PHY-GEO: 14-16 November 2026, online. Instructor: J. Salvador Arias (Instituto de Biologia Subtropical, CONICET-UNaM, Argentina).

Phylogenetic biogeography with PhyGeo, taught by the author of the program. This workshop runs online, so participants may join without traveling to Bogota.

PRE-REGISTRATION

Workshops 2 and 3 share the same dates, so each participant may take only one of them. Pre-register here:

<https://www.google.com/url?q=https://forms.gle/3kkXKUHCuDpvJVdG8&source=gmail&ust=1786655915915000&sa=E> Applicants then receive payment

instructions by email, and payment confirms the place. The deadline is 31 August 2026.

TRAVEL AWARDS

The Willi Hennig Society funds students, postdoctoral researchers, and early-career researchers who present at the XLIII Annual Meeting. Priority goes to students who present their work and also participate in one of the workshops. Applications close on 31 August 2026, the same day as workshop pre-registration. Details and the application form are at <https://www.google.com/url?q=https://cladistics.org/awards/&source=gmail&ust=1786655915915000&sa=E>. CONTACT

Local organizers (Universidad Nacional de Colombia): hennigXLIII_bog@unal.edu.co

Willi Hennig Society: hennig.society@gmail.com

Meeting page: <https://www.google.com/url?q=https://cladistics.org/meetings/&source=gmail&ust=1786655915915000&sa=E> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

Course Online Advanced QGIS Spatial Analysis

Hello EVOLDIR members Geographic data can clarify how environmental patterns relate to biological variation. Advanced QGIS: Spatial Analysis led by Nick Bearman (University College London and Geospatial Training Solutions) is now available as an on-demand streaming seminar. Spatial overlays, point-based access analysis, spatial joins, and metric creation support investigation of geographic patterns in evolutionary and ecological data. Researchers can integrate coordinates, postal data, and other GIS sources to examine distributions, habitats, and spatial relationships relevant to their questions. Critical interpretation of spatial data methods helps align analytical choices with the limits of available evidence. Course details: The full course outline is available on the Instats course page.

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Live online course Model-Based Evolutionary Biogeography

Dear colleagues, Registration is open for Transmitting Science's live online course "Model-Based Statistical Inference in Evolutionary Biogeography" Instructor: Dr. Nick Matzke (University of Auckland, New Zealand). Course webpage: <https://www.transmittingscience.com/courses/evolution/model-based-statistical-inference-evolutionary-biogeography-2/> This course offers a structured, hands-on introduction to methods for inferring historical biogeography using phylogenetic and spatial data. Participants will learn how to estimate ancestral geographic ranges, compare probabilistic models, and interpret biogeographic patterns using real data. The course moves from introductory training in R, phylogenies, and BioGeoBEARS, through likelihood-based model testing and visualisation, to advanced topics such as trait-dependent dispersal, state-dependent diversification models, and large-scale analyses using PhyBEARS.jl in Julia. It also incorporates the integration of GIS and paleogeographic data (e.g., via GPlates), equipping participants with a comprehensive toolkit for studying lineages across space and time. For any questions, please write to courses@transmittingscience.com Best regards, 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 Advanced QGIS Spatial Analysis 2 0 Aug11-12

Hello EVOLDIR members

A reminder - Map geographic patterns that can sharpen questions about populations and environments. Advanced QGIS: Spatial Analysis 2.0 is a 2-day seminar livestreaming August 11-12 with Nick Bearman (University College London and Geospatial Training Solutions). Spatial overlays, point-based access analysis, and spatial joins can turn occurrence records and environmental layers into interpretable geographic mea-

sures. Learn to integrate XY coordinates, postal data, and other GIS sources, then aggregate results into research metrics. Apply these QGIS techniques to investigate spatial patterns relevant to evolutionary and ecological research.

Details and registration: The seminar page includes the full schedule and registration details. Best wishes

Michael Zyphur Professor and Director Instats

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Online Advanced R Programming 27-30 October

Dear all,

Registrations are now open for the 4-day online course - Beyond Beginner R: Advancing Your Coding Skills - 27-30 October.

Course website: <https://www.physalia-courses.org/courses-workshops/course47/>

The course covers advanced R programming, project organisation, functional programming, reproducible reporting with Quarto, publication-quality visualisation with ggplot2, version control with GitHub, and the critical use of AI coding assistants.

