EvolDir

June 2, 2026

Month in Review

Foreword

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

2026 AMS Meeting Registration DEADLINE May15

The Friday, May 15 registration and abstract deadlines for AMS 2026 are fast approaching! We look forward to receiving your registration and seeing you in Syracuse, June 15-19. Your presentation and poster contributions will help make this a great meeting. For any questions or issues, please contact Dr. Rebecca Rundell (`rundell@esf.edu`). You can complete your registration and abstract submission through the meeting website: `https://ams.wildapricot.org/AMS-2026`Our meeting features an opening session and Keynote speaker focused on Indigenous Mollusk Research, Uses, and Relationships. We are honored to celebrate the important connection between mollusks and North American history through wampum. For more information about our speakers, please see: `https://ams.wildapricot.org/AMS-2026-Program`Registration includes lunches catered by ESF's Trailhead Cafe each day (Tuesday, Wednesday, Thursday), two coffee/tea/snack breaks per day, and reception appetizers (Welcome, Poster, and Student Fundraising Auction receptions). The Banquet will be held at Ithaca's Museum of the Earth, within their Marvelous Mollusks exhibition. `https://www.museumoftheearth.org/exhibit/marvelous-mollusks` Banquet and field trip tickets are not included and must be purchased separately. Housing is available at ESF, right near the conference venue. Purchasing your housing with us is highly recommended, because it is affordable, convenient, and includes breakfast (and free parking)! Please note that there are no hotels in walking distance to campus. You can sign up for your housing here: `https://ams.wildapricot.org/AMS-2026-Registration`While you are registering, don't forget to add some conference merchandise to your purchase: `https://ams.wildapricot.org/AMS-2026-Merch`The AMS 2026 logo was designed by graphic artist Pablo Marin of Dega Designs: `https://degastudios.threadless.com/about`Items available include notebooks, keychains, stickers, bottle opener magnets, and t-shirts. Two design versions are offered (Pride logo and Blue logo). The 100There is also an optional workshop on Land Snail Identification Through Dissection, featuring hands-on training by Dr. Morgan Bullis (USDA APHIS). Space is limited. To sign up for the workshop, please contact Dr. Bullis directly at `morgan.bullis1@usda.gov` The optional field trip will be held on Friday, June 19, and will include a tour of Chittenango Falls State Park, home of the rare Chittenango ovate amber snail, followed by hands-on fossil collecting in New York's Devonian Seas. Boxed lunch and transportation are included. If you have any donations of items for our Student Fundraising Auction, please contact Rebecca Rundell at `rundell@esf.edu`. You can send items in advance (preferred) or bring them along. Items can be mailed directly to Rebecca at 1 Forestry Drive, Dept. of Environmental Biology, SUNY-ESF, Syracuse, NY 13210. We look forward to seeing you at the meeting! Thank you, Rebecca evoldir@evoldir.net) evoldir@evoldir.net)

Antwerp Belgium 7EuropeanConservationGeneticsMeeting new deadline

On August 26-28 this year, the 7th European Conservation Genetics Meeting will happen in Antwerp, Belgium. The deadline for submitting an abstract is now May 20th. The deadline for early bird registration is still June 15th.

Please visit our Website (7th European Conservation Genetics meeting - ZOO Science) with information on the themes, keynote speakers, preliminary schedule, abstract submission, registration/payment link, hotel accommodation and venue. (https://www.zooscience.be/en/7th-european-conservation-genetics-meeting/) This is an in-person meeting with 5 non-parallel sessions and poster sessions every day. We pay special attention to open (panel) discussions and early career researchers, and offer possibilities for an artistic experience and guided excursions to a nature reserve. Please, spread the news!

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Bangkok Nov2-6 Reminder 10th International Barcode of Life Abstract submiss

Dear friends and colleagues, This is a reminder that the abstract submission deadline for the 10th International Barcode of Life Conference is only two weeks away. Submit and secure a spot in one of our sessions. We are looking for abstracts across a wide range of topics related to our conference theme Building on Barcodes: Impacting Science & Society (https://dnabarcodingconference.com/abstracts/). The abstract submission deadline is May 29, 2026. Join us from November 2-6, 2026, in Bangkok to exchange the latest scientific discoveries and advancements in biodiversity genomics. Have a look at our impressive plenary speaker line up: https://dnabarcodingconference.com/program/plenary-speakers/We are looking forward to meeting you at the Siam Kempinski Hotel Bangkok, our venue for the conference. Ideally situated in the heart of Bangkok, the hotel is easily accessible via public transit, with direct connections to the BTS Skytrain at Siam Station and links to Bangkok's airport rail and metro systems. Sign up for our newsletter to make sure you don't miss anything: http://eepurl.com/jvhKFAAll the best, Dirk Steinke on behalf of the Conference Organizing Committee

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BournemouthU UK 8thInternationalMouseMeeting 9-11June2026

8th International Mouse Meeting Bournemouth University, UK 9 - 11 June 2026 (https://8thinternationalmousemeeting.my.canva.site/) The International Mouse Meeting series is a scientific conference where researchers from around the world gather to share and discuss the latest research on the evolutionary biology, population genetics, applied genetics, archaeology, behaviour and ecology of the house mouse (Mus musculus) and related species, focussing on wild populations or wild-derived individuals in a laboratory setting. The meeting has helped to foster the house mouse as one of the best-studied species from an evolutionary and population genetic standpoint, extending on the status of the species as the foremost laboratory model for mammals. The series began in 2009 in Plon, Germany, and has been held regularly since then, generally every two years and with about 50 participants. If you wish to attend, please register using the following link: (https://www.eventbrite.co.uk/e/the-8th-international-mouse-meeting-tickets-1984379596792?aff=oddtdtcreator) There is the opportunity to present a talk or a poster. Looking forward to seeing you at the meeting!

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Conference Portugal Jul8-10 EvolutionaryRoleOfStructuralVariation

CONFERENCE ON THE EVOLUTIONARY ROLE OF STRUCTURAL VARIATION 8th - 10th of July 2026, Vila do Conde, Portugal !!!! LAST CALL FOR REGISTRATION!!!! Dear colleagues, we still have a few places available for participating in the TIBE-STRiVE conference "Trends in Biodiversity and Evolution: the evolutionary role of structural genomic variation" (TiBE-STRiVE)" that will feature cutting-edge research presentations, foster interdisciplinary discussions, and initiate collaborative projects spanning the breadth of structural variant research (https://structuralvariantsstn.github.io/). Thanks to the very generous funding by the American Genetics Society recently awarded to TiBE-STRiVE, we decided to support: 1. Participants with dependent-care responsibilities 10 Childcare subsidies are available, which can be used to pay children travel and/or some accompanying person that takes care of them (max. of 250 euros per participant). If you are interested, please e-mail us as soon as possible (ruifaria@cibio.up.pt) to know the conditions and how to apply. 2. Participants from under-represented countries or facing additional costs linked to disability, accessibility, or social inequality. Support (amount not defined yet) will be available to pay costs related with accommodation and or travel costs. Please e-mail us as soon as possible (ruifaria@cibio.up.pt) to know the conditions and how to apply. IMPORTANT INFORMATION and LINKS: Venue-Location: Quinta do Crasto, Vairao, Vila do Conde, Portugal Dates of the conference: 8th to 10th of July, 2026 Registration deadline: 20 of May 2026 Websites: https://structuralvariantsstn.github.io/porto_about/ and/or https://tibe.biopolis.pt/ How to register: https://structuralvariantsstn.github.io/porto_registration/How to become STRiVE member (not mandatory to participate in the meeting): https://structuralvariantsstn.github.io/committee/Follow us on Bluesky (@strivestn.bsky.social) Looking forward to see you in TiBE-STRiVE! Rui Faria, PhD 1. Researcher and SEAGEN Group Leader CIBIO, Centro de Investigacao em Biodiversidade e Recursos Geneticos, InBIO Laboratorio Associado BIOPOLIS Program in Genomics, Biodiversity and Land Planning Campus de Vairao Rua Padre Armando Quintas, no 7 4485-661, Vairao, Portugal 2. Invited Assistant Professor, Department of Biology Faculty of Sciences at the University of Porto, Rua Campo Alegre s/n 4169-007, Porto, Portugal Webpages: Littorina Research Community https://littorina.at.biopolis.pt/https://rmigueldefaria.wixsite.com/farialab-1https://sites.google.com/biopolis.pt/littorina/winklewatch (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Firenze Evolution2026 Sep6-10

ITALIAN SOCIETY FOR EVOLUTIONARY BIOLOGY Congress 6-10 September 2026, Firenze, Italy ———1 week left to submit your abstract——————— Dear friends and colleagues, this is a friendly reminder that there is still 1 week left to submit your abstract for the SIBE Evoluzione 2026 Congress. We look forward to your contributions! The congress will take place in Firenze from 6 to 10 September. The scientific program will be organized around the following symposia: Symposium 1 "Host-microbiome interactions" Symposium 2 "Evolutionary roots of behavioural diversity" Symposium 3 "Phylogeography and Conservation Genomics: understanding evolutionary history to sustain species resilience" Symposium 4 "Human evolution" Symposium 5 "The evolution of ecological diversification: mechanisms, interactions, and outcomes" Symposium 6 "Evolutionary biology without borders" Each symposium will open with a plenary lecture by an international invited speaker, including Stephen Palumbi, Mihai Netea, David Caramelli, Martin Giurfa, Jacintha Ellers, Mirte Bosse, and Maurizio Mencuccini. In addition to the scientific sessions, the congress will offer several events, including a dedicated poster session, a free crash course on wet-lab techniques in genomics, the meeting of the Italian Group for Conservation Genetics and Genomics, the original outreach theatre event "Botanica Queer", and a social dinner at the Florence Botanical Garden. The congress will take place across several venues in the city. All scientific sessions will be held in the Novoli district, at the University's Social Sciences Campus, while social events and the poster session will take place in the historic city centre. Participants may therefore choose to stay either in the city centre or in Novoli, two areas conveniently connected by the tram line. Please note that the last tram runs at around 00:30; after this time, public transportation options become more limited. September is a high season for tourism in Florence, and other conferences are scheduled in the Novoli area during the same period. We therefore strongly recommend booking accommodation well in advance. For further details about Evoluzione 2026, please visit the website: `www.sibe-iseb.it/firenze2026`We look forward to welcoming many of you to Firenze, The Organizing and Scientific Committee

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JacquesMonod Roscoff France 21-25September2026

Jacques Monod - Roscoff, France - Mechanistic and evolutionary basis of programmed DNA elimination - 21-25 September 2026 The Jacques Monod Conference "Mechanistic and evolutionary basis of programmed DNA elimination" will be held from Monday September 21 to Friday 25, 2026 in Roscoff, France. It aims to bring together researchers working on DNA elimination as well as other unusual chromosome biology across the tree of eukaryotes. We would be very keen to include researchers working on related phenomena, such as drive and conflict, B chromosomes, and on the mechanisms and regulation of genome stability, chromosome segregation and germline development. Registration is open until May 20, 2026. Available slots for selected talks. Prices for poster and oral presentations from early career researchers. `https://cjm.sb-roscoff.fr/en/conference/mechanistic-and-evolutionary-basis-programmed-dna-elimination` Registration cost includes food and accommodation. Reduced rates for students. Also Roscoff is a fantastic place to visit and has great facilities (and food). Best wishes, Sandra Duharcourt and Laura Ross

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MPI Ploen Tracing Evolution through Cell Lineages Oct12-14

We are pleased to announce the symposium "Tracing Evolution through Cell Lineages", which will take place 12-14 October 2026 at the Max Planck Institute for Evolutionary Biology in Plon, Germany. This workshop aims to bring together researchers at the interface of evolutionary, developmental, and stem cell biology to explore how evolutionary change is mediated through cell lineages. While phenotypic evolution is often studied at the level of whole organisms, this symposium focuses on the cellular processes–cell states, lineage architecture, fate decisions, and dynamics–that ultimately generate morphological and functional diversity. Particular emphasis will be placed on how changes in lineage topology, timing, and spatial deployment contribute to the emergence of novel cell types and to phenotypic diversification across and within taxa. The workshop will begin with a kick-off session on the evening of Monday, October 12, followed by two full thematic days. The second day will focus on how cellular processes underpin phenotypic change, while the third day will emphasize the evolution and diversification of cell types and lineages. The program will include invited speakers, contributed talks, a poster session, structured discussions, and ample time for informal exchange. Invited speakers include: Gunther Wagner Athanasia Tzika Leslie Babonis Alexa Sadier Henrik Kaessmann Detlev Arendt Patrick Tschopp Andrea Streit Arnau Sebe-Pedros We welcome contributions from researchers working within this framework. Participants may present their work as a poster or be considered for a short talk. Register here: `https://workshops.evolbio.mpg.de/event/145/overview`With kind regards, the organizing committee: Gianmarco Cavalli, Nathalie Feiner, Linda Kappes, Marketa Kaucka, Robin Pranter

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Online ESEB PolyAdaptSTN May28

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 28th May, 2026, 4 pm CET. Our speaker for this seminar is Dr. Samuel Yeaman from University of Calgary, Canada. Title: What can we learn by studying the repeatability of adaptation? Abstract: Genotypic redundancy is a basic parameter of fundamental importance in evolutionary biology, yet we know very little about its magnitude. If the mapping from genotype to phenotype to fitness involves considerable redundancy, then there are many different ways that species can adapt to a given environment, and evolution is highly flexible. On the other hand, if this mapping involves minimal redundancy, evolution is highly constrained as only certain genes can contribute to adaptation. We may naively expect that traits that integrate across many developmental or molecular pathway or tissue types may involve more redundancy, but we have very limited understanding of this parameter in nature. Studying the repeatability of adaptation provides an indirect way to quantify redundancy, as high repeatability should only happen when redundancy is minimal (and vice versa). This presentation will explore we can study and interpret observations about the repeatability of adaptation, starting with a brief review of theoretical models of adaptation and some recent results. I will then discuss projects studying the genomic basis of local and global adaptation to climate in plants, which show some significant signals of repeated adaptation, but also imply considerable flexibility. Interestingly, genes that contribute to local vs. global adaptation tend to have different characteristics, consistent with theoretical predictions. Much remains to be learned about the genetic basis of adaptation before we can understand the extent to which evolution is flexible vs. constrained, but data is rapidly accumulating that will help answer this question. Meeting details: Date: May 28, 2026 Time: 4 PM CET Zoom link to join the seminar: `https://eu02web.zoom-x.de/j/63438967177?pwd=uAl2uZ01cEc3BcdXdgd3aNaHsBLgaj.1`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/`

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Online Universe25MouseUtopiaExperiment Jun10

Last chance: Course:Online.Universe 25 Mouse Utopia Experiment.Jun 10 Hello EVOLDIR members Last chance - Our upcoming livestream seminar explores how physical environments shape social dynamics and behavioral outcomes. Universe 25: The Mouse Utopia Experiment (Free Seminar) is a 2-day seminar livestreaming June 10 with Paolo Trucillo (University of Naples Federico II). Evolutionary researchers can apply these socio-material frameworks to model how resource distribution and spatial constraints drive behavioral adaptation in animal populations. By analyzing the breakdown of social structures under extreme density, you can generate novel hypotheses regarding the evolutionary pressures on social organization and cooperative behaviors. This conceptual toolkit will help you design comparative frameworks that link environmental architecture directly to phenotypic and behavioral shifts in your own study systems. Sign up today (`https://instats.org/seminar/universe-25-the-mouse-utopia-experiment`) to secure your spot, and please share this opportunity with colleagues and students who might benefit! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Paris-Saclay Oct7-9 2026 International conference on Mixing for Agroecology

Dear Colleagues, We are pleased to invite you to the international and interdisciplinary conference: "Mixing crops, varieties, disciplines, and know-hows for agroecology" October 7-9, 2026 – ENS Paris-Saclay, France This meeting will bring together researchers from genetics to economics, to explore how within-field crop diversification can promote ecosystem services and drive the agroecological transition. The programme includes an interdisciplinary plenary day with renowned invited speakers, followed by two days of parallel sessions – including symposia on genetics of social interactions, host/pathogen coevolution, soil ecology, and ecophysiological modelling. Key Dates - Abstract submission deadline: June 15, 2026 - Early bird registration deadline: July 15, 2026 Full programme and registration: `https://mix4agroecology.colloque.inrae.fr/`We strongly encourage early-career researchers to submit an abstract for a selected talk slot. We would greatly appreciate your help in circulating this announcement within your lab and networks. Just as in agroecology, the most fertile ground for ideas is a diverse and well-mixed community – we very much look forward to seeing you in Paris-Saclay! Best wishes, Jerome Enjalbert and Jean-Benoit Morel, for the Organizing Committee

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Roscoff HostParasiteCoevolution Nov2-6

REMINDER registration deadline

Dear Colleagues,

This is a reminder that the ABSTRACT & REGISTRATION DEADLINE (6 June) is approaching for the Jacques Monod Conference "Ecology and evolution of host-parasite interactions in a changing world.