Requirements: working knowledge of R, including data frames, vectors, basic functions and plotting, plus familiarity with RStudio and R projects.

The course will run 13:00-19:00 Berlin time each day and will combine practical exercises with discussion.

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 AI for Data Visualization and Dashboards

Hello EVOLDIR members

Clarify complex evolutionary evidence through accessible, reproducible visual communication. AI for Data Visualization and Dashboards led by Hadi Fariborzi (Bissett School of Business, Mount Royal University, Calgary) is now available as an on-demand streaming seminar. Create reproducible visualizations and dashboards from quantitative, spatial, temporal, textual, and mixed-methods data using AI-assisted workflows. Practice data cleaning, chart selection, calculated measures, annotation, accessibility checks, and cross-platform replication with ChatGPT, Power BI, Tableau, Python, and R. Evolutionary researchers can apply these methods to communicate genetic, trait, geographic, or temporal evidence with transparent visual narratives.

Course details: Further information is available on the Instats course page.

Best wishes

Michael Zyphur Professor and Director Instats

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Online Analysis of DNA Methylation 20

Hello EVOLDIR members

Epigenetic variation can be investigated alongside evolutionary and genomic processes. Analysis of DNA Methylation 2.0 led by Aline Muyle (Institute of Evolutionary Science of Montpellier (ISEM)) is now available as an on-demand streaming seminar. Process WGBS, PacBio, and Oxford Nanopore data to infer methylation patterns from genome-scale sequencing. Analyse cytosines, differentially methylated regions, haplotype-specific methylation, gene expression, and natural selection using bioinformatic workflows and R. Apply these methods to evolutionary questions in organisms with

a draft reference genome, including epigenetic diversity and adaptation.

Course details: The full course outline is available on the Instats course page.

Best wishes

Michael Zyphur Professor and Director Instats

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Online Ancient DNA Analysis Oct26-30

Ancient DNA Analysis (ADNA01) - Applications for Evolutionary Biology <https://prstats.org/course/ancient-dna-analysis-adna01/> Delivered by experienced researchers in ancient DNA, palaeogenomics, bioinformatics, and population genomics. Learn how to analyse ancient DNA (aDNA) using modern bioinformatics workflows, with methods that are transforming evolutionary biology, population genetics, palaeogenomics, and evolutionary genomics. The course covers the complete analytical workflow, from sequencing data processing and authentication through to population genomic analyses and evolutionary interpretation. Ancient DNA has revolutionised evolutionary biology by providing a direct genetic window into the past. Rather than inferring evolutionary history solely from modern genomes, researchers can now reconstruct demographic history, investigate natural selection, quantify admixture and introgression, trace migration events, and study adaptation through time using DNA recovered from ancient specimens. This course provides comprehensive, hands-on training in the bioinformatics and analytical methods required to process, analyse, and interpret ancient genomic datasets. What you'll gain - A strong understanding of ancient DNA technologies and laboratory challenges - Practical experience processing and analysing ancient sequencing datasets - Skills in quality control, authentication, mapping, variant calling, and population genomic analyses - Understanding of contamination assessment, DNA damage patterns, and downstream evolutionary analyses - Confidence applying ancient DNA methods to evolutionary research Course format - Live, instructor-led online training - Hands-on bioinformatics using real ancient DNA datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready

workflows Who is this course for? - Evolutionary biologists - Population geneticists and evolutionary genomic researchers - Palaeogeneticists and molecular evolution researchers - Bioinformaticians and computational biologists - PhD students and quantitative life scientists Why take this course? Ancient DNA has fundamentally changed our understanding of evolution by allowing researchers to observe evolutionary change directly through time. These methods are increasingly used to reconstruct population histories, identify adaptive evolution, investigate hybridisation and introgression, estimate historical effective population sizes, and examine the genetic consequences of climate change, extinction, and domestication. As sequencing technologies continue to advance, ancient DNA has become an essential tool for studying evolutionary processes across humans, animals, plants, and other organisms. This course equips you with the practical skills needed to process, analyse, and interpret ancient DNA sequencing data using modern bioinformatics workflows. Whether you're studying population history, adaptation, speciation, phylogeography, natural selection, domestication, or evolutionary genomics, you'll gain the analytical toolkit needed to confidently apply ancient DNA methods to your own evolutionary research. Learn more & enrol PR Stats course page for Ancient DNA Analysis (ADNA01) <https://prstats.org/course/ancient-dna-analysis-adna01/> Questions? Email: oliver@prstats.org

Oliver Hooker Managing Partner

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

Online Backbone of biodiversity data for anyone working with species

Dear EvolDir community,

How important are species' names in your research? Do they not really matter, or are they crucial to the integrity of your study? How confident are you in your species names – how did you identify them? Could someone else pick up where you leave off, or is your biodiversity data not repeatable?

To orient anyone to the above questions, I'm very excited to open the registration for a crash course enti-

titled "Decoding Species: The Foundation of Biodiversity Data": <https://www.transmittingscience.com/courses/evolution/decoding-species-the-foundation-of-biodiversity-data/> The course will be in English and will address: - How to view species identification as a diagnostic process - Can you trust the names in data repositories, such as GBIF or GenBank? - Do you have one species or two, or subspecies? What is a species? Is it fluid? - Why do species' names change? - How to tell if you have a new species, and what to do about it. - What is the impact of these problems on conservation? - What is the "dark taxa" problem? - The future of identifying species with AI and genomics/barcoding This is a topic that is largely ignored by universities, so researchers are not getting this foundation before launching their projects. Therefore, this course is aimed at working professionals but students are also welcome.

Do not hesitate to send me questions about the course: bernardj@hawaii.edu. For questions regarding registration, please contact courses@transmittingscience.com.

Thank you, Jared Bernard

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Online ChatGPT with Stata Panel Data Analysis

Hello EVOLDIR members

Develop a stronger framework for analysing change across populations and time. ChatGPT with Stata: Panel Data Analysis led by Tor Georg Jakobsen (Norwegian University of Science and Technology) is now available as an on-demand streaming seminar. Model longitudinal genetic and population data using pooled, fixed, random, and dynamic panel approaches. Assess temporal relationships while accounting for unobserved differences among populations, species, or study units. Use Stata commands and AI-assisted troubleshooting to select models and interpret results for evolutionary research.

Course details: Please circulate this information if it is relevant to colleagues or students.

Best wishes

Michael Zyphur Professor and Director Instats

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Online Course on the Analysis of DNA Methylation

Dear all, I teach an online seminar on the Analysis of DNA Methylation, available for replay: <https://instats.org/seminar/analysis-of-dna-methylation-20-1> Please do not hesitate to contact me if you have any question. Best wishes, – Aline Muyle CNRS researcher <https://sites.google.com/view/muyle-lab/home> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Functional Trait Space Analyses in R 14-16September

Dear all,

We are pleased to announce the upcoming online course Functional Trait Space Analyses in R, taking place from 14 to 16 September.

Course website: <https://www.physaliaa-courses.org/courses-workshops/functional-trait-space-analyses-in-r/>

This course provides a combination of theoretical background and hands-on practical sessions in R, offering participants an overview of current approaches and tools for functional trait space analyses.

Throughout the course, participants will learn how to:

- Understand the theory and methods underlying functional trait space analyses
- Build, visualise and interpret functional trait spaces
- Apply methods including SMA regression, PCA and kernel density approaches
- Link functional trait spaces to other ecological dimensions
- Use R packages such as smatr, TPD and funspace
- Explore intraspecific trait variability and resampling approaches
- Plot and export the results of functional trait space analyses

Basic experience with R is strongly recommended. All slides and R scripts will be shared with participants and explained in detail during the course.

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

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

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Online IntroductionToComputationalBiology

We are pleased to announce Introduction to Computational Biology, a five-day online hands-on training course taking place 28 September-2 October.

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

The course provides an introduction to modern computational approaches used in genomics, transcriptomics, and multi-omics research, combining short lectures with practical, project-based learning using real biological datasets.

Topics covered include: -Long-read sequencing & genome assembly -Metagenomics & pangenomics - Single-cell RNA sequencing -Metabolomics & multi-omics integration

Throughout the course, participants will work in small groups on guided mini-projects, developing practical skills in data analysis, biological interpretation, and scientific communication. The course is aimed at PhD students, early-career researchers, wet-lab biologists, researchers transitioning into computational biology, and industry professionals working with genomic or multi-omics data.