The conference will take place in Roscoff (Brittany, France), from 2-6 November 2026.

Contributions will be organised around three main themes: (1) Abiotic stressors and the evolution of host and parasite ecological niches, (2) Predicting disease emergence: Epidemics, connectivity and evolution, (3) Evolution in multi-species interactions and ecological networks.

Information about the conference, invited speakers and instructions on how to apply can be found here: `https://cjm.sb-roscoff.fr/en/conference/ecology-and-evolution-host-parasite-interactions-changing-worldhttps://cjm.sb-roscoff.fr/en/how-register` The registration site is open and the deadline for applications is 6 June, 2026. There are 75 slots available for participants, who will either give a short talk or present a poster. Don't hesitate to contact us if you have any questions (`Oliver.kaltz@umontpellier.fr`, `bkoskella@berkeley.edu`).

Looking forward to seeing you in Roscoff!

Britt Koskella & Oliver Kaltz ************

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Switzerland Orthology Aug29-30

Quest for Orthologs meeting (QfO9) August 29-30, 2026, Lausanne LAST CALL: abstract submissions for talks and posters. Submission deadline: June 1st, 2026 Registration deadline: July 1st, 2026 Webpage: `https://qfo2026.unil.ch/`Keynote Speakers: Erich Bornberg-Bauer (University of Munster), Katharina Hoff (University of Greifswald), Ekaterina Osipova (Harvard University), Lucy J. Colwell (University of Cambridge, Google). The QfO Consortium addresses key challenges in molecular evolutionary biology and strives to develop large-scale methods for inferring orthology among fully sequenced genomes, and to reconstruct the complement of protein-coding genes in common ancestral genomes across the tree of life. The QfO meetings aim to bring together researchers around the world who work in the field to accelerate progress through sharing of ideas, methods, and research findings. QfO 9 will take place ahead of ECCB 2026 (both in Switzerland). Travel awards for early-career researchers are available. Best regards, QfO 9 organizing committee

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UppsalaSweden BioSystEU Aug17-19

Early bird registration for BioSyst.EU ends May 31. The BioSyst.EU conference will be held in Uppsala, Sweden, August 17-19 this summer. A three-day conference celebrating European systematics and biodiversity research at its origin. The keynote speakers will be Paul Hebert, Sandra Knapp, and Fredrik Ronquist. https://event.trippus.net/Home/Index/AEAKgIPwqKKWT7_SUqROJHxpngiuR_Ar-WnoIpJEmrOJXRjejtinxGf-l9u33-Qlc_WMNyFX-EVK/AEAKgIPVez3SLTiEhaIHxCFryKd8RUd-yJ44Dr4G8YZOPaJ726e9xecN6DJ5vDWgmuyJqg185wPS/engMartin Ryberg Systematic Biology Department of Organismal Biology Uppsala University

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Virtual SORTEEconference Oct13-14

The next conference organized by the Society for Open, Reliable and Transparent Science in Ecology & Evolutionary Biology (SORTEE) will take place virtually on 13-14 October 2026. The conference is a forum to discuss, initiate and teach initiatives and practices for making research in fields related to ecology and evolutionary biology more open, transparent and reliable. Content proposal submissions are open until June 7th via the following form (https://forms.gle/R1pTxmmxKwf2DMzB9). We welcome three types of submissions: unconferences, hackathons and workshops. If you have an idea related to open science or reproducible research, don't hesitate to submit a proposal! For more information, see https://sortee.org/upcoming/. If you have any questions, don't hesitate to contact us at conference@sortee.org.

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GradStudentPositions

AutonomousUniversityBarcelona Simulating evolution under complex genotype-phenotype maps

Graduate position Simulating evolution under complex genotype-phenotype maps

Four year position to do a PhD at the Autonomous University of Barcelona (UAB). This position is ideal for biologists with an interest in theory and in the evolution of complex phenotypes. This also includes students interested in evolution, evo-devo, evolutionary theory, quantitative genetics, population genetics and embryonic development. 1. Introduction to the topic of research Living organisms are very complex. Humans and other animals, for example, have complex organs with an exquisite distribution of cell types and tissues over space that lead to a functional whole. How has this complexity arisen in evolution? Moreover, how is it possible that such complexity arose not only through evolution but also arises in each individual and generation from the relative simple zygote. How are those two processes, evolution and development, related? Ultimately, this complexity has to do with genes but how? Certainly genes have to interact in networks and with the mechanical properties of cells for complex phenotypes to arise. The question of this project is, thus, how have genes been wired in development and over evolution to lead to the complexity we see in life. Current evolutionary theory provides the basic principles to understand such evolution; but its theoretical core, population genetics, was built at a time when not much was known about how genes and cells interact to construct the body in each generation (e.g. from a zygote). In fact, most of evolutionary theory relies, directly or indirectly, on simple and outdated models of the relationship between genetic and phenotypic variation (the genotype-phenotype map). This project uses existing models, developed in the group, to simulate the evolution of complex 3D phenotypes (i.e. morphologies made of thousands of cells) under natural selection. These models consider a population of individuals, their genotypes, mutation, drift, the phenotype of each individual and natural selection based on these phenotypes. The model considers the genetic and cellular interactions possible in animal development. Each genotype is, in fact, a developmental gene network from which the phenotype arises. Through mutations these gene networks can change and, thus, lead to different individual phenotypes and underlying development. This way we do not have to assume that the genotype-phenotype map is in a certain way, we can just let it evolve. Since classical evolutionary theory does not consider the genotype-phenotype map, development or how these evolve, this models also allows to explore questions not classically addressable, e.g. how development itself or the genotype-phenotype map evolve. Ultimately the question is how development could evolve to lead to complex phenotypes and how does development affect evolutionary dynamics. For more detailed outlines of the research ask (`isaac.salazar@uab.cat`) and check the group's webpage: `https://webs.uab.cat/salazar-ciudad-lab/`2. Requirements: - Candidates should have a University Degree and a Master's Degree in biology or related topics within the European Higher Education System (minimum 300 ECTS) or equivalent by September 2022. -Scientific programming skills or a willingness to acquire them are required. -The most important requirement is a strong interest and motivation for science and evolution. A capacity for creative and critical thinking is also required. 3. Salary and conditions: -The salary would be the standard one graduate students in Spain. Full-time employment 4. The application must include: -Application letter including a statement of interests and motivation. -CV including degrees obtained, subjects included in degree (for the bachelor and master), grades obtained (for the bachelor and masters), average grade. Foreign applicants, especially non-EU applicants, should attach an explanation of their University's grading system. All documents should be in English, no official translation is required in the initial application but may be requested afterwards. Applications should be sent to Isaac Salazar-Ciudad by email: `isaac.salazar@uab.cat` 5. Starting: Starting date to be negotiated (from september 2026 to early 2027). 6. Work environment: Salazar-Ciudad group is the Genetics and microbiology deparment in the UAB (`www.uab.cat`). The Genetics and Microbiology department is very international and, thus, not being able to speak Catalan or Spanish is not a problem. The UAB is one of the largest and best Universities in Spain. 7. References: Salazar-Ciudad I, Marin-Riera M.Adaptive dynamics under development-based genotype-phenotype maps. Nature. 2013 May 16;497(7449):361-4.

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

France INRAE Avignon PhDinLandscapeGenomics

Bonjour, We are offering a funded PhD position in landscape genomics at the Plant and Horticultural Cropping Systems Research Unit (PSH, INRAE, Avignon, France). The project will investigate the spatio-temporal dynamics of adaptation to a biocontrol agent in a major insect pest of apple orchards, the codling moth (Cydia pomonella). The PhD will rely largely on already available genomic datasets and aims to understand how local and landscape-scale selection pressures interact with dispersal and agricultural landscape structure to shape the spatio-temporal dynamics of resistance to the codling moth granulovirus (CpGV). We are looking for a highly motivated candidate with strong skills in data processing and statistical analyses in R, including spatial analysis approaches. Interest in landscape genomics, population genomics and spatial ecology will be highly appreciated. More information about the PhD project and application procedures is available at: `https://site-atelier-basse-vallee-durance.fr/offre-de-these/` `https://psh.paca.hub.inrae.fr/actualites/proposition-de-these-financee`Application deadline: May 20, 2026. Please feel free to circulate this opportunity to potentially interested students. Best regards, Bertrand Bertrand GAUFFRE Charge de Recherche, Axe CBC UR 1115 Plante et Systeme de culture Horticole `https://site-atelier-basse-vallee-durance.fr/https://psh.paca.hub.inrae.fr/axes-de-recherche/axe-cbc-controle-biologique-par-conservation`inrae.f r

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IMTLucca Italy ProtistMovementComplexSystems-Deadline25May

A PhD opportunity is available at the IMT School for Advanced Studies Lucca, Italy, within the Complex Systems & Networks track of the PhD programme in Systems Science. Application deadline: 25 May 2026. The opportunity may be relevant to students interested in protistology, microbial ecology, organismal biology, ecology, evolutionary biology, biophysics, quantitative biology, or complex systems. Although the track is not specifically devoted to protistology, it may offer a suitable interdisciplinary framework for projects using protists as model systems to study movement, organism-organism interactions, spatial patterns, ecological networks, and the modelling of complex biological systems. Further information on the track: `https://sys.imtlucca.it/program-overview/complex-systems-and-networks-cn`Application information: `https://sys.imtlucca.it/how-to-apply_1`For informal enquiries, prospective candidates may contact: Dr Andrea Perna Assistant Professor, IMT School for Advanced Studies Lucca `andrea.perna@imtlucca.it`

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JagiellonianU-Krakow Sanger-Cambridge SexANDTardigradeEvolution

PhD studentship in tardigrade and sex evolution Fully funded 4-year PhD studentship in tardigrade evolution at the Jagiellonian University in Krakow (Poland) in the team of Prof. Lukasz Michalczyk, in collaboration with Prof. Mark Blaxter (Wellcome Sanger Institute, Cambridge, UK). The main goal of the project is to take a unique advantage of applying cutting-edge methodology of genome sequencing to a fascinating model, tardigrades, in order to answer one of the fundamental questions in life sciences: why are some asexual lineages able to persist over long evolutionary time, whereas the majority of them seem to be evolutionary dead ends? Given that genetic recombination seems to be the key to evolutionary success, the prediction is that ancient asexual lineages exhibit genomic signatures of recombination, whereas most recent asexuals do not. In other words, the project will provide first large scale, systematic comparative analysis of the genomic architecture of ancient and recent asexuals. The PhD studentship presents a great and unique opportunity to answer one the fundamental questions in life sciences using a fascinating model and cutting edge methods. Importantly, the position also offers additional training in genomics and transcriptomics in one of the world's leading institutions in genomics, the Wellcome Sanger Institute in Cambridge, UK. Prof. Mark Blaxter, Head of the Tree of Life Programme at Sanger, is a formal and the key collaborator on the project. Although the evolution of sex and tardigrades are the central project aims, the system provides potential for a dedicated student to explore their own ideas on other topical tardigrade biology and evolutionary questions. A dedicated student will have a great chance not only to learn a range of transferable skills, but also to build a sound publication record which will help them to get an attractive PostDoc or industry position in the future. The successful candidate will be involved in will be involved in field work (sample collection), tardigrade identification, culturing, DNA extraction, genome & transcriptome sequencing and assembly, as well as in phylogeny reconstruction. The PhD Student will be also required to prepare first drafts of some manuscripts and will be involved in the promotion of results at seminars and conferences. The PhD programme in Biology at the Jagiellonian University is run entirely in English and it includes some obligatory and facultative classes. The programme is open to all nationalities and there are no tuition fees. The PhD stipend is 6 300 PLN per month (typically, cost of life in Krakow for a PhD student is ca. 4 000 PLN/month). Deadline for applications: 31st of May 2026. More information on the project, university, our team and the application procedure is available here: https://asex.project.uj.edu.pl/phd-position-2026Prof. Lukasz Michalczyk LM@tardigrada.net

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Krakow InvasionGenomics

Graduate position: Krakow, Poland. PhD in Invasion Genomics of Invasive Hemipteran Pests Applications are invited for a fully funded PhD position within the project: "Invasion success through genomic lens: insights from whole-genome diversity of invasive Hemiptera pests" funded by the Polish National Science Centre. PROJECT DESCRIPTION Biological invasions are increasing worldwide and represent a major threat to biodiversity and ecosystem functioning. Understanding the genetic mechanisms underlying invasion success remains a central challenge in invasion biology. This project will investigate the genomic basis of invasion success using two invasive Hemipteran insect species, Cinara curvipes and Leptoglossus occidentalis, as model systems. Using whole-genome sequencing data, we will examine population genomic differentiation, structural variants (SVs), transposable elements (TEs), and gene family expansions potentially associated with adaptation and successful range expansion. We will also investigate the role of facultative bacterial endosymbionts in promoting invasiveness.

The successful candidate will participate in: - de novo genome sequencing, assembly and annotation of Cinara curvipes, - analyses of structural variation, TE content and gene family evolution, - investigation of bacterial endosymbiont diversity and distribution. The project combines molecular laboratory work with bioinformatic and population genomic analyses, with a stronger emphasis on genomic data analysis. SUPERVISION AND COLLABORATION The PhD student will be supervised by Dr Aleksandra Biedrzycka at the Institute of Nature Conservation, Polish Academy of Sciences, Krakow, Poland, and will collaborate with Dr Pierre Nouhaud (INRAE-CBGP, Montpellier/Marseille, France). REQUIREMENTS Applicants must hold an MSc degree by the start of the position and should have: - a strong interest in evolutionary genomics, population genomics, or invasion biology, - experience or interest in bioinformatics and genomic data analysis, - good English communication skills, - good organizational skills and motivation for independent research. FUNDING The position is funded for 48 months. - approximately 5000 PLN gross gross/month before the mid-term evaluation, - approximately 6500 PLN gross gross/month after the mid-term evaluation. APPLICATION Please submit first an informal application to: Dr Aleksandra Biedrzycka biedrzycka@iop.krakow.pl Applicants should submit: - a cover letter describing their background, skills and motivation, - a CV, - contact details of at least one academic referee. Formal applications will be submitted through the Doctoral School of Natural and Agricultural Sciences. Detailed information regarding required documents and recruitment procedures will be published on the Doctoral School website: https://botany.pl/en/doctoral-school-en/admissions-enDEADLINE Application deadline: 7 August 2026 Starting date: 1 October 2026 We welcome applications from motivated students interested in evolutionary genomics, biological invasions and biodiversity research. Dr hab. Aleksandra Biedrzycka Instytut Ochrony Przyrody Polskiej Akademii Nauk Al. Adama Mickiewicza 33 31-120 Krakow

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LaTrobeUniversity Australia

PhD position in Sensory Biology Institution: La Trobe University, Melbourne, Australia Start: 2026/2027 We are seeking a PhD student to join a research group investigating the evolution and function of sensory systems and coloration, with a particular focus on insects. The projects address how animals perceive their environments, how sensory constraints and ecological conditions shape signal design, and how these interactions influence behaviour and fitness. The student will be based in the School of Agriculture, Biomedicine and Environment at La Trobe University and will be part of a collaborative, international research network. Project: Evolution of deep-red vision and infrared heat sensitivity in jewel beetles This project investigates how jewel beetles detect and use long-wavelength light and heat cues, and why these sensory abilities have evolved. Key questions include how deep-red vision and thermal sensing contribute to habitat selection, mate finding, and host detection. The project combines field and laboratory approaches, including behavioural experiments, electrophysiology, and microscopy, and involves collaboration with international experts in visual and thermal sensory biology. Environment and training La Trobe University is located in Melbourne, Australia, and offers a vibrant research environment with access to modern facilities and a diverse academic community. Students will receive training in evolutionary theory, experimental design, and quantitative approaches, and will be encouraged to develop independent, hypothesis-driven research programs. Applicants should have a strong interest in evolutionary biology, sensory ecology, or behavioural ecology, and hold a First-Class Honours or Master's degree (or equivalent). Prior research experience and publications are advantageous. Application deadline: 26th June 2026 To apply, please send the below to Amanda: 1. A cover letter outlining relevant skills, experience and research interests 2. A CV 3. Academic transcripts/grades 4. Contact details for two referees (including a research supervisor) For enquiries, contact Dr Amanda Franklin (a.franklin@latrobe.edu.au) www.amanda-franklin.com (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UAarhus DK PhD position plant computational biology

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Python.for.Bioinformatics(IPYB02)-EvolutionaryBiologyApplications Category: WOrkshops / Courses Content: Python for Bioinformatics (IPYB02) - Evolutionary Biology Applications https://prstats.org/course/introduction-to-python-for-bioinformatics-ipyb02/Delivered by experienced bioinformaticians and computational biologists. Learn Python programming for evolutionary biology, genomics, and sequence analysis – no prior coding experience required. From phylogenetics and population genetics to comparative genomics and molecular evolution, modern evolutionary biology relies heavily on computational tools. This hands-on course introduces the core Python programming skills needed to work efficiently with evolutionary and genetic datasets in research workflows. What you'll gain - A strong foundation in Python programming for evolutionary biology - Practical experience working with sequence and genomic data - Skills in file handling, loops, functions, and biological data structures - Understanding of coding workflows used in phylogenetics and population genetics - Confidence in writing and debugging reproducible analysis scripts Course format - Live, instructor-led online training - Hands-on coding with real biological datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Evolutionary biologists and geneticists new to programming - Researchers working with genomic or sequence datasets - PhD students and early-career researchers - Anyone interested in computational evolutionary biology Why take this course? Evolutionary biology increasingly depends on computational approaches to process and interpret large genetic datasets. Whether analysing

DNA sequences, automating phylogenetic workflows, or exploring genomic variation, Python has become an essential tool for modern evolutionary research. This course provides an accessible introduction to programming, equipping you with the skills to automate analyses, handle biological data efficiently, and build reproducible computational workflows for evolutionary biology research. Learn more & enrol PR Stats course page for Introduction to Python for Bioinformatics (IPYB02) Questions? Email: oliver@prstats.org

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UAlaska Fairbanks NSFprogram EMERGE Alaska

We are recruiting 8 PhD students at the University of Alaska Fairbanks, College of Fisheries and Ocean Sciences through a new NSF program: EMERGE Alaska. Faculty in our departments of Fisheries, Marine Biology and Oceanography conduct evolutionary biology research, including phylogenomics, population genomics, environmental DNA, ichthyology, transcriptomics and biogeography, on fishes, birds, invertebrates, plankton and marine mammals. This opportunity is only for US citizens, nationals or green card holders who received an Honorable Mention from the National Science Foundation's Graduate Research Fellowship within the last 3 years (since 2023). Fellowships provide 3 years of full support (salary, stipend, health care, fees). Students should first identify and reach out to a prospective faculty advisor before applying on NSF ETAP's website. Applications are due by 9/15/2026. For a list of participating faculty and their research interests, as well as detailed information about the program and how to apply, please look at our website: https://www.uaf.edu/cfos/academics/emerge-alaska/index.phpContact Dr. Jessica Glass (jrglass@alaska.edu) with any questions.

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UAlberta GraduatePosition

Graduate position - Ecology and Evolution of Host-parasite Interactions

A graduate research position (MSc or PhD) is available in Dr. Lien Luong's research group (https://grad.biology.ualberta.ca/luong/) at the University of Alberta. Our lab investigate how exposure to parasites can lead to changes in host behavior, morphology, or physiology, even in the absence of infection. These non-consumptive effects (NCE) or risk-induced trait responses can be understood in the context of the "ecology of fear". Students interested in this field or the ecology & evolution of parasite-host interactions generally are encouraged to apply.

The Department of Biological Sciences at U of A is one of the largest and most scientifically diverse departments of its kind in Canada. We offer research-orientated, thesis-based graduate programs at both the MSc and PhD levels. Study programs are tailored individually to graduate student needs and emphasize interdisciplinary thinking. All students accepted into our MSc program have guaranteed funding for at least 2.3 years and 5 yrs for the PhD program. Teaching training is provided and is mandatory for all students on graduate teaching assistantships. With 200 graduate students, ¿50 full-time faculty, excellent support facilities and ample research funding, a vibrant and exciting learning environment is provided. For more information about applying to the graduate program: http://www.biology.ualberta.ca/programs/graduate/prospective/ To apply, please send a brief explanation of your research experience and interests and a copy of your curriculum vitae to lluong@ualberta.ca. For more information, please contact Dr. Lien Luong (lluong@ualberta.ca). Application deadline for January 2027 entry is August 1, 2026; Fall 2027 entry is February 1, 2027.

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U Bristol NestArchitecture Ants

Fully funded PhD position on nest architecture in ants at the University of Bristol (UK) Project title: Adaptive architecture in animal societies: how ants tune their nests to optimise performance under competing pressures (`https://stroeymeyt-lab.co.uk/open-positions/`) Application deadline: 5 June 2026 Background Many social animals construct complex environments that shape how their societies function, from insect nests to coral reefs and human cities. These structures are not passive: their architecture regulates movement, interactions, and the flow of information, resources, and disease. Understanding how such architectures can be tuned to balance competing demands is a fundamental challenge - and one with direct relevance beyond biology. During the recent pandemic, architects and urban planners explored how spatial design could limit contagion; biological systems shaped by millions of years of evolution may already have solved versions of these problems. Social insects provide a uniquely powerful model, as they build elaborate nests that control how individuals move and interact, and can be reshaped in response to changing pressures. Yet despite their importance, these systems remain surprisingly understudied, largely because they are buried underground, placing them beyond the reach of conventional experimental approaches. The project In this interdisciplinary project, you will study how ant colonies remodel their nest architecture in response to competing pressures, and how these changes influence collective performance. (1) You will use controlled laboratory experiments to map how colonies reshape their nests under specific pressures - pathogen exposure, resource availability, seasonal variation - revealing architectural solutions refined by millions of years of evolution. (2) You will test whether these architectural responses are adaptive by building faithful replicas of real nests and measuring their effects on colony performance and resilience - quantifying, for the first time, to what extent architecture underpins a colony's ability to withstand stress. (3) You will extend these findings beyond simplified laboratory systems, studying nests in natural and semi-natural contexts, combining direct excavation and casting with emerging geophysical approaches for non-destructive imaging, to ask whether the same architectural principles operate in the wild. Methods and approaches To address these questions, you will use a combination of advanced imaging, fabrication, and analytical methods that make underground nest architecture fully accessible to experimental investigation. You will use microCT scanning and 3D surface scanning to map nest architecture in three dimensions. To analyse these data, you will develop custom code in R, Python, and/or C++ to convert nest scans into spatial networks and visibility graphs. You will apply network-based analyses to quantify connectivity, accessibility, and robustness, generating predictions about how individuals, resources, and disease spread through the nest. You will then test these predictions in controlled manipulative experiments by producing faithful physical replicas of real nests using a combination of 3D printing and lost-wax casting in aerated concrete. Finally, fieldwork will take you beyond the laboratory, including setting up mesocosms, casting natural nests, and working with geophysical experts to deploy ground-penetrating radar for non-destructive imaging of field nests. In addition, you will benefit from the University of Bristol's doctoral training environment, with access to a wide range of courses in data analysis, programming, scientific writing, and presentation skills, as well as opportunities for interdisciplinary collaboration and career development. The team The project will be based in the Ant Lab led by Dr Nathalie Stroeymeyt at the University of Bristol, within a dynamic and collaborative research environment. The work is part of the ERC-funded SMARTNESTS programme (June 2026-May 2031), which brings together expertise in behavioural biology, imaging, and experimental system design. The student will interact with an interdisciplinary team and benefit from collaborations with engineers and geophysicists. Candidate profile We are looking for highly motivated candidates with a strong interest in biological systems, collective behaviour, or complex systems. Applicants should hold (or be close to completing) a degree in biology, ecology, physics, engineering, computer science, or a related discipline, with a final grade of 2:1 or more. The project combines experimental work, quantitative analysis, and computational approaches. Prior experience in one or more of these areas (e.g. programming, data analysis, imaging, or experimental design) is desirable but not essential. Curiosity, creativity, and a willingness to work across disciplines are key. Expected start date

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UGdansk-Poland PhDposition-CanineGenomics

PhD position in canine genomics at the University of Gdansk, Poland Dr Malgorzata Pilot, a leader of a research group in mammalian evolutionary genomics at the University of Gdansk, Poland is looking for candidates for a PhD position in canine genomics. The PhD project will be focused on the evolution of phenotypic traits considered as part of Domestication Syndrome in dogs. The project will be carried out in collaboration with the Domestication Lab at VetMed University Vienna. The start date for the PhD studies is the 1st of October 2026, and the duration is 4 years. This position will involve laboratory work to prepare DNA for the genotyping on SNP arrays and Next Generation Sequencing (including DNA extraction and quantification, and preparation of NGS libraries) and the analysis of the genomic datasets alongside the phenotypic data. The work will require learning new methods of data analysis, and therefore strong self-motivation and willingness to learn is essential. The work will involve preparation of research papers as a first author and contribution of the work on research papers as a team member. The project will not involve fieldwork, but there will be an opportunity to visit the project's field site. The PhD studies involve participation in lectures and other activities being part of the curriculum as well as contribution to undergraduate teaching. The PhD studies commence on the 1st October 2026 and should be completed with the thesis submission within 4 years. A stipend is available for the 4 years of the PhD studies and is not extendable. The stipend is sufficient to cover life expenses of a single person. The Doctoral School does not charge tuition fees. Research environment The University of Gdansk offers education to 22 thousand students and carries out research in most fields of academic knowledge. The University is highly committed to gender equality and has achieved fourth position globally in the CWTS Leiden Ranking 2019, which measures the participation of women in scientific publications at universities. The University is a member of a consortium of European University of the Seas - SEA-EU, which is intended as a first step towards establishing an international, multilingual European University. The research group is based at the Faculty of Biology, and is part of the Department of Evolutionary Genetics and Biosystematics. The research at the Department is focused on a broad range of themes in animal evolution and ecology, including systematics, biogeography, molecular ecology, and evolutionary genomics. The Faculty of Biology is based in a large modern building opened in 2012. Gdansk is a historic city at the coast of the Baltic Sea and a popular tourist destination (https://visitgdansk.com/home.qbpage?setLanguage=en). Requirements - MSc degree in biological sciences or a related area, awarded or to be awarded before July 2026 - Good theoretical knowledge of population genetics - Experience with molecular genetics labwork and the analysis of DNA - sequence data - Good knowledge of English - Experience with NGS data analysis and/or with programming will be an advantage Candidates should send a Curriculum vitae (including the list of publications and/or manuscripts in preparation, conference presentations and other outputs) and a short motivation letter (maximum one A4 page) to Dr Malgorzata Pilot (malgorzata.pilot@ug.edu.pl) no later than 5th of June 2026. The title of the message should be "Application for a PhD position in canine genomics". Informal inquiries can be addressed to Malgorzata Pilot. The candidates will be assessed based on the information in the submitted documents and may be invited for an online interview, which will be carried out in mid-June. The selected candidate will be requested to submit an application to the Doctoral School and attend an oral entry exam (online or in person).

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UGeneva PhDPosition in Evolutionary Biology-Phylogenomic

Project Title ? Genomic and phylogenetic bases of evolutionary insular plant radiations, the case of the Sapotaceae in Madagascar Host Institution ? Geneva Botanic Garden (GBG) ? University of Geneva (UNIGE), Faculty of Science, Department of Plant Sciences Supervisors ? Prof. Yamama NACIRI (UNIGE, Geneva Botanic Garden) ? Dr. Charles Pouchon (Geneva Botanic Garden) Duration ? 5 years (start date: 01.09.2026) Location ? Geneva Botanic Garden Scientific Background Evolutionary radiations, defined as the rapid diversification of a single lineage into an exceptionally large number of descendant species, are considered a major driver of current biodiversity on Earth. Studies in plants and animals have identified key innovations (e.g., morphological or behavioural traits) and key environments (e.g., oceanic islands, sky islands) that correlate with radiations. However, evolutionary radiations have rarely been examined within a single family under a shared biogeographic framework, using extensive sampling and standardized molecular markers. As a result, heterogeneity in data can significantly affect phylogenetic reconstructions of diversification and biogeographic patterns. Several genetic factors have also been proposed as drivers of evolutionary radiation, including hybridization, gene/genome duplications, activation of transposable elements (TEs), and genetic drift during the early stages of radiation. Yet, most of these processes remain poorly studied, particularly in plants. This project aims to bridge this gap by investigating multiple, independent radiations within the Sapotaceae family in Madagascar, using an innovative combination of phylogenomic and genomic approaches. Building on two previous projects, we developed a targeted gene capture kit that allowed a thorough revision of the family's systematics and phylogeny, doubling the known number of species and providing a robust backbone for further research. A remarkable feature of the family is that 55This PhD project aims to deepen understanding of both extrinsic factors (environmental variables such as climate, geography, landscape, and soil) and intrinsic factors (trait syndromes, genomic changes, TE dynamics, demographic processes, adaptive evolution, gene duplications) driving these radiations. To achieve this, we will leverage previous phylogenomic reconstructions, incorporating extensive sampling (200 species, ¿1000 specimens), targeted gene capture for broad coverage, and whole genome sequencing for a subset of 20 species. By combining high-resolution phylogenomic data, broad taxonomic sampling, and the complementary expertise of the two principal investigators and three international collaborators in evolutionary biology and ecology, this project will establish a novel integrative framework for testing key hypotheses in insular evolutionary radiations. Additionally, the project will include outreach and educational activities to communicate evolutionary processes to the public in both Switzerland and Madagascar. Research Objectives The PhD will explore the phylogenetic and genomic drivers of evolutionary radiations in Sapotaceae in Madagascar, addressing the following research questions: ? Diversification patterns: How do the tempo, mode, and geography of diversification differ across genera radiating within Madagascar's insular environment? ? Neutral vs adaptive processes: What is the relative influence of neutral processes (e.g., small ancestral populations, genetic drift) versus adaptive processes (e.g., natural selection) on diversification? ? Genomic mechanisms: What genomic factors (e.g., transposable elements, genome duplications, gene losses, epigenetic modifications) underlie these radiations? Methodology The PhD candidate will work with a comprehensive dataset including: ? Phylogenomic data from target gene capture across 200 species and ¿1000 specimens ? Genome and transcriptome sequencing for a subset of 20 species ? Existing taxonomic, ecological, and environmental data Approaches will include: ? Field works ? Phylogenomic and divergence time reconstructions ? Collect of morphological, ecological and environmental datasets ? Comparative analyses of diversification rates across lineages by modelling trait evolution and diversification processes ? Genomes reconstruction and annotation ? Genomic analyses (TE dynamics, genome duplications/loss, adaptive evolution) Expected Outcomes ? Publications in high-impact journals in evolutionary biology and genomics ? Novel insights into the intrinsic and extrinsic drivers of evolutionary radiations ? Development of an integrative framework applicable to other insular radiations ? Contribution to biodiversity research and conservation in Madagascar Candidate Profile Education