For the full list of our courses and workshops, please visit: <https://www.physalia-courses.org/courses-workshops/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Introduction to QGIS Spatial Data

Hello EVOLDIR members

Spatial evidence can clarify patterns across populations, environments, and distributions. Introduction to QGIS & Spatial Data led by Nick Bearman (University College London and Geospatial Training Solutions) is now available as an on-demand streaming seminar. Learn to import, explore, join, classify, and style vector and raster spatial data in QGIS. Build publication-ready maps with legends and scale information while preparing spatial data for analysis. Evolutionary researchers can apply these methods to map genetic variation, species distributions, and other geographically structured evidence.

Course details: The course page includes the curriculum and enrollment details.

Best wishes

Michael Zyphur Professor and Director Instats

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Online Introduction to Spatial Data and R as a GIS 2 0 Aug18-19

Hello EVOLDIR members

A reminder - Explore geographic patterns alongside evolutionary and genetic evidence. Introduction to Spatial Data and R as a GIS 2.0 is a 2-day seminar livestreaming August 18-19 with Nick Bearman (University College London and Geospatial Training Solutions). Import, manage, process, and map spatial data in R using spatial formats and the sf library. Create choropleths, customise map presentation, automate repeated outputs, and introduce interactive maps. Evolutionary researchers can apply these techniques to visualise geographic patterns in populations, traits, and genetic data.

Details and registration: Further information is available on the seminar page.

Best wishes

Michael Zyphur Professor and Director Instats

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Online Invasion Genomics in R 12-14-16October

Dear all, Registrations are open for our online course "Invasion Genomics in R", taking place 12, 14 & 16 October.

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

Designed to foster international participation, the course combines recorded lectures, self-paced practical tutorials with annotated R scripts, and live remote instructor support. Participants can progress through the materials at their own pace while having the opportunity to ask questions and discuss challenges with the instructor. The format is particularly suited to participants across different time zones.

The course provides a practical introduction to invasion genomics, focusing on three key themes: - Movement dynamics – investigating invasion sources, dispersal pathways, genetic diversity, and population structure - Adaptation dynamics – applying selection outlier detection methods to investigate adaptive processes - Environmental adaptation – using genotype-by-environment association (GEA) methods to explore how environmental conditions shape adaptive outcomes The course is aimed at graduate students, researchers, and professionals interested in applying genomic approaches to invasion biology.

Includes: Recorded lectures, guided practicals, annotated R scripts, and live remote support Participants will gain both fundamental knowledge and practical experience to help them apply invasion genomic approaches in their own research.

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

Best regards,

Carlo

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

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Online live course:Species concepts in biodiversity studies

Dear Evoldir members, Transmitting Science is offering the short live online course "Decoding Species: The Foundation of Biodiversity Data". Course webpage: <https://www.transmittingscience.com/courses/evolution/decoding-species-the-foundation-of-biodiversity-data/> Species are the basic units of biodiversity, and therefore the basic units in many ecology, evolution, and conservation biology studies, yet most researchers receive little formal training in what defines a species or how much biodiversity remains hidden, which can impact their research. This short course addresses the basic concepts you need to know to work with biodiversity in your research. We will also discuss the changing role of taxonomy/systematics in an era of declining interest, genomics, and AI. For any questions, please write to courses@transmittingscience.com Best regards Sole – Soledad De Esteban-Trivigno, PhD Director Transmitting Science www.transmittingscience.com/courses Bluesky @soledeesteban.bsky.social X @SoleDeEsteban Orcid: <https://orcid.org/0000-0002-2049-0890> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Markov and Hidden Markov Models with R 1-4September

Dear all,

there are still a few seats for the upcoming online course Markov and Hidden Markov Models with Applications in R, taking place 1-4 September.

Course website: <https://www.physalia-courses.org/courses-workshops/markov-and-hidden-markov-models-with-applications-in-r/>

The course provides a practical introduction to Markov and hidden Markov models for longitudinal data, covering model specification, estimation, interpretation,

model selection, and applications to continuous and categorical data, including missing values.

Participants will gain hands-on experience applying these methods in R using the LMest package, with practical exercises and real-world examples throughout the course.

R experience: Basic familiarity with R is desirable but not required.