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UGreifswald Germany DoctoralResearchAssociate

Graduate Position, Doctoral Research Associate University of Greifswald, Germany A researcher position suitable for conducting a PhD project is available at the Zoological Institute and Museum of the University of Greifswald in the Uhl lab. `https://zoologie.uni-greifswald.de/struktur/abteilungen/allgemeine-und-systematische-zoologie/`The position is funded for three years by the German Research Foundation (DFG) at the salary level E 13 TV-L (65One of the research fields investigated in the Uhl lab are animal reproductive strategies in an evolutionary context and anatomical and functional aspects related to reproduction and sexual selection. The position is linked to a DFG funded project on ”Sperm uptake and release in male spiders: a functional, biomechanic and neurobiological perspective”. Background: Animals with internal fertilization have evolved diverse structures for sperm transfer from males to females. These include spermatophores deposited externally and taken up by females, as well as specialized body parts, such as penes connected to testes. Some species have developed secondary sperm transfer devices and use modified appendages. Sperm transfer structures are highly complex and species-specific, and go beyond simple sperm delivery. This complexity makes the male genitalia important for species identification and for evolutionary biology research on sexual selection, sexual conflict, and speciation. Our research project aims to elucidate the mechanisms of sperm uptake and transfer in male spiders that use specialized palpal organs (POs). Despite nearly two centuries of observation, the functioning of spider POs remains unclear. Focusing on two species representing major spider clades, the project will employ advanced imaging techniques, biomechanical testing, and experimental manipulations to investigate the following: 1. Structural and material properties of POs, including sclerites, membranes, and sperm-bearing spermophors. 2. Roles of muscles, hemolymph pressure, glandular secretions, and innervation in sperm uptake. 3. Dynamics of sperm release from PO to female during mating. The project combines expertise in spider mating behavior, ultrastructural anatomy, and functional morphology of copulatory organs in the Uhl lab (Greifswald) with state-of-the-art methods of micromechanics in the Gorb lab (Kiel). The candidate will work closely together with another candidate working on complementary aspects in the Gorb lab. By elucidating the intricate mechanisms of sperm transfer in spiders, this study will significantly advance our understanding of arachnid reproductive biology and may inspire novel technological applications in microfluidics and related fields. Your tasks: * Plan and execute experiments to understand the dynamics of sperm uptake and release * Generate and analyse morphological data from a range of microscopy techniques (Cryo-SEM, FE-SEM and TEM) to investigate the functional morphology of sperm transfer organs in male spiders. * Investigate general and species-specific differences using a comparative approach * Collaborate with project partners, particularly with associated PhD candidate at Uni Kiel * Coordinate a team of student helpers * Publish results in scientific journals and present the work at scientific conferences on the national and international level. Your profile: * A master's degree or equivalent in biology or other biology-oriented disciplines. * A strong motivation to unravel the details of sperm storage and release mechanisms * Experience and interest in overarching questions (reproductive strategies to biomechanical functioning) * Experience and skills in independent scientific work, ideally conducted using morphological methods and imaging (SEM, TEM, CT). * Comfortable when working in a team and good communication skills * Reliability and skills in project management * Fluent in English, both written and spoken. Advantages for you: * You will work on a state-of-the-art research project in an internationally recognized research laboratory with an excellent infrastructure and a friendly atmosphere. * You closely work together with another group of experts and thus expand your network * You will be able to participate in conferences and workshops * University of Greifswald offers participation in a qualification program to gain additional qualifications during your doctoral studies. * Greifswald is a historic city on the Baltic Sea coast in north-east Germany. Its large student population contributes to a vibrant and dynamic social atmosphere. Greifswald offers a high standard of living with affordable costs, with most destinations reachable by bicycle. How To Apply:

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UHaifa EvolutionaryBiology

Molecular Biology Ph.D., postdoctoral and researcher positions open - University of Haifa The Sagol Lab for Evolution Research at the University of Haifa, directed by Prof. Adi Livnat, studies fundamental questions about how evolution occurs, focusing on the mechanisms of mutation. For more than a century, it has been thought that mutations are random with respect to fitness; namely, that while mutation rates vary across the genome, the causes of individual mutations bear no meaningful relationship to their biological consequences. Recently, however, a new methodology that enabled the measurement of de novo origination rates of individual mutations for the first time uncovered empirical patterns that were unexpected under this view. Our lab studies a range of exciting questions that follow from this new evidence, with potentially fundamental implications for our understanding of evolution. We are currently looking for highly motivated individuals with a strong background in molecular biology and a record of academic excellence for empirical studies on the origin of mutations. Ph.D., postdoctoral and researcher positions are available. For more information, read about our recent work (`https://www.pnas.org/doi/10.1073/pnas.2424538122`) or see our website. Requirements: Background in molecular biology/molecular genetics, high motivation and a record of excellence. To apply: Send a CV and a cover letter to adi.livnat@sci.haifa.ac.il, and arrange for 2-3 referees to send a letter of recommendation to the same address.

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UmeaU Sweden Infant Microbiome Evolution

PhD position in infant microbiome evolution Application details and submission link: https://umu.varbi.com/en/what:job/jobID:927502/For more details on the research area, contact Chinmay Dwibedi (dwibedilab.org) at chinmay.dwibedi@umu.se We welcome your application!

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UppsalaU Sweden PhDposition-EvolutionaryEcologyGenomics AmphibianMicrobiomes

A fully funded 4-year PhD position is available at the Department of Ecology and Genetics (Evolutionary Biology Centre, Uppsala University) within the Animal Ecology programme. The project, "Amphibian skin microbiomes and infectious diseases," will investigate how host evolutionary history, environmental factors, and pathogens shape skin microbiome diversity across populations and latitudinal gradients. The student will use integrative approaches including metabarcoding, shotgun metagenomics, metatranscriptomics, and population genomics to characterize microbial communities (bacteria, fungi, viruses, protists) in wild amphibians. The project combines fieldwork, molecular lab work (DNA/RNA extraction, library preparation for Illumina and long-read sequencing), and advanced bioinformatics.

Applicants should hold a Master's degree in evolutionary ecology or a related field, with experience in genomics, bioinformatics, and molecular techniques. Fieldwork experience and microbiome analysis skills are advantageous. A valid driving licence (B) is required.

**Start date: 1 October 2026 (or as agreed). **Appli-

Interested applicants should contact Dr. Margres directly at margres@usf.edu and provide (1) CV, (2) statement of interest, and (3) contact information for three references. The desired start date is Spring/Fall 2027.

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UTuebingen HomininEvolution

PhD position - How did climate shape the movements, interactions, and evolution of hominin populations? The Genotype-Phenotype Evolution in Space (GPS) Lab, led by Dr Cecilia Padilla-Iglesias, is seeking a PhD candidate to investigate one of the central questions in human evolution: how past climate shaped the distribution, dynamics, and interactions of hominin populations, and how these processes contributed to the origins and diversity of Homo sapiens. Understanding human origins requires understanding population dynamics. During the Middle and Late Pleistocene, multiple hominin groups inhabited Eurasia and may have interacted with one another and, eventually, with H. sapiens populations dispersing out of Africa. Yet, key questions remain unresolved: how were these populations related, where and when did they interact, and how did climate shape the extent and consequences of these interactions? In this project, we will combine population genetics, species distribution models, and palaeoclimate reconstructions to build models of past human population dynamics. The aim is to reconstruct how climatic changes influenced the movements, persistence, and interactions of different human groups from the Middle Pleistocene onwards, and how these processes contributed to the exceptional range of H. sapiens, the disappearance of other lineages, and present-day human diversity. Type of work The student will use climate-informed spatial genetic models (see Padilla-Iglesias et al. 2025), a framework that integrates ecological, genetic, and climatic data to study responses to past environmental change. The project is primarily computational and involves training across several disciplines. The student will work closely with a group of students and postdocs developing quantitative tools for ecological and evolutionary questions, with scope to incorporate morphological, isotopic and archaeological data depending on the student's interests and the direction the project takes. What we look for Applicants should have a strong interest in human evolution, proficiency in R, some experience with bioinformatics or population genetic data, and enthusiasm for interdisciplinary, quantitative work. Experience in archaeology, anthropology, or evolutionary biology is desirable, but candidates from related backgrounds are also encouraged to apply. We are looking for a curious, proactive, and intellectually independent candidate who is excited to make the project their own and bring their own questions and ideas to it. What we offer We offer a 3-year fully funded PhD position (E13, 65The successful candidate will join a highly international and interdisciplinary research environment, with outstanding opportunities for collaboration across genetics, palaeoanthropology, cultural evolution, and biomolecular archaeology. The project will be supervised by Dr Cecilia Padilla-Iglesias, in close collaboration with Prof Cosimo Posth at the Archaeo- and Paleogenetics Group at the University of Tubingen and Prof Andrea Manica and the Evolutionary Ecology Group at the University of Cambridge. The student will benefit from close supervision and mentoring, weekly coding sessions with the Evolutionary Ecology Group in Cambridge, and opportunities to develop strong coding and quantitative skills in R and potentially other languages. There will also be opportunities to engage in collaborative projects and, potentially, to take part in anthropological fieldwork in Africa. Tubingen is a vibrant university town with a strong international research community and an outstanding environment for doctoral training.

How to apply Please send a single PDF to Dr Cecilia Padilla-Iglesias by the 7th of June 2026 at cecilia.padilla-iglesias@uni-tuebingen.de including: . a letter of motivation, including information on previous scientific work and publications, if available . a CV with a complete listing of academic certificates and credentials . contact details for two referees . if available, a copy of your Master's thesis Informal inquiries are also very welcome. If this type of work sounds interesting to you, feel free to get in touch by email before applying. Reference Padilla-Iglesias, C., Xue, Z., Leonardi, M., Paijmans, J. L., Colucci, M., Hovhannisyan, A., ... & Manica, A. (2025). Pan-African metapopulation model explains Homo sapiens genetic and morphological evolution. bioRxiv. Dr Cecilia Padilla-Iglesias Group Leader in Genotype-Phenotype Interactions Human Origins Cluster of Excellence University of Tubingen

Jobs

IowaStateU AssistantProfessor FreshwaterEcology

We are excited to share that the Iowa State University Ecology, Evolution, & Organismal Biology (EEOB) Department is hiring an Assistant Professor Freshwater Ecology including folks with an evolutionary interest in this area. This position is a great opportunity to join our supportive, collegial, and intellectually vibrant department. https://isu.wd1.myworkdayjobs.com/IowaStateJobs/job/Ames-IA/Assistant-Professor-in-Freshwater-Ecology_R19216 Assistant Professor in Freshwater Ecology

The Department of Ecology, Evolution & Organismal Biology (EEOB) seeks applications for a tenure-track Assistant Professor of Freshwater Ecology. We define freshwater ecology broadly (including lake, river, stream, and wetland ecosystems) but will give preference to candidates whose research includes a pathway for application to lakes and reservoirs in Iowa and the midwestern USA. The successful candidate will develop an externally funded, research-intensive program that contributes foundational knowledge in freshwater ecology–spanning organismal, population, community, ecosystem, or biogeochemical perspectives–while addressing processes and mechanisms relevant to inland waters of agricultural and human-dominated landscapes. Research may be at any biological scale (genes, individuals, communities, populations, ecosystems), with any group of organisms. We are particularly excited about candidates who use innovative empirical, analytical, computational, or modeling approaches in their research. The successful candidate will also contribute to undergraduate and graduate education, including the teaching of a course in aquatic ecology. Research programs that integrate basic ecological discovery with use-inspired or management-relevant questions are particularly encouraged. There will be opportunities for leveraging ongoing partnerships with state and federal agencies, as well as collaborations with a large assemblage of ISU scientists involved in research on water and environmental resources and with the Iowa Nutrient Research Center, the Iowa Water Center, and the Leopold Center for Sustainable Agriculture, all located at ISU in Ames, IA. This is a tenure-track position in the College of Agriculture and Life Sciences at the rank of assistant professor. The distribution of effort for this position is 70

Candidates must be legally authorized to work in the U.S. on an ongoing basis without sponsorship. Immigration sponsorship is not available for this position.

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Job Molecular Lab Coordinator UConn

Molecular Lab Coordinator X Plant Computational Genomics Lab Appointment: Full-time, on-site; initially offered as a temporary position with planned transition to a staffrole within six months Compensation: $27V32$/hr, commensurate with experience Description: The Plant Computational Genomics (PCG) Lab at the University of Connecticut (Storrs campus) seeks a Molecular Lab Coordinator to support an interdisciplinary research program focused on biodiversity and conservation genomics. The coordinator will manage daily laboratory operations, develop scalable sample-tracking infrastructure, and lead high-throughput sequencing efforts across diverse organisms, with a particular emphasis on plants and other recalcitrant sample types. The position coordinates high throughput sample extraction, library prep, and sequencing, as well as the associated data infrastructure. It is perfect for someone who is highly organized, communicates clearly across technical and non-technical audiences, and values sample provenance, reproducibility, and data integrity. Responsibilities Design, document, and maintain SOPs for high-throughput sample processing, including barcoded sample tracking (e.g., SmartSheet) from accessioning through sequencing and downstream analysis. Oversee inventory management, reagent ordering, equipment maintenance, and coordination with core facilities, including the Center for Genome Innovation (CGI). Implement and enforce laboratory biosafety protocols and institutional compliance standards. Extract DNA and RNA from diverse and challenging samples, including plant tissues with high polysaccharide, polyphenol, or secondary-metabolite content (e.g., CTAB-based protocols and modifications for recalcitrant tissue), animal samples, and environmental samples. Prepare and optimize sequencing libraries for short-read (Illumina) and long-read (Oxford Nanopore, PacBio HiFi) platforms, including whole-genome sequencing (WGS), reduced-representation approaches such as ddRAD, RNA-seq, and amplicon workflows. Troubleshoot extraction and library preparation across taxa with variable quality. Ensure metadata standards and sample identifiers propagate cleanly from bench through sequencing runs to downstream analysis, supporting reproducibility and downstream data sharing. Train and mentor undergraduate and graduate students, postdoctoral researchers, and visiting scientists in laboratory techniques, safety, and documentation practices. Required Qualifications Bachelor's or Master's degree in molecular biology, genomics, plant biology, or a related field. Two or more years of molecular laboratory experience beyond coursework. Demonstrated experience with high-throughput sequencing workflows, including DNA/RNA extraction and library preparation. Hands-on experience with Illumina and at least one long-read platform (Oxford Nanopore and/or PacBio). Experience with barcoded samples and high-throughput sample tracking systems. Strong organizational skills and meticulous attention to detail in managing complex, parallel workflows. Demonstrated commitment to laboratory documentation, reproducibility, and data integrity. Ability to work independently and collaboratively in a fast-paced academic environment. Preferred Qualifications Three or more years of molecular laboratory experience beyond coursework. Experience extracting nucleic acids from plant tissues, particularly recalcitrant or non-model species (CTAB/modified CTAB or column-based protocols optimized for high-polysaccharide or polyphenolic samples). Experience with sequencing diverse, non-model organisms. Experience with Hi-C library preparation and related chromosome conformation capture methods. Familiarity with one or more additional techniques relevant to the lab's research: Single-cell sequencing (e.g., 10x Genomics). Methylation profiling (bisulfite sequencing or long-read methylation calling). Familiarity with liquid-handling automation platforms Experience training users across a range of expertise levels. Environment: The successful candidate will join a collaborative research environment associated with the Institute for Systems Genomics and closely aligned with the Center for Genome Innovation. The PCG Lab integrates molecular and computational approaches to address conservation genomics questions. Please send a cover letter, resume/CV, and contact information for three professional references to: Jill Wegrzyn (`jill.wegrzyn@uconn.edu`). Ideal start date between July 1st and August 1st.