The course is suitable for students, researchers, and practitioners in academia, industry, and consultancy who want to learn how to apply Markov and hidden Markov models.

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 Metabolomics with R-Bioconductor 17-20November

Dear all,

the Physalia online course Metabolomics with R/Bioconductor will take place in November 17-20.

More information and registration: <https://www.physalia-courses.org/courses-workshops/course55/>

The course is aimed at students and researchers who want to learn how to work with metabolomics data in R and Bioconductor, covering the whole process from study design and data preprocessing to statistical analysis. We will work with both targeted and untargeted metabolomics data, with plenty of hands-on work in R. The practical sessions will include xcms, PCA, univariate and multivariate analyses, missing data and feature annotation.

The course will run online from 09:30 to 13:30 Berlin time each day and will combine lectures, practical exercises and discussions.

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

[rses-workshops/](https://www.physalia-courses.org/courses-workshops/) Best regards, Carlo —————
– Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR
info@physalia-courses.org

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

Online Metagenomic Data Analysis of Microbial Communities Oct26-30

Metagenomic Data Analysis of Microbial Communities (MGMC01) - Applications for Evolutionary Biology <https://prstats.org/course/metagenomic-data-analysis-of-microbial-communities-mgmc01/> Delivered by experienced computational biologists and microbiome researchers with expertise in metagenomics, microbial ecology, evolutionary genomics, and bioinformatics. Learn how to analyse shotgun metagenomic sequencing data to investigate the taxonomic composition, functional potential, and evolutionary dynamics of microbial communities. This course provides practical training in modern bioinformatics workflows for analysing complex metagenomic datasets. Metagenomics has transformed evolutionary biology by allowing researchers to study the evolution of entire microbial communities directly from environmental samples, without the need for cultivation. These approaches provide unprecedented opportunities to investigate microbial diversity, adaptation, natural selection, horizontal gene transfer, genome evolution, host-microbe co-evolution, and the evolutionary processes shaping microbial ecosystems. This course provides comprehensive, hands-on training in the computational analysis of shotgun metagenomic sequencing data, from quality control through to evolutionary interpretation. What you'll gain - A strong understanding of shotgun metagenomics and microbial community analysis - Practical experience processing and analysing metagenomic sequencing datasets - Skills in taxonomic and functional profiling of microbial communities - Understanding of microbial diversity, comparative genomics, and evolutionary analyses - Confidence applying metagenomic methods to evolutionary research Course format - Live, instructor-led online training - Hands-on bioinformatics using real metagenomic datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Evolutionary biologists - Evolutionary microbiologists and microbial ecologists - Population genomic and comparative genomic researchers - Bioinformaticians and

computational biologists - PhD students and quantitative life scientists Why take this course? Microbial genomes evolve rapidly, making metagenomics one of the most powerful approaches for investigating evolutionary processes in natural populations and communities. Researchers increasingly use shotgun metagenomics to study microbial adaptation, strain evolution, horizontal gene transfer, host-microbe coevolution, the evolution of antimicrobial resistance, and the functional evolution of microbial ecosystems. As sequencing technologies continue to advance, metagenomic analysis has become an essential tool for evolutionary research across environmental, host-associated, and experimental systems. This course equips you with the practical skills needed to process, analyse, visualise, and interpret metagenomic sequencing data using modern bioinformatics workflows. Whether you're studying microbial evolution, comparative genomics, adaptation, coevolution, environmental microbiomes, or evolutionary ecology, you'll gain the analytical toolkit needed to confidently apply metagenomic methods to your own evolutionary research. Learn more & enrol PR Stats course page for Metagenomic Data Analysis of Microbial Communities (MGMC01) <https://prstats.org/course/metagenomic-data-analysis-of-microbial-communities-mgmc01/Questions?> Email: oliver@prstats.org

Oliver Hooker Managing Partner

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

Online Multivariate Analysis of Biotic Communities

Hello EVOLDIR members

Develop a clearer analytical workflow for complex ecological and evolutionary datasets. Multivariate Analysis of Biotic Communities led by Oliver Miler (North-west Indian Fisheries Commission) is now available as an on-demand streaming seminar. Multivariate concepts, data preprocessing, R workflows, and visualization provide ways to examine biotic-community patterns alongside environmental variables. Work with ecological datasets to prepare data, manage missing values and transformations, and interpret multivariate results. Evolutionary researchers can apply these ap-

proaches when comparing community composition, environmental associations, and ecological context across study systems.

Course details: Further information is available on the Instats course page.

Best wishes Michael Zyphur Professor and Director Instats

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Online Network Analysis Systems Biology with R-Bioconductor 5-8 Oct

There are still a few seats available on the upcoming Physalia online course "Network Analysis in Systems Biology with R/Bioconductor", taking place 5-8 October. Course website: <https://www.physalia-courses.org/courses-workshops/network-in-systems-biology/>

This hands-on course will introduce methods for inferring, analysing, comparing, and integrating biological networks from RNA-seq data using R and Bioconductor.

Topics include: Gene co-expression networks (GCNs) Network comparison and functional analysis Network-based gene discovery and SNP-to-gene mapping Gene regulatory networks (GRNs) Network visualization The course is aimed at researchers and students in systems biology with a working knowledge of R. Familiarity with RNA-seq and Bioconductor is helpful but not essential.

For the full list of our courses and workshops, please visit: <https://www.physalia-courses.org/courses-workshops/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Phylogenomics 30November-4December

Dear all,

Join our Phylogenomics course, held online from 30 November to 4 December, and learn how to infer evolutionary relationships and divergence times from multilocus genomic data.

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

Across five hands-on days, you will learn how to: - Build and analyse phylogenomic datasets - Perform maximum-likelihood and Bayesian phylogenetic inference - Infer species trees under the multispecies coalescent - Detect and quantify introgression and gene flow - Estimate divergence times from genomic data The workshop combines lectures, practical exercises and expert-led discussion, with a strong focus on understanding methods and interpreting results rather than simply running software.

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
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Online PR stats upcoming live courses

Hi everyone, Below is a list of our upcoming live courses covering evolutionary biology and related methods, including population genetics, genomics, phylogenetics, bioinformatics, and computational approaches with strong applications to evolutionary research. Please feel free to share this email with colleagues, friends, and others within your institute, organisation, or wider re-

search network.

Bioinformatics / Genomics / Genetics Machine Learning for Evolutionary Genomics (MLEG01) <https://prstats.org/course/machine-learning-for-evolutionary-genomics-mleg01/> Machine Learning for Evolutionary Genomics: learn predictive modelling, data analysis, and AI methods for genomic data.

RNA-Seq Analysis (RNAA02) <https://prstats.org/course/rna-seq-analysis-rnaa02/> RNA-Seq analysis training - live online course covering experiment design, data QC, alignment, gene expression, DESeq2 differential expression, PCA, visualisation, and functional analysis.

Genomic Prediction of Complex Traits (GPCT01) <https://prstats.org/course/genomic-prediction-of-complex-traits-gpct01/> Genomic Prediction of Complex Traits: learn predictive modelling, polygenic prediction, and genomic methods for analysing complex traits.

Population Genomics and Structure Analysis (PGSA01) <https://prstats.org/course/population-genomics-and-structure-analysis-pgsa01/> Learn population structure analysis for evolutionary biology using genetic data, population genetics methods, and evolutionary inference.

Deep Learning for Evolutionary Genomics (DLEG01) <https://prstats.org/course/deep-learning-for-evolutionary-genomics-dleg01/> Deep Learning for Evolutionary Genomics: learn neural networks, predictive modelling, and AI methods for genomic data analysis.

Spatial Phylogenetics and the Bayesian Phylogenetic Mixed Model (PMM) (BPMM01) <https://prstats.org/course/spatial-phylogenetics-and-the-bayesian-phylogenetic-mixed-model-pmm-bpmm01/> Learn spatial phylogenetics and Bayesian phylogenetic mixed models in R. Practical online training in phylogenetic modelling and comparative workflows.

Single cell RNA-Seq analysis (SCRN03) <https://prstats.org/course/single-cell-rna-seq-analysis-scrn03/> Learn single cell RNA-Seq analysis with Seurat, 10x Genomics, and advanced QC methods. Gain cell type-specific insights in this live online course.

Ancient DNA Analysis (ADNA01) <https://prstats.org/course/ancient-dna-analysis-adna01/> Ancient DNA Analysis: learn bioinformatics workflows, population genetics, and genomic analysis for ancient DNA research.