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NTNU Norway Researcher position

We are hiring a 2-year Researcher at the NTNU (Norwegian University of Science and Technology) University Museum, Department of Natural History, to work on the Horizon Europe project TETTRIX, a major initiative aimed at advancing taxonomy in the genomic era. This position sits at the interface of evolutionary biology, systematics, and biodiversity informatics, with a focus on how species are discovered, delimited, and represented in an age of rapidly expanding molecular data. The project addresses a central challenge in evolutionary biology: much of Earth's diversity–particularly among hyperdiverse and poorly sampled ”dark taxa”–remains undescribed and underrepresented in biodiversity knowledge systems. The successful candidate will contribute to developing frameworks for integrating these unnamed evolutionary lineages into data infrastructures, enabling more complete representations of biodiversity and improving our ability to study patterns of diversification, speciation, and evolutionary history at scale. Responsibilities include conducting research on species delimitation and integrative taxonomy, developing approaches to represent taxonomic hypotheses (e.g. molecular clusters, OTUs) in a stable and reproducible way, and working closely with European partners to link molecular data, natural history collections, and digital biodiversity platforms. The position also involves coordination within a large international consortium and contributing to collaborative publications and future research initiatives. Qualifications: Applicants should hold a PhD in evolutionary biology, systematics, taxonomy, or a related field, with experience in species delimitation, molecular systematics, or integrative taxonomy. Experience with biodiversity data, collections, or large-scale collaborative projects is advantageous. Strong communication, organizational, and collaborative skills are essential. This position offers a unique opportunity to contribute to shaping how species are defined and operationalized in modern evolutionary biology, within a highly collaborative European research environment. Position Details This is a full-time position for 2 years. Location: Trondheim, Norway (NTNU University Museum) Start date: To be agreed/by end of year Application Materials Applicants should apply through the official job portal: https://www.jobbnorge.no/en/available-jobs/job/298989/researcher-position-in-the-horizon-eu-tettrix-projectIf you have any questions regarding the position, please contact Associate Professor Emily Hartop, email emily.hartop@ntnu.no. If you have questions regarding the recruitment process, please contact HR Senior Consultant Anne Karin Henning, email anne.karin.henning@ntnu.no Application deadline: 21.05.2026

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ThreeInstructorPositionsatUniversityofLouisiana Lafayette

Emergency Temporary Instructor- The School of Biological Sciences has multiple openings for Emergency Temporary Instructors. These positions require a minimum of a MS degree. The candidate would be expected to teach Introductory Biology at the non-major and major level, in combination with courses such as Field Techniques, Principles of Ecology, Diversity/Systematics, or laboratory sections of Anatomy and Physiology. The teaching load will be equivalent to 15 credits. Courses with large enrollments count as double credits (i.e. 6 credits for a large 3 credit course), some laboratory coordination duties may also contribute to the course load. The work expectation is equivalent to an 80Salary commensurate with experience. Successful applicants will have a robust academic record, and will be active educators in their discipline, cultivating a student body that is intellectually curious and civically engaged. Faculty members should pursue innovation informed by best practices and serve as advisors and mentors to students to encourage success. Applicants should provide a cover letter, curriculum vitae, contact information of 3 references, and a statement of teaching interests. To ensure full consideration, applications should be received by May 15th. These materials should be emailed as a single pdf file to sophie.plouviez@louisiana.edu. Appointment will be contingent upon verification of eligibility to work in the U.S. and is expected to begin August 1, 2026. The University of Louisiana at Lafayette does not discriminate on the basis of race, color, national origin, age, religion, sex, sexual orientation, or disability in admission to, access to, treatment in, or employment in its programs and activities as required by Title VI and Title VII of the Civil Rights Act of 1964, Age Discrimination in Employment Act of 1967, Age Discrimination Act of 1975, the Equal Pay Act of 1963, Title IX of the Education Amendments of 1972, Executive Order 11246, Section 503 and 504 of the Rehabilitation Act of 1973, Section 402 of the Vietnam Era Veterans Readjustment Assistance Act of 1974 and the 1990 Americans With Disabilities Act. - See more at: http://personnel.louisiana.edu/employment-opportunities/policy-nondiscriminationA Member of the University of Louisiana System

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UAlabamaBirmingham ResTech AgingEvolutionaryGenomics

We are hiring a laboratory researcher / coordinator to work in my primate genomics lab–the Primatology Alabama (PrimAL) lab–in the Department of Biology at the University of Alabama at Birmingham (UAB). Interested applicants can apply through the official job posting: https://uab.taleo.net/careersection/ext/jobdetail.ftl?job=T235391 The ideal candidate is a highly motivated individual with a minimum of an undergraduate degree and experience in genetics, next-gen sequencing, and/or other molecular biology labwork. The position would be well-suited for a recent graduate who is interested in gaining expertise in functional genomics and aging research before going to graduate school. Our lab is highly interdisciplinary and is a good fit for individuals with training in biology, genetics/genomics, ecology/ethology, anthropology, psychology, neuroscience, or related fields.

Located in Birmingham, Alabama, the PrimAL Lab studies the intersection of sociality, ecology, genomics, and health in primates. We are interested in the biological and evolutionary underpinnings of health and aging, focusing on (1) how social experiences and other environmental stimuli influence health disparities by altering physiology, physiology, and aging; and (2) how population dynamics and natural selection influence physiology and health.

Ongoing projects in our lab include those understanding:

1) how evolutionary, genetic, and socioecological differences among species influence the trajectory of epigenetic aging among primate species, 2) how social experiences influence the trajectory of gene expression aging in the primate brain, 3) how dietary differences shape gene expression aging in microglia and other brain cells of the primate brain, 4) how aging is associated with declining musculoskeletal function via gene regulation and gene expression in primate cartilage.

More information is available on our website: https://primallab.org Birmingham, Alabama is an innovation hub of the South and was recently ranked as the 6th best place to live in the United States on Livability's 2026 index (see https://livability.com/al/birmingham/?top-100=2026), reflecting the city's upward rise, vibrant and cosmopolitan culture, and high quality of life.

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UArkansas ResAssist NeuroEvoDevo

The Nakanishi Lab at the Department of Biological Sciences, University of Arkansas, (https://wordpressua.uark.edu/nakanishi-lab/) seeks a research associate to assist in studying cnidarian neural development and evolution. The laboratory's research uses the sea anemone Nematostella Vectensis and the Moon Jellyfish Aurelia sp.1 as cnidarian experimental models. The research associate will be responsible for feeding, breeding and maintaining wildtype and transgenic Nematostella Vectensis and Aurelia sp.1 at the aquarium facility. In addition, the research associate will provide technical support for research activities in the laboratory, which may involve nucleic acid extraction, PCR, cloning, sequencing, immunohistochemistry, in situ hybridization, microinjection, microdissection, transgenesis, genome editing via CRISPR/Cas9, and confocal microscopy. This person will facilitate research in the laboratory by ordering and maintaining lab equipment and supplies, ensuring EH&S compliance in the laboratory.

This is a 1-year appointment, renewable based on the need for the position, availability of funding, and continued satisfactory level of performance in the role. Regular, reliable, and non-disruptive attendance is an essential job duty, as is the ability to create and maintain collegial, harmonious working relationships with others. Qualifications: Minimum Qualifications: - Bachelor's degree in biology or related field from an accredited institution of higher education - Experience with basic molecular biology techniques

Preferred Qualifications - Master's degree in biology or related field from an accredited institution of higher education - Experience with cnidarians or other marine invertebrates

Knowledge, Skills, and Abilities: - Must possess excellent written and oral communication skills

Additional Information: This position is renewable annually based on continued need for the position, availability of funding, and satisfactory job performance.

Salary Information: Commensurate with education and experience Required Documents to Apply: Cover Letter/Letter of Application, List of three Professional References (name, email, business title), Resume Optional Documents: Proof of Veteran Status Recruitment Contact Information: Nagayasu Nakanishi, Associate Professor, nnakanis@uark.edu Apply here: https://uasys.wd5.myworkdayjobs.com/UASYS/job/Fayetteville/Laboratory-Assistant-II---Biological-Sciences_R0085884 (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UArk ResAssist NeuroEvoDevo

The Nakanishi Lab at the Department of Biological Sciences, University of Arkansas, (https://wordpressua.uark.edu/nakanishi-lab/) seeks a research associate to assist in studying cnidarian neural development and evolution. The laboratory's research uses the sea anemone Nematostella Vectensis and the Moon Jellyfish Aurelia sp.1 as cnidarian experimental models. The research associate will be responsible for feeding, breeding and maintaining wildtype and transgenic Nematostella Vectensis and Aurelia sp.1 at the aquarium facility. In addition, the research associate will provide technical support for research activities in the laboratory, which may involve nucleic acid extraction, PCR, cloning, sequencing, immunohistochemistry, in situ hybridization, microinjection, microdissection, transgenesis, genome editing via CRISPR/Cas9, and confocal microscopy. This person will facilitate research in the laboratory by ordering and maintaining lab equipment and supplies, ensuring EH&S compliance in the laboratory. This is a 1-year appointment, renewable based on the need for the position, availability of funding, and continued satisfactory level of performance in the role. Regular, reliable, and non-disruptive attendance is an essential job duty, as is the ability to create and maintain collegial, harmonious working relationships with others. Qualifications: Minimum Qualifications: * Bachelor's degree in biology or related field from an accredited institution of higher education * Experience with basic molecular biology techniques Preferred Qualifications * Master's degree in biology or related field from an accredited institution of higher education * Experience with cnidarians or other marine invertebrates Knowledge, Skills, and Abilities: * Must possess excellent written and oral communication skills Additional Information: This position is renewable annually based on continued need for the position, availability of funding, and satisfactory job performance. Salary Information: Commensurate with education and experience Required Documents to Apply: Cover Letter/Letter of Application, List of three Professional References (name, email, business title), Resume Optional Documents: Proof of Veteran Status Recruitment Contact Information: Nagayasu Nakanishi, Associate Professor, nnakanis@uark.edu Apply here: https://uasys.wd5.myworkdayjobs.com/UASYS/job/Fayetteville/Laboratory-Assistant-II---Biological-Sciences_R0085884 (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UCalifornia USA DNA Manipulation and Sequencing Specialist

Position title: DNA Manipulation and Sequencing Specialist (Junior Specialist Rank) Salary range: Commensurate with qualifications and experience. The posted UCSC Salary Scales (https://academicpersonnel.ucsc.edu/compensation/salary-scales/) set the minimum pay determined by rank and step at appointment. See the scale titled, Represented Specialist Series Fiscal Year. A salary that is higher than the published system-wide salary at the designated rank and step, are offered when necessary to meet competitive conditions. A reasonable estimate for this position is $55,000-58,600$. Percent time: Full-time (100Anticipated start: As soon as possible after the initial review of applications. Position duration: Initial appointment will be for one year, with the possibility of reappointment. Should the hiring unit propose reappointment; a review to assess performance will be conducted. Reappointment is also contingent upon the availability of funding. Position description The UCSC Paleogenomics Laboratory (https://pgl.soe.ucsc.edu/) at the University of California, Santa Cruz (UCSC) invites applications for a DNA Manipulation and Sequencing Specialist. The Paleogenomics Laboratory is a joint venture between Ecology and Evolutionary Biology Professor Beth Shaprio and Biomolecular Engineering Professor Ed Green. Under the direction of Dr. Ed Green, the successful candidate will support and assist in research that uses a genomics approach to understand how genetic variation is distributed among populations over geographic space, and how this changes through time. The duties of this job are to: 1) extract DNA from a variety of tissues, including bone, hair, and other tissues, using in-house protocols; 2) assess the quality of DNA extractions using PCR and other quantitation methods; 3) prepare and quantify genomic libraries for next-generation sequencing; 4) perform next generation sequencing using standard Next Generation Sequencing (NGS) equipment; and 5) perform preliminary quality control analyses of recovered data using bioinformatics approaches. The selected candidate must be able to learn new techniques and implement protocols with attention to detail and to participate in the research of UCSC faculty through DNA extraction, genomic library preparation, sequencing, analytical measurements, and through training and supervision of users. We are particularly interested in identifying a candidate with experience using the Illumina sequencing platform. The hiring unit will not sponsor employment-eligible immigration statuses for this position. Ecology and Environmental Biology Department: `https://www.eeb.ucsc.edu/`*Qualifications* *Basic qualifications* (required at the time the application is submitted) - Bachelor's degree or higher (or equivalent foreign degree) in molecular biology, evolutionary biology, or a related scientific field. - A minimum of six months' previous experience in laboratory research (this may include experience gained while earning degree). - Knowledge of and experience with troubleshooting DNA extraction, PCR amplification, genomic library preparation, and DNA sequencing protocols. - Bioinformatic skills, including knowledge of command-line interfaces and UNIX as well as pipelines for analysis of quality control of NGS data. Your application must demonstrate (e.g., in your C.V. or cover letter) that you meet all of the basic qualifications when you submit your application. There are no exceptions to this requirement. *Application Requirements* Document requirements Curriculum Vitae - Your most recently updated C.V., which must include a minimum of three professional references along with their contact information. The search committee will contact the references of those applicants who are under serious consideration. Cover Letter - Letter of application that briefly summarizes your qualifications and interest in the position. Apply link: `https://recruit.ucsc.edu/JPF02047`Help contact: `regreen@ucsc.edu`; `sford1@ucsc.edu` This application closed June 4th, 11:59PM Pacific.

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UGrazAustria FullProfessor MechanismsOfAdaptation

Professorship Mechanisms of Adaptation at the University of Graz, Austria The University of Graz (Austria) is seeking to hire a full professor in the field of evolutionary and developmental biology. The primary focus of this professorship is the experimental investigation of the molecular mechanisms underlying adaptations. This includes, but is not limited to, the elucidation of molecular, physiological, and/or developmental processes by which animals adapt to diverse environmental conditions. An organismal research perspective with an emphasis on aquatic systems is preferred. For more information, please see: `https://jobs.uni-graz.at/en/jobs/9b80dc8f-946b-e3cb-5799-69f0b49f712c`Application deadline is June 17. For more information on the position and to submit applications, please see: `https://jobs.uni-graz.at/en/jobs/9b80dc8f-946b-e3cb-5799-69f0b49f712c`Dr. Kristina Sefc (`kristina.sefc@uni-graz.at`)

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UHaifa EvolutionaryBiology

Molecular Biology Ph.D., postdoctoral and researcher positions open - University of Haifa The Sagol Lab for Evolution Research at the University of Haifa, directed by Prof. Adi Livnat, studies fundamental questions about how evolution occurs, focusing on the mechanisms of mutation. For more than a century, it has been thought that mutations are random with respect to fitness; namely, that while mutation rates vary across the genome, the causes of individual mutations bear no meaningful relationship to their biological consequences. Recently, however, a new methodology that enabled the measurement of de novo origination rates of individual mutations for the first time uncovered empirical patterns that were unexpected under this view. Our lab studies a range of exciting questions that follow from this new evidence, with potentially fundamental implications for our understanding of evolution. We are currently looking for highly motivated individuals with a strong background in molecular biology and a record of academic excellence for empirical studies on the origin of mutations. Ph.D., postdoctoral and researcher positions are available. For more information, read about our recent work (https://www.pnas.org/doi/10.1073/pnas.2424538122) or see our website. Requirements: Background in molecular biology/molecular genetics, high motivation and a record of excellence. To apply: Send a CV and a cover letter to adi.livnat@sci.haifa.ac.il, and arrange for 2-3 referees to send a letter of recommendation to the same address.