Metagenomic Data Analysis of Microbial Communities (MGMC01) <https://prstats.org/course/metagenomic-data-analysis-of-microbial-communities-mgmc01/>

omic-data-analysis-of-microbial-communities-mgmc01/ Learn metagenomic data analysis for microbial communities. Analyse shotgun sequencing data, profile microbiomes, and interpret microbial diversity using R.

Genome-Wide Association Studies (GWAS) for Evolutionary Biology (GWAS01) <https://prstats.org/course/genome-wide-association-studies-gwas-for-evolutionary-biology-gwas01/> GWAS for Evolutionary Biology: learn genome-wide association studies, quantitative trait analysis & genomic methods for evolutionary data.

Ancient Environmental Metagenomics (AEMG01) <https://prstats.org/course/ancient-environmental-metagenomics-aemg01/> Ancient Environmental Metagenomics: learn bioinformatics workflows, taxonomic profiling, and genomic analysis of ancient environmental DNA.

Introduction to Snakemake (SNKM03) <https://prstats.org/course/introduction-to-snakemake-snkm03/> Learn Snakemake to automate data workflows. Build reproducible, scalable pipelines for research with hands-on training in this 4-day live online course.

Genomics and Bioinformatics for Non-Model Organisms (BNMO01)

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up

at <https://evoldir.net/brian/evoldir/evoldir.html>

Online scRNAseq With R Bioconductor 16-20November

Dear all,

Join our Single-Cell RNA-seq Analysis with R/Bioconductor course, taking place 16-20 November, online.

Course website: <https://www.physalia-courses.org/courses-workshops/course18/>

In this hands-on course, you'll learn the key steps of a modern scRNA-seq analysis workflow, from quality control and normalization to cell clustering, annotation and downstream analysis. Whether you are a biologist looking to analyse your own scRNA-seq data or a bioin-

formatician looking to strengthen your single-cell analysis skills, this course will provide a practical foundation for working confidently with scRNA-seq data.

You'll gain practical experience with: - Processing and QC of scRNA-seq data - Normalization and batch-effect correction - Dimensionality reduction and visualization - Cell clustering and annotation - Differential expression analysis - Pseudotime and temporal analysis - Reproducible R/Bioconductor workflows The course combines expert-led lectures with practical exercises, giving you the opportunity to apply the methods directly to real datasets and understand how to interpret the results.

For the full list of our courses and workshops, please visit our website: <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 Shotgun Metagenomics 23-26Nov

Dear all,

Join our online course on "Shotgun Metagenomics Processing and Analysis", taking place 23-26 November, designed for researchers and students who want to gain practical expertise in the analysis of high-throughput microbiome datasets.

Course website: <https://www.physalia-courses.org/courses-workshops/course33/>

Across four days, you will explore the complete metagenomics workflow – from raw data processing and taxonomic profiling to strain-level analysis, genome reconstruction, functional profiling, and advanced statistical approaches. Through a combination of expert lectures and hands-on sessions, you will work with leading bioinformatics tools and reproducible workflows used in modern microbiome research.

For the full list of our courses and workshops, please visit our website: <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 RNA-Seq Analysis 26-29Oct

Single-cell RNA-Seq Analysis (SCRN03) - Applications for Evolutionary Biology <https://prstats.org/course/single-cell-rna-seq-analysis-scrn03/> Delivered by experienced bioinformaticians with expertise in single-cell transcriptomics, RNA sequencing, and computational biology. Learn how to analyse single-cell RNA sequencing (scRNA-seq) data in R using Seurat, with methods that are increasingly relevant to evolutionary biology, evolutionary developmental biology, and comparative genomics. Single-cell transcriptomics makes it possible to study gene expression at the level of individual cells, revealing cellular diversity and regulatory variation that are often hidden in bulk RNA-Seq data. These approaches are opening new opportunities to investigate the evolution of cell types, developmental pathways, phenotypic diversity, adaptation, and gene regulation across populations and species. This hands-on course provides practical training in modern scRNA-seq workflows, including quality control, normalisation, clustering, dimensionality reduction, differential expression, and cell type identification. What you'll gain - A strong understanding of single-cell RNA-Seq technologies and experimental design - Practical experience analysing scRNA-seq datasets using Seurat in R - Skills in quality control, normalisation, clustering, dimensionality reduction, and cell type annotation - Understanding of differential expression analysis and downstream biological interpretation - Confidence applying single-cell transcriptomics to evolutionary research Course format - Live, instructor-led online training - Hands-on coding with real single-cell RNA-Seq datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Evolutionary biologists and evolutionary developmental biologists - Comparative genomic and transcriptomic researchers - Population geneticists and molecular evolution researchers - Bioinformaticians and computational biologists - PhD students and quantitative life scientists Why take this course? Single-cell transcriptomics is becoming an important tool for studying