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UIowa AssistantProfessor EvolutionaryEcology

The Department of Biology at the University of Iowa invites applications for a tenure-track Assistant Professor of Evolutionary Ecology, with the position to begin at the start of the 2027-2028 academic year: https://jobs.uiowa.edu/faculty/view/75951We invite applications from candidates whose research addresses how the interactions of organisms, populations, or species with their environments affect, or are affected by, evolutionary processes. Candidates whose research can connect with the Biology Department's emphasis area "Resilience and Adaptation" are especially encouraged to apply. Existing strengths within Biology (https://biology.uiowa.edu/) include sex and meiosis, speciation, cell and developmental biology, behavior, neurobiology, and genomics. Opportunities also exist for collaboration with scholars in other departments on campus (e.g., Anthropology, Earth, Environment, and Sustainability, Psychological and Brain Sciences, Mathematics). The successful candidate will also be expected to teach courses in areas connected to evolutionary ecology, mentor undergraduate and graduate students, and foster a welcoming and respectful academic and work environment. The Department of Biology is in the heart of downtown Iowa City, IA (https://downtowniowacity.com/), a lively and accessible midwestern college town. A UNESCO City of Literature (the first in the U.S.) and the site of several annual cultural festivals, Iowa City has been named one of the happiest and most livable small cities in the country. Informal inquiries about the position can be directed to Dr. Tina Tootle, Chair of Biology (tina-tootle@uiowa.edu) or to Dr. Andrew Forbes, Chair of the Hiring Committee (andrew-forbes@uiowa.edu)

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VisitingAssistantProfessoratUniversityofLouisiana Lafayette

The School of Biological Sciences seeks a visiting assistant professor with expertise in Zoology or Organismal Biology. This position will have an assignment of research, teaching, advising and mentoring undergraduate research. Teaching will consist of junior/senior level courses in one of the following disciplines: Herpetology, Invertebrate Zoology, Ornithology, Mammalogy, Environmental Toxicology, Field Techniques, Principles of Ecology, or Diversity of Life/Systematics. The courses selected would depend on the department's needs and the hire's expertise. Most labs include TA support; however, the instructor would be involved in laboratory supervision and instruction and could teach a lab section if needed. This position is for the 2026-2027 academic year, with the possibility of a similar assignment in 2027-2028 depending on departmental needs and administrative approval. The teaching load would be the equivalent of 6 or 7 credit hours per semester. Research endeavors aimed at establishing a record of peer reviewed publications are expected. Collaboration with research faculty at the University is strongly encouraged. Salary will be commensurate with experience. Successful applicants will have a robust academic record, and will be active educators in their discipline, cultivating a student body that is intellectually curious and civically engaged. Faculty members should pursue innovation informed by best practices and serve as advisors and mentors to students to encourage success. Applicants should provide a cover letter, curriculum vitae, contact information of 3 references, statement of research interests, and a statement of teaching interests that addresses inclusive pedagogy and how the candidate's cultural, experiential, or academic background contributes to building an equitable scholarly environment. These materials should be emailed as a single pdf file and emailed to Karen.smith@louisiana.edu. To ensure full consideration, applications should be received by May 18th. Appointment will be contingent upon verification of eligibility to work in the U.S. and is expected to begin August 1, 2026. The University of Louisiana at Lafayette does not discriminate on the basis of race, color, national origin, age, religion, sex, sexual orientation, or disability in admission to, access to, treatment in, or employment in its programs and activities as required by Title VI and Title VII of the Civil Rights Act of 1964, Age Discrimination in Employment Act of 1967, Age Discrimination Act of 1975, the Equal Pay Act of 1963, Title IX of the Education Amendments of 1972, Executive Order 11246, Section 503 and 504 of the Rehabilitation Act of 1973, Section 402 of the Vietnam Era Veterans Readjustment Assistance Act of 1974 and the 1990 Americans With Disabilities Act. - See more at: http://personnel.louisiana.edu/employment-opportunities/policy-nondiscriminationA Member of the University of Louisiana System

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WashingtonDC US Center Head Center for Conservation Genomics Smithsonians National Zoo and Conservation Biology Institute

Center Head - Center for Conservation Genomics at the Smithsonian's National Zoo and Conservation Biology Institute in Washington DC. Details about the position and how to apply are contained via the announcement links below (for Supervisory Research Zoologist, GS-410-14/15). Note that the position will be open for applications from Thursday 5/28/26 through Wednesday 6/24/26. The DEU announcement below is open to the public for applications. The MPA announcement is for applications from current federal employees, veterans and other limits as listed in the announcement. DEU-https://www.usajobs.gov/GetJob/ViewDetails/870869600 MPA - https://www.usajobs.gov/GetJob/ViewDetails/870868000 (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Other

2026 SORTEE Conference Reminder SubmitYourContentProposal-byJune7th

Dear Colleague,

This is just to remind you that content submissions are still open for the sixth annual SORTEE conference (The Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology), which will be held virtually in October 2026. The conference will run continuously from 13th October 07:00 UTC to 14th October 10:00 UTC to cover all time zones.

To submit a content proposal, please go to: https://www.sortee.org/upcoming We accept the following types of proposals:

Unconferences: Facilitated discussions on how to make ecology, evolutionary biology, and related disciplines more open, reliable, and transparent. The goal of an unconference is to generate understanding and ideas around a topic.

Hackathons: Group projects with well-defined goals (papers, techniques, software, protocols, organisations, etc.). The goal of a hackathon is to bring people together to produce a concrete deliverable.

Workshops: Facilitators will teach tools to implement open, reliable, and transparent practices. The goal of a workshop is for attendees to learn an open science practice.

Submissions will close on June 7th.

The conference is a forum for discussing and developing ideas, while also exploring current practices for advancing research in fields related to ecology and evolutionary biology. If these topics interest you, then please consider becoming a member: https://www.sortee.org/join. The conference will be FREE for SORTEE members.

Interested in hosting a session at the 2026 SORTEE Conference, but not sure where to start? Join us to learn how to submit a proposal, develop your idea, and confidently facilitate a session. We'll walk through the process and leave time for your questions. We're offering two sessions at different times to make it easier for attendees across time zones to join. Please join whichever session works best for your schedule.

?Register to receive a calendar invite (optional): https://forms.gle/qH3mmVk2otiqHKmi9

? Option 1: Tue, May 5, 2:00 PM UTC ? Option 2: Wed, May 6, 2:00 AM UTC

You are also welcome to submit a proposal and facilitate your session in a language other than English. We will organise live translation during the conference to support this.

We strongly encourage proposals for all contribution types from people at a wide range of career stages and from members of underrepresented groups. We welcome proposals from small teams, as well as individuals. We encourage teams to include diverse perspectives, for instance, with facilitators from different countries and balanced in terms of gender and career stage. Facilitation by early career researchers (students or early career postdocs) is warmly encouraged.

Everything you need to know about the conference accessibility is available at https://sortee.org/upcoming/#accessibility. Conference registration will also soon open on the SORTEE webpage: https://www.sortee.org/upcoming. For more information on the conference, do not hesitate to contact us at conference@sortee.org

We hope to see you in October.

Sincerely, The SORTEE Conference Committee (https://sxsoty.ff62.fdske.com/e/c/01kqsffmgfy38gt7q98ma29tby/01kqsffmgfy38gt7q99fc3z163)

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AGA ResearcherCommunityEngagementAward

The American Genetic Association is excited to announce a funding opportunity for Researcher Community Engagement (RCE). RCE Award grants may be used 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.

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 local (defined as rural and under-resourced urban communities) and/or Indigenous communities. Eligible Applicants AGA members at any career stage working in biological, ecological, or genomic sciences who demonstrate a commitment to ethical, culturally respectful engagement with a specific community. Award Details Learn more about the award and application process at: `https://www.theaga.org/rce-awards-form`Applications are due June 30, 2026

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Call ESEBStudentRepresentative 2026

2026 Call for ESEB Student Representative

ESEB welcomes statements of interest for one of the two Student Representative positions. The appointed student will serve a two-year term starting in August 2026. Student Representatives provide a student perspective to the ESEB Council. They will attend ESEB Council meetings (3-4 per year, online) and develop activities to promote student involvement and interests in the Society. Student members should develop ways to promote ESEB among biology students and ways in which ESEB can better serve its student members. Student representatives should aim to attend one EMPSEB meeting and/or one ESEB congress. ELIGIBILITY Applicants must meet the following criteria: Hold an active ESEB Student Membership. Currently pursue a PhD in evolutionary biology or related area. Be able to commit to the role on a voluntary basis for the full two-year term. APPLICATION

Applications must include - a maximum one-page statement of interest, including a proposal what you would promote as ESEB student representative - a CV, and - a short support letter by the supervisor including the confirmation of the PhD status.

Please submit your application as one pdf file (not exceeding 10 Mb) by email to the ESEB Office (`office@eseb.org`; subject: StudRep2026).

Deadline: Friday, 19 June 2026

We will confirm receipt of all applications within a week. If you do not receive this confirmation, please contact the ESEB Office again.

ELECTION PROCESS The Secretary together with the current Student Representatives will screen the applications for eligibility. The names and motivation letters of the eligible candidates will be forwarded to student membership in an election. The candidate with the most votes will be appointed as the next Student representative. European Society for Evolutionary Biology — `www.eseb.org` — `office@eseb.org`

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DAMBE update

Dear Colleagues: I have just uploaded a substantially revised version of DAMBE for both Windows and Max OS (which I have tested with both the old Intel-based MACs and the new ARM64-based M-series MACs). Please download from `https://dambe.bio.uottawa.ca/DAMBE/dambe.aspx`It takes only a few clicks to install DAMBE in Windows, but many more mouse clicks for installation on MacOS. 1. Added support for IQ-TREE, which is needed for reconstructing large trees. PhyML is faster for small trees but does not use parallel computing. To access the tree-reconstructing function of IQ-TREE in DAMBE: Phylogenetics — Maximum likelihood — IQ-TREE IQ-TREE is a complicated program, so it is hard to find the optimal design of the graphic user interface, e.g., how to group connected options together. I should appreciate your feedback. The GUI is extremely cluttered at present. I did not do an exhaustive test of all meaningful combinations of options. Please let me know if you find some option combinations that do not work. 2. IQ-TREE also facilitates the selection of the best substitution models. This function can be accessed by clicking Phylogenetics — Find best sub. model 3. IQ-TREE can also simulate sequence evolution along a tree. This function can be accessed by clicking Sequences — simulate sequence evolution When you simulate multiple sequences, you naturally would need to align them all and perhaps do phylogenetic reconstruction or other analyses on all simulated data sets. Such batch-processing functions have been added. 4. Alignment with secondary structure. This is an experimental function. DAMBE will first reconstruct the secondary structure of each sequence and then align them with the secondary structure information. A default substitution matrix is included but can be replaced by your own. The matrix is 12 by 12 because each nucleotide can be in three different states: 1) in the stem (paired region) at the 5' side, 2) in the stem at the 3' side, and 3) in the loop. This function is accessible from 'Alignment — Align with secondary structure'. 5. Multiple sequence alignment with a user-supplied guide tree. This is a convenience when you access the MAFFT function in DAMBE. 6. Many new tables with 1) codon frequencies from highly expressed genes and 2) background frequencies for computing ITE. 7. The nucleotide and amino acid coloring is now more friendly to color-blind users. 8. Keep in mind that sequence alignment and phylogenetics represent only a small fraction of DAMBE functions. Other functions in DAMBE are described in my book (Xia, X. 2026. Bioinformatics and the cell: modern computational approaches in genomics, proteomics, and transcriptomics. Springer. Switzerland. 3rd edition. https://link.springer.com/book/10.1007/978-3-032-18842-7). This new book does not include any chapter on molecular phylogenetics because I am currently writing a separate book entitled "Molecular phylogenetics". A major revision is likely to introduce bugs. Please report to me if you notice anything unusual. If I have time, I will write a more detailed report on the update. ***IQ-TREE, PhyML, MUSCLE, and MAFFT are separate programs. The authors graciously granted me permission to incorporate their functions in DAMBE. I designed the graphic user interface mainly for my own research because I cannot remember all the command-line options. If you call these programs within DAMBE, please cite the paper that I have included in the graphic user interface. Best. Xuhua Gendron 278/287 Professor, Department of Biology University of Ottawa https://scholar.google.ca/citations?hl=en&user=fbAS_FcAAAAJ&view_op=list_works (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

ESEB Call Policy Evolutionary Biology Funds Sep30

ESEB 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 im-

Interactive viewer of the Open Tree of Life

EvolDir members may be familiar with the Open Tree of Life project https://tree.opentreeoflife.org/about/open-tree-of-life that curates a phylogeny of all life based on a synthesis of taxonomy and phylogenies (the "synthesis tree").

I have created an alternative viewer for the synthesis tree at https://iphylo.org/ott-viewer. The viewer is at the "proof of concept" stage, but I'm hoping it will be a useful starting point for anyone interested in exploring the Open Tree of Life synthesis tree. Feedback welcome.

Regards,

Rod Page

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Online Movie An extraordinary guest to celebrate Sir D Attenborough

An extraordinary guest to celebrate Sir David Attenborough Sir David Attenborough turned 100 on Friday! Sure, we do what we do for the science of development and evolution ... but also out of fascination for the beauty and complexity of Life. So, we decided to produce a 3.5-minute movie in which an extraordinary guest celebrates Attenborough's birthday. See for yourself: https://youtu.be/oAwsMkMdAMA We hope that our movie will contribute to honouring the man who helped the world fall in love with nature. Social media links: - X/Twitter: https://x.com/LANEVOL/status/2052621779261124672?s - Bluesky: https://bsky.app/profile/lanevol.bsky.social/post/3mlcysxxa3s25 - LinkedIn: https://www.linkedin.com/Have a great Attenborough weekend! Michel & Athanasia https://www.lanevol.org/news/article/extraordinary-guest-celebrate-sir-david-attenborough https://www.lanevol.org (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

ResearchExchangeFunding WildAnimalMicrobiomeAndEvolution WAME

Dear all, The ESEB Wild Animal Microbiome and Evolution (WAME) special topic network are pleased to announce the next round of funding for early career research exchanges. We invite applications from early career researchers working in the field of microbiome science who wish to visit a lab/group with complementary research interests. This can be to learn new methods, discuss future collaborations, grant or fellowship proposals, or just to go and present your work and hear about theirs! WHO CAN APPLY Early career researchers - postgrad research students, postdocs and junior research fellows. Applicants of any nationality and country of residence are welcome to apply. WHAT CAN BE FUNDED: Up to EUR1400 towards travel and accommodation required for the research visit only. HOW TO APPLY: Applicants should fill out the WAME ECR Research Visit form (https://drive.google.com/file/d/10ah_pBY0ls1VptLTUNEUli54hZbJo4bT/view?usp=sharing) and submit this in a single PDF file to stn.wame@gmail.com along with two short letters of support (one from current supervisor / line manager) and one from host research group. KEY DATES: Deadline for applications Friday 19th June 2026 Awards announced at the end of June 2026 All costs must be claimed before end of May 2027 Best regards, WAME organising committee

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Scicomm LIFT Recruiting evolution instructors to test scicomm training initiatives 2026-2027

Dear Colleagues,

We are recruiting professors, instructors, and trainers of students in evolution, ecology, behavior, and/or conservation (EEBC) to participate in an exciting new research project (Scicomm LIFT) that seeks to enhance graduate students' ability to communicate science effectively and ethically with non-specialist audiences (NSF DGE 2429657 Leveraging Institutional capacity for eFfective graduate student Training).

If you are looking for ways to offer or improve science communication training for your evolution graduate students and would like to get more support (and even a stipend!) for the scicomm training opportunities you provide, you might be a great fit.

At this time we are seeking potential participants who:

1. Teach a graduate course in an EEBC field or teach a full term scicomm course (in the 2026/2027 academic year) 2. Are willing to engage their students in educational interventions that teach ethical scicomm

There are many perks to participating! - A stipend for your time and effort - Collaboration with a growing community of practice focused on teaching scicomm in evolution fields - Access to vetted scicomm teaching resources - Support to overcome barriers that may prevent instructors from embedding science communication (scicomm) training in graduate programs

You can express interest in participating by taking a 5-minute survey here! https://docs.google.com/forms/d/e/1FAIpQLSdZxHtDFXpyHtvNiPX0n66jRrJrwZ6x4r7WD_6pJWpCEmSHGg/viewform If selected, you will take part in one of three intervention trainings: a one-hour workshop, a one-week module, and/or a full-term course. Onboarding will include synchronous virtual training on July 9 or 10, 2026 with a second training option offered in mid August, 2026.

For more information about this study, visit us at https://www.scicommlift.com/aim-2. Many thanks, The Scicomm LIFT in Classrooms team

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Siberian jay project Field Assistant Bird Research

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

We are seeking one highly motivated field volunteer to support a long-term ecological research project on Siberian jays led by Dr. Michael Griesser (University of Konstanz) and Dr. Miya Warrington (Oxford Brookes University). For the upcoming field season (11 Sept - 31 Oct 2026) we are looking for 1 assistant to help with our work on foraging ecology in Siberian jays. The assistants will help with catching and ringing birds, do behavioural observations, do field experiments, and assist with data management. Observe that temperatures in the end of the season can be as low as -20C, and field work involves walking up to 15km per day. An overview over our past work can be found here: `https://www.youtube.com/watch?v=JaH6wjAYAiE` Essential qualifications: 1) Bird ringing and mist-netting experience 2) Field work experience, involving behavioural observations and experiments 3) Ability to work in small teams and sociable personality 4) Driving license (manual transmission) 5) Fluent in English 6) Highly motivated

Applications received before 1 June July 2026 will be given full consideration.

If you wish to apply, send a motivation letter, CV, and two contacts for references (as a single PDF) to `michael.luondua@gmail.com`

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SmallGrantOpportunity AGAHumaneGenomicsEducationAward

Dear Colleagues,

The American Genetic Association has recently created two awards that may be of interest to EvolDir.

The Award for Humane Genomics Education (HGE) is a pilot program from the American Genetic Association 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. The award will support a variety of educational programs, with up to 2000*availabletoeachapplicant.ProposalswillbeacceptedupuntilJune*1.

Inquiries regarding the HGE award may be made to the award coordinator, Klaus-Peter Koepfli: `klauspeter.koepfli527@gmail.com`

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 local (defined as rural and under-resourced urban communities) and/or Indigenous communities. The award will provide up to 2000*infinancialsupportforcommunityengagementactivitiesthatfalloutsidetypicalresearchfunding,includingextendedstays giving(cashgiftsnotallowed),andotherrelationship−buildingexpenses.ProposalswillbeacceptedupuntilMay*15.

Inquiries regarding the RCE award may be made to the award coordinator, Katie Lotterhos: `k.lotterhos@no` rtheastern.edu

The full text of the announcements is below:

¡https://us3.campaign-archive.com/?e=__test_email__&u=8bb5b89e00b071fa27c043310&id@e7bdee99>[image: Logo] ¡https://www.theaga.org/> Humane Genomics Education Award (HGE) ¡https://theaga.us3.list-manage.com/track/click?u=8bb5b89e00b071fa27c043310&id/a9210d5c&e|56e537c1>

Deadline 1 June 2026 i? 1/2 " Awards announced 1 July 2026

The American Genetic Association provides HGE grants to support humane genomics education, aiming to enhance student understanding of genetics and combat bias within genetics and evolutionary biology.

Overview

The Award for Humane Genomics Education 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. As developed and described by Donovan et al (2024), humane genomics education focuses on teaching the complexity of human genomics that is not captured by a basic introduction to Mendelian genetics. This approach focuses on describing the distribution of genetic variation within and between populations and the multifactorial basis of complex human traits, including polygenic inheritance and genotype by environment interactions. Integrating these principles provides a comprehensive understanding of human diversity that directly counters the deterministic narrative that human traits and social identities are fixed, inevitable products of our DNA.

Purpose

The Award for Humane Genomics Education is a pilot program from the AGA to support educational activities and initiatives at the high school or undergraduate level that promote understanding of human genetics and genomics. 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.

Eligible Applicants

Professional educators teaching at the high school and undergraduate levels, including 2-year and 4-year institutions. It is anticipated that applicants will be currently teaching classes in Biology, Genetics, Molecular Biology or Biological Chemistry, or expect to be teaching in these areas in the near future. However, interdisciplinary teams that include educators working in other areas are welcome. Applications from instructors at under-resourced institutions are particularly encouraged to apply.

— / —

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

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SpecialIssue GenomicAndFitness-ConsequencesOfGeneFlow

Molecular Ecology - Special Issue on the Genomic and Fitness Consequences of Gene Flow Submission Deadline: Monday, 30 November 2026 https://onlinelibrary.wiley.com/page/journal/1365294x/call-for-pap ers/si-2026-000452 Gene flow represents one of the primary mechanisms of evolution for populations and species. Introduction of genetic material may counteract or facilitate evolution by natural selection, and can be a mechanism for diversification. This special issue will cover all aspects of gene flow among individuals (horizontal transfer), populations, and species (introgression) with a focus on the fitness consequences of genetic exchange. Appropriate submissions include empirical, theoretical, and methodological contributions aimed at improving our understanding of the genomic and fitness consequences of gene flow.

Topics of interest for this call for papers include but are not restricted to the following:

Contributions to adaptation; Counteracting selection; Introgression between lineages stalled by barrier loci; Introgression between lineages contributing to adaptation; Contributions to purging of genetic load; Counteracting genetic drift; The spread of adaptive genetic variation.

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SSB Mentorship Program for 2026-2027

SSB is recruiting new mentees and mentors to participate in the Mentorship Program for 2026-2027! The Mentorship Program helps facilitate new professional relationships between graduate students and postdocs with more-established members of the systematics community, such as faculty, curators, teachers, researchers, etc. Mentoring pairs typically meet virtually once per month throughout the year. It's a great way to find your community, meet new people, support your colleagues, and get a fresh perspective on systematics research. Apply by completing this form: https://forms.gle/1daBQbswoFqjGZXx9. Applications are open until June 12th, 2026. Visit https://www.systbio.org/mentorship-program.html to learn more about the program. Please contact mentorship@systematicbiologists.org with any questions or comments. The SSB Mentorship Program Team Michael Landis, Laura Kubatko, Uhunwa Precious Igho-Osagie, Sean McHugh

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Study Scientific Reasoning

Invitation to participate in a study about scientific reasoning Dear colleague,

We are a research team from Carnegie Mellon University, the Santa Fe Institute, and Johns Hopkins University. We are conducting a study that explores how scientists reason about research findings. Your insights as a biologist would be essential for this research, and we invite PhD students, postdocs, research scientists and faculty to participate.

The study involves completing one online survey (approximately 20 - 40 minutes). In the survey, you will be invited to read a series of research findings and provide judgments about them, explain them, and reflect on possible follow-up studies that could be conducted to better understand these findings. Your participation will help advance our understanding of how scientists reason about and build on prior research findings.

Participation is entirely voluntary, and your responses will remain anonymous. To thank you for your time, you will be compensated with a $30 Amazon Gift Card following completion of our survey.$

If you are interested in participating, please contact the research team via email at scientificreasoningstudy@gmail.com.

Thank you for considering this opportunity to contribute to a project exploring how scientists reason about and build on prior research findings. Your insights will make a meaningful contribution to this research!

Best, Di Liu, Johns Hopkins University (`https://www.di-liu.com/`) Marina Dubova, Santa Fe Institute (`https://www.mdubova.com/`) Kara Kedrick, Carnegie Mellon University (`https://sites.google.com/andrew.cmu.edu/kara-kedrick?usp=sharing`)

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Support Graduate Students on their Research Journey

The Society for the Study of Evolution is raising funds for our Graduate Research Excellence Grants (`https://www.evolutionsociety.org/content/society-awards-and-prizes/graduate-research-excellence-grants.html`), which provide graduate students around the globe with funds for evolutionary biology research projects. In this competitive program, recipients gain not only the funds to fuel their creative and impactful research projects, but also the confidence, skills, and experience to help launch them into a future career in evolutionary biology.

The GREG program is a key component of SSE's mission. Each year, we receive many more outstanding GREG proposals than we can fund. In 2025, we received 334 proposals, and were able to fund only 31. This year, with additional revenue from our society-owned journals Evolution and Evolution Letters, we can award up to 50 grants. But with current and increasing cuts to science funding and academic opportunities, we want to provide even more support for students.

Check out our campaign to donate. Or, share the link with your networks:

`https://www.gofundme.com/f/support-students-on-their-scientific-research-journey`Thank you for your support! – Kati Moore she/her Communications Manager Society for the Study of Evolution `communications@evolutionsociety.org` `www.evolutionsociety.org` (to subscribe/unsubscribe the EvolDir send mail to `evoldir@evoldir.net`) `evoldir@evoldir.net`)

ULeipzig Germany Masters Program in Evolutionary Anthropology

Our new Masters Program in Evolutionary Anthropology between the Max Planck Institute for Evolutionary Anthropology and the University of Leipzig, Germany has just been officially announced. Please help us to spread the word to interested students that might be excited to join the program: `https://www.uni-leipzig.de/en/studying/prospective-students/courses-of-study/degree-programme/course/show/evolutionary-anthropology-m-sc-1`The deadline for applications is end of May 2026. The program will start in October this year. There us usually no tution fees at German universities. This Master's program in Evolutionary Anthropology at UL offers a distinctive opportunity for students to enter the field while gaining a comprehensive understanding of human evolution. It provides a broad, interdisciplinary perspective on the development, diversity, origins, and history of our species, equipping students with the theoretical knowledge and analytical skills needed to engage with key questions about humanity's past. We very much look forward to engage with the first cohort of students

PostDocs

Avignon France Eco-evolutionary modelling

As part of the BackOut ANR project (Eco-evolutionary feedback loops out from the laboratory), we hire a postdoc having strong quantitative training, experience in statistical modelling and scientific programming, and a PhD in ecology, evolution, biostatistics, applied mathematics, or in a closely related field. The position is especially well suited to candidates interested in hierarchical and Bayesian modelling, eco-evolutionary dynamics, quantitative genetics, population dynamics, and the development of mechanistic inference from complex biological data.

PROJECT DESCRIPTION: BackOut seeks to understand whether, how, and when eco-evolutionary feedback loops shape the stability and functioning of natural systems. These feedback loops arise when ecological conditions, such as population density or environmental variation, influence selection and evolution, while the resulting phenotypic changes in turn affect population dynamics, species interactions, and ecosystem functioning. Although such reciprocal links are increasingly recognised as central to the dynamics of populations and communities, they remain extremely difficult to quantify in natural systems from observational data alone. BackOut addresses this challenge by developing new inferential frameworks to recover these feedbacks from empirical data.

(1) The postdoc will develop and apply extended capture-recapture animal models (CRAMs) to investigate body-size-dependent eco-evolutionary feedback loops in brown trout. CRAMs combine capture-recapture approaches, which account for imperfect detection while estimating survival and population den-

sity, with animal models from quantitative genetics, which infer breeding values and the additive-genetic component of phenotypic variation. In the trout system, the aim is to integrate capture histories, phenotypic measurements, incomplete growth information, and pedigree data within a single hierarchical framework in order to quantify both directions of the feedback loop: how ecological conditions shape selection, and how phenotypic variation in turn affects fitness and population dynamics.

(2) The postdoc will also link individual-based inference in CRAMs to population-level inference based on mechanistic difference-equation models designed to recover hidden eco-evolutionary feedbacks from simpler abundance-and-phenotype time series. This line of research will build on recent mechanistic-statistical and neural differential equation approaches. In practice, the postdoc will work at the interface between detailed individual-based data and lower-dimensional time-series inference, helping to connect the direct estimation of feedbacks from capture-recapture-with-pedigree data with their indirect reconstruction from mechanistic dynamical models.

(3) Finally, the postdoc will contribute to the development of related CRAM approaches for crayfish data generated within the project and, in close interaction with project members, will take part in the broader cross-system comparison involving trout, crayfish, and medaka time series. This comparative perspective is an important component of BackOut, whose ambition is not only to estimate eco-evolutionary feedbacks in a single empirical system, but also to assess the generality of the underlying mechanisms and inferential tools across contrasted biological contexts.

POSITION DETAILS: This is a full-time, 20 months position, with the potential to extend pending additional funding. The successful candidate will be based at INRAE BioSP in Avignon, where we develop mathematical and statistical methods for spatial and spatio-temporal processes, notably in ecology and evolutionary ecology. The postdoc will be co-supervised by Julien Papaix and Eric Edeline, and will work in close connection with Eric Edeline's group at INRAE DECOD in Rennes. The project will also include interactions with the broader BackOut consortium and trips to Oslo to work with Asbjorn Vollestad's group, where the trout dataset was collected and where long-term knowledge of the study system has been developed.

SALARY: The monthly salary will be around EUR3,500 gross (approximately EUR2,800 net) and will be set according to the current INRAE salary scale, depending on the candidate's experience.

APPLICATIONS: send a CV and a cover letter to Julien Papaix (julien.papaix@inrae.fr) and Eric Edeline (eric.edeline@inrae.fr) before June 21st 2026.

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Bangor EvolutionaryEcologyInsects

Postdoc: Insect evolutionary ecology and their responses to the invasive plant Rhododendron ponticum. We are seeking a Postdoctoral Research Officer for a project focusing on the phenotypic and genomic mechanisms that native insect species may be using to utilise a non-native and invasive host plant, Rhododendron ponticum. The post will involve fieldwork collecting herbivory data, collecting and analysing genomic data of a diversity of species, and lab experiments. Submit your application before the deadline of the 5th of June 2026. Contact Dr Benjamin Jarrett (b.jarrett@bangor.ac.uk) for informal inquiries. More information and to apply see here: https://jobs.bangor.ac.uk/details.php.en?id=QLYFK026203F3VBQB7V68L0TX&nPostingID=9116&nPostingTargetID=9943&mask=stdext&lg=UK (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Cambridge Postdoc EvolutionaryNeurobiology

A postdoctoral Research Associate post is available with Professor Stephen Montgomery's Research Group in the Department of Zoology at the University of Cambridge. This position is part of a recently awarded Wellcome Trust Discovery grant on the developmental control of neural cell number and type. The applicant will work on understanding the evolution of neural circuits associated with a major expansion of the insect learning and memory centre, the mushroom bodies, in Heliconius butterflies. The principal aim for this post is to develop methodologies to map and analyse, whole brain projectomes, quantifying patterns of connectivity and cell morphologies across closely related species with divergent neural morphologies. The approach may include a combination of spatial transcriptomics, immunohistochemistry, and nanotomography. A very strong background in quantitative analysis and established skills in bioimaging and/or molecular biology will be essential, and prior experience with, or demonstrable interest in, insect neurobiology is highly desirable. The successful candidate will join a productive and supportive team based in Zoology, alongside researchers with complementary expertise in bioinformatics, development, neuroscience and behaviour. There will be opportunities for collaboration across the project, and close teamwork and a collaborative spirit will be essential. The successful applicant will also be expected to demonstrate scientific independence matching their technical expertise while perusing their own, specific objectives. There will be opportunities to contribute to training new team members and to general project management, as well as to participate in public engagement and community-orientated activities. The successful applicant will have a dedicated training budget and a supportive and engaged supervision team. For more information, please see: `https://www.cam.ac.uk/jobs/research-associate-fixed-term-pf49578`Informal enquiries are welcomed and should be directed to: Professor Stephen Montgomery [email: `shm37@cam.ac.uk`]. Prof Stephen Montgomery He/Him `www.shmontgomery.co.uk` (to subscribe/unsubscribe the EvolDir send mail to `evoldir@evoldir.net`) `evoldir@evoldir.net`)

CambridgeUK Molecular evolution functional genomics

Dear evoldir community, We invite applications for a 4-year Postdoctoral Research Associate position in Molecular Evolution and Functional Genomics, jointly supervised by Dr Gamze Gursoy and Dr Nicola De Maio at the University of Cambridge. For more information on the post, and to apply, please visit `https://www.jobs.cam.ac.uk/job/55572/`.Thank you, and please share with anyone who may be interested, Gamze and Nicola

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ConservationGenomics 2years UWisconsin Madison

We are hiring a 2-year Postdoctoral Research Associate to conduct a genomics study on the ecological and evolutionary underpinnings of dispersal and range expansion of invasive barred owls in California. This work is part of a collaborative project funded through the California Department of Fish and Wildlife's Cannabis Restoration Grant in partnership with the Hoopa Valley Tribe. The project seeks to unravel the ecological and evolutionary mechanisms sharing individual dispersal patterns and population range expansion of invasive barred owls (Strix varia) in California. Using genomic kinship and landscape genomics approaches, the project integrates existing and newly generated SNP data (Oxford Nanopore sequencing) to understand movement pathways and environmental drivers of dispersal. Additional genomics-based projects of mutual interest can be developed. Because barred owls are an invasive species in the Pacific Northwest and California, this work is situated within a broader management context that includes lethal removal. Applicants should be aware of and comfortable working within this applied conservation framework. Responsibilities: Oxford Nanopore library preparation and sequencing; generate and analyze genomic data; perform population and landscape genomic analyses to address project objectives; lead preparation of at least two peer-reviewed manuscripts

Required: Ph.D. in ecology, evolutionary biology, genetics, genomics, wildlife biology, or a related field; experience with molecular laboratory techniques and genomics data analysis; strong scientific writing skills and history of publishing impactful peer-reviewed papers in ecology, evolutionary, or conservation journals; willingness to work with samples derived from invasive species removal Preferred: Experience with next-generation sequencing (NGS) library preparation; familiarity with Linux and high-performance computing environments; experience analyzing SNP and/or whole genome datasets; background in conservation genomics or molecular ecology

The postdoctoral researcher will work directly with Dr. Emily Fountain in a collaborative genomics lab that emphasizes shared learning, mentorship, and teamwork. The selected applicant will also work under supervision and collaboration with Dr. Zach Peery. This position involves engaging with the Peery Lab through meetings and group activities, with opportunities for interdisciplinary collaboration and community-building.