how cellular functions, developmental programmes, and gene regulatory systems evolve. By comparing gene expression across cell types, tissues, populations, or species, researchers can investigate cell-type evolution, developmental divergence, adaptive responses, and the molecular basis of phenotypic innovation. This course equips you with the practical skills needed to process, analyse, visualise, and interpret single-cell RNA-Seq data using modern R-based workflows. Whether you're studying the evolution of cell types, developmental systems, gene regulation, adaptation, comparative physiology, or non-model organisms, you'll gain the analytical toolkit needed to apply single-cell transcriptomics confidently to evolutionary research. Learn more & enrol PR Stats course page for Single-cell RNA-Seq Analysis (SCRN03) <https://prstats.org/course/single-cell-rna-seq-analysis-scrn03/> Questions? Email: oliver@prstats.org

Oliver Hooker Managing Partner

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

Online Spatial Proteomics in R-Bioconductor 10-12November

Dear all,

We are pleased to announce the online course "Spatial Proteomics Data Analysis in R/Bioconductor: From Mass Spectrometry to Subcellular Maps", taking place 10-12 November (12:00-16:00 Berlin time each day).

Course website: <https://www.physalia-courses.org/courses-workshops/spatial-proteomics-in-r/>

This hands-on course will introduce participants to the analysis and interpretation of MS-based subcellular spatial proteomics data using R/Bioconductor tools and reproducible computational workflows. Through practical exercises, participants will learn data processing and quality control, exploratory analysis, protein annotation, dimensionality reduction, clustering, and machine-learning approaches for protein localisation prediction, culminating in the generation of comprehensive subcellular maps.

We welcome participants from around the world and encourage anyone interested in computational proteomics and subcellular protein localisation to join us.

For further information about our courses and workshops: <https://www.physalia-courses.org/courses-workshops/spatial-proteomics-in-r/>

Best regards,

Carlo

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

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

yond SNPs and small indels.

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

Best regards,

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

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Online Structural Variant Analysis 30 November-2 December

Dear all,

Structural variants are an important source of genomic variation, but their detection and comparison remain challenging. This three-day online course will provide a practical introduction to SV analysis, covering approaches based on both short- and long-read sequencing.

Registration is now open for the only Physalia course: Structural Variant detection and comparison.

30 November - 2 December — Online 14:00-20:00 Berlin time

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

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

- Identify Structural Variants using mapping or assembly approach
- Identify Structural Variants from long and short read data.
- Compare and filtering Structural Variants.
- Annotate of Structural Variants (gene overlap, Population frequency)
- Generate a trio / population VCF file for Structural Variants
- Identify mosaic / somatic Structural Variants

For researchers interested in evolutionary, comparative or population genomics, this is an opportunity to develop practical skills for studying genomic variation be-

Virtual RNAseq Analysis Aug25-27

The Computational Biology Core at the University of Connecticut is hosting virtual bioinformatics workshops this summer! We still have space available in our RNA-seq Analysis Workshop (virtual but live instruction - Aug. 25-27).

This hands-on workshop will guide participants through the complete RNA-seq analysis workflow using a reference genome and annotation. You'll learn about experimental design, high-throughput sequencing basics, quality control, alignment, differential expression analysis, and gene ontology/gene set enrichment—using real datasets and widely used tools.

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

Learn more & register here: [<https://bioinformatics.uconn.edu/cbc-workshops/>] (<https://bioinformatics.uconn.edu/cbc-workshops/>)

WHERE: Virtual (MS Teams) WHEN: 10:00 AM - 2:00 PM EST COST: \$500 (UConn affiliates)/\$600 (External participants)

Registration is first come, first served.

Questions? E-mail: cbcsupport@helpspotmail.com

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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.