This project is conducted in partnership with the Hoopa Valley Tribe, and we welcome applicants interested in research at the intersection of genomics, conservation, and Tribal natural resource priorities. We value diverse perspectives, interdisciplinary experiences, and community-engaged approaches to science.

Website: https://peery.russell.wisc.edu/ Position Details This is a full-time, 2-year position, with the potential to extend pending additional funding. This position will be based full-time, on site, at the University of Wisconsin - Madison. Salary: $70,000 + benefitsAnticipatedstartdate : Earlieststartdateisanticipatedtobe15June2026$

Application Materials To apply, please submit the following materials to Dr. Emily Fountain at efountain@wisc.edu: A current resume/CV, a cover letter briefly describing qualifications relevant to the positions, and three professional references. Applications will be considered on a rolling basis, but priority will be given to applications received by 18 May 2026.

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Cornell AntimicrobialPeptide-Evol-QuantGenet

The Lazzaro Lab at Cornell University is recruiting postdocs for a research project on the molecular evolution and quantitative genetics of antimicrobial peptides in Drosophila and other insects. Antimicrobial peptides (AMPs) are ubiquitous in animals and plants. They are particularly abundant in barrier epithelia where they protect against opportunistic bacterial infection. AMPs are the major mechanism for antibacterial immune defense in adult Drosophila melanogaster and other insects. This project will examine the varied roles of distinct D. melanogaster AMPs in fighting a spectrum of bacterial infections, using evolutionary and functional genetic approaches in combination with cell biology and protein biochemistry. We are particularly looking for scientists with expertise and/or interest in molecular evolutionary and population genetic analysis of AMPs in D. melanogaster and across the genus Drosophila, and/or in quantitative genetic analysis of AMP allelic variation in natural populations. Interested candidates should directly contact Prof. Brian Lazzaro at bplazzaro@cornell.edu. Please include a CV and a brief statement of research background and interests. Candidates must hold a PhD when starting the position. For more details about our work, visit our lab website at https://www.lazzarolab.org (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Cornell EvolutionaryModeling

The Messer Lab at Cornell University is recruiting a postdoctoral researcher Our group studies the population genetics of rapid evolution using mathematical models, computer simulations, and genomic data from both natural and laboratory populations. Our overarching goal is to develop models that more accurately capture the dynamics of rapid evolutionary processes. Building on these models, we create new statistical and computational tools to study rapid evolution through a quantitative lens and better predict its outcomes (https://messerlab.org). We are seeking to hire a scientist with a strong quantitative background who is interested in addressing research questions in one or more of the following broad areas: - Spatial population genetics - Eco-evolutionary dynamics - Gene drive modeling - Conservation genomics - Machine learning and SLiM simulations - Theory and modeling at the interface of ecology and evolution The position is fully funded for at least two years by grants from the Gordon and Betty Moore Foundation and the Simons Foundation, and offers a competitive salary, full benefits, as well as generous discretionary research funds. As part of the Gordon and Betty Moore postdoctoral fellow cohort at Cornell, you will be invited to several specialized convenings throughout your appointment. The position also provides extensive opportunities for collaborations within Cornell, across the US, and internationally. The start date is no later than September 1, 2026. Interested candidates should contact Prof. Philipp Messer at messer@cornell.edu. Please include a CV and a brief statement of research background and interests.

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Madrid MicrobialEvolution CompetitiveFellowship

MSCA Postdoctoral Fellowship Opportunity

We are seeking a highly motivated early-career researcher to apply with us for the upcoming MSCA Postdoctoral Fellowship, the top scheme of this kind for early-career researchers from the European Commission. We are looking for someone passionate about understanding the rules that guide rapid adaptation in microbes, in particular how the interplay between epistasis and mutation biases shapes adaptive predictability (see Couce 2024 Science; Melero-Jimenez 2025 Nat Commun; Barber & Couce 2026 Nat Commun). The ideal candidate has demonstrated experience in experimental evolution, molecular biology, or bioinformatics, and is able to work with a high degree of independence. The candidate is expected to contribute ideas to shape the project to be submitted. We will prioritize projects focusing on the evolution of microbial consortia, either in the context of the human microbiota adapting to antibiotics, or plant-associated and pathogenic bacteria. The call deadline is 9 September 2026. This highly regarded fellowship provides generous funding for a 2-year period. Feedback from the call is expected in early 2027, and, if successful, the estimated starting date would be between April-May 2027 (extendable up to September 2027). Eligibility (MUST READ; strict criteria, candidates not fitting the eligibility criteria will not be considered): - Candidates must hold a doctoral degree and have a maximum of 8 years of postdoctoral experience. - The call is extremely competitive, candidates should have ¿=3 first-author research articles in prominent journals (specialist or multidisciplinary; reviews and opinion pieces do not count). - International mobility is required. At the call deadline (9 September 2026), candidates must not have resided or worked in Spain for more than 12 of the previous 36 months. To apply, please send a single PDF to acouce@cnb.csic.es including: - A complete CV (with contact information) - A 1-page motivation letter outlining your 3-5 most relevant research contributions - A brief 1-page proposal of your future research project Please include ”MSCA-IF.MicrobialEvolution” in the subject line. The call is highly competitive; only candidates truly meeting ALL requirements will be considered.

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NHMLondon AncientDNA

Dear EvolDir community, A Postdoctoral Research Assistant position in Ancient DNA is available with PI Dr Selina Brace, at the Natural History Museum (NHM) in London, UK Position Description: A Leverhulme funded PDRA position is available for 3 years working on ”Human-dog co-evolution as a driver of behaviour change in the Upper Palaeolithic” . This is a biomolecular based research project that will generate aDNA and isotope data to analyse canid specimens alongside existing human genetic, archaeological and environmental data. We are seeking an enthusiastic Postdoctoral Researcher who holds a PhD including working with ancient DNA. Work experience in an a-DNA lab using aDNA extraction and library building methods for NGS sequencing is essential. Experience in the application of custom bioinformatics pipelines for the computational analyses of degraded genomic data, using programs relevant for phylogenetic and nuclear DNA population level analyses are also required. Your role will also include the interpretation of isotopic data and developing species-distribution models and agent based modelling. Full Details and application pack can be found here: https://jobs.nhm.ac.uk/Job/JobDetail?JobId=809&source=JobTrainRSSFeedLocation: NHM London UK Duration: 3 years Closing Date: 16/06/2026 Start Date: 01/10/2026 For informal enquires please email Selina Brace: s.brace@nhm.ac.uk

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NTNU Norway Researcher position

We are hiring a 2-year Researcher at the NTNU (Norwegian University of Science and Technology) University Museum, Department of Natural History, to work on the Horizon Europe project TETTRIX, a major initiative aimed at advancing taxonomy in the genomic era. This position sits at the interface of evolutionary biology, systematics, and biodiversity informatics, with a focus on how species are discovered, delimited, and represented in an age of rapidly expanding molecular data. The project addresses a central challenge in evolutionary biology: much of Earth's diversity–particularly among hyperdiverse and poorly sampled "dark taxa"–remains undescribed and underrepresented in biodiversity knowledge systems. The successful candidate will contribute to developing frameworks for integrating these unnamed evolutionary lineages into data infrastructures, enabling more complete representations of biodiversity and improving our ability to study patterns of diversification, speciation, and evolutionary history at scale. Responsibilities include conducting research on species delimitation and integrative taxonomy, developing approaches to represent taxonomic hypotheses (e.g. molecular clusters, OTUs) in a stable and reproducible way, and working closely with European partners to link molecular data, natural history collections, and digital biodiversity platforms. The position also involves coordination within a large international consortium and contributing to collaborative publications and future research initiatives. Qualifications: Applicants should hold a PhD in evolutionary biology, systematics, taxonomy, or a related field, with experience in species delimitation, molecular systematics, or integrative taxonomy. Experience with biodiversity data, collections, or large-scale collaborative projects is advantageous. Strong communication, organizational, and collaborative skills are essential. This position offers a unique opportunity to contribute to shaping how species are defined and operationalized in modern evolutionary biology, within a highly collaborative European research environment. Position Details This is a full-time position for 2 years. Location: Trondheim, Norway (NTNU University Museum) Start date: To be agreed/by end of year Application Materials Applicants should apply through the official job portal: https://www.jobbnorge.no/en/available-jobs/job/298989/researcher-position-in-the-horizon-eu-tettrix-projectIf you have any questions regarding the position, please contact Associate Professor Emily Hartop, email emily.hartop@ntnu.no. If you have questions regarding the recruitment process, please contact HR Senior Consultant Anne Karin Henning, email anne.karin.henning@ntnu.no Application deadline: 21.05.2026

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Population and Landscape Geneticist

Postdoctoral Researcher - Population and Landscape Geneticist - wildturkeyDNA

Job Description and Position Summary: We seek a Postdoctoral Researcher in population and landscape genetics, who will be mentored by Dr. Philip Lavretsky in the Department of Biological Sciences at the University of Texas at El Paso (UTEP), and co-mentored by Dr. Michael Chamberlain in the Warnell School of Forestry and Natural Resources at the University of Georgia (UGA). Researcher will work primarily on all aspects of wildturkeyDNA (https://wildturkeydna.com), a state-of-the-art, citizen-assisted research project launched in 2025. The project was created through a partnership between the Wild Turkey Lab at UGA, the Lavretsky Lab at UTEP, the National Wild Turkey Federation, Ducks Unlimited, and the Low Country Game Bird Foundation. The researcher will collaborate with a team of researchers at both UTEP and UGA to study population genetics of wild turkeys at multiple spatial scales using the most comprehensive genetic dataset ever collected on the species. Specific objectives of wildturkeyDNA on which the researcher can focus include: 1. Assess population structure within and between wild turkey subspecies. 2. Evaluate population genetic connectivity within and among states 3. Calculate levels of hybridization, with particular interest in regions where multiple subspecies were translocated during restoration activities. 4. Assess levels of standing genetic diversity, inbreeding coefficients, and effective population sizes within and among states. 5. Continue determining the origin of odd plumage traits and the prevalence of genetics linked to domestic and domestic x wild turkey crosses in wild populations. Beyond the aforementioned project objectives, the researcher will be given ample opportunity to pursue research topics of interest to them. The rich dataset now includes thousands of samples with each sample accompanying metadata (i.e., date, location, plumage, movement data) that has the potential to answer important questions spanning across evolutionary, ecological, and conservation biology.

ABOUT UTEP: Located in one of the largest binational communities in the world, The University of Texas at El Paso is unique among R01 research institutions, with an enrollment of ¿25,000 students today. The Department of Biological Sciences, with doctoral programs in Ecology and Evolutionary Biology and Bioscience, is among the most productive departments on campus. Core facilities in the NIH sponsored Border Biomedical Research Center include capacities for genomic sequencing, bioinformatics, and statistics; Biodiversity Collections, multiple vivaria, and the 45,000 acre Indio Mountains Research Station provide research opportunities. More information is available at the Department of Biological Sciences website. Essential Job Duties: The postdoctoral fellow will lead wildturkeyDNA research objectives as part of the Lavretsky Lab at UTEP. The fellow will coordinate day-to-day wildturkeyDNA efforts with respective staff and doctoral students to ensure continuous samples collection and processing. The fellow will have ample opportunity to mentor at the undergraduate and graduate levels, including building their own research foci as they relate to wildturkeyDNA and other projects currently going on at the Lavretsky lab (`https://www.utep.edu/science/lavretskylab/`). The fellow will not only work alongside Lavretsky to ensure that ancestry analyses are done timely for the project but will be tasked to generate peer-reviewed publications. The fellow will need to demonstrate an ability to communicate regularly with project PIs, but also effectively to constituents and the public through various popular media outlets.

Minimum Qualifications - PhD in genetics, conservation genetics, or a related discipline - Experience in handling large genomic datasets, including essential bioinformatic pipelines and subsequent methods to attain summary statistics, genetic ancestry, population connectivity, etc. Preferred Qualifications - Understanding of landscape and wildlife ecology - Strong quantitative and/or modeling skills - Experience working on collaborative research projects - Strong communication, project, and time organizational skills - Demonstrated ability to interact successfully with an interdisciplinary team and with project partners, including state and federal agencies, along with non-governmental conservation organizations - Experience with analysis and software such as ADMIXTURE, vcftools/bcftools, Plink, and/or other similar tools required for bioinformatics and post-processing genomic datasets for various questions.

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RutgersU FunctionalMorphologyVertebratePaleontology

The brand new Formorphology Lab at Rutgers University (New Jersey) is looking to hire a three-year postdoc starting this Fall 2026. Salary: 65, 000.

Lab Website: `https://www.formorphologylab.com/` The lab's focus will be on the functional and biomechanical drivers and underpinnings of secondarily aquatic transformations in amniotes, ideally from a postcranial lens. I am seeking applicants with strong backgrounds in the following areas: vertebrate and functional morphology, paleontology, biomechanics, comparative anatomy, and phylogenetics. I would also be keen on those with skills in computational fluid dynamics and kinematics.

If interested, please fill out the form below.

`https://forms.gle/Vnag3EWDqWdLqQWG7` (to subscribe/unsubscribe the EvolDir send mail to `evoldir@evoldir.net`) `evoldir@evoldir.net`)

Stockholm Sweden Postdoc Brown bear spatio-temporal dynamics

Postdoc: Brown bear spatio-temporal dynamics, Stockholm (SWEDEN)

The Swedish Museum of Natural History is advertising a post-doctoral position in spatio-temporal modelling of large carnivore populations. The Swedish Museum of Natural History is a government agency with a mandate to promote knowledge, research and interest in our world. It is a prominent research institution and Sweden's largest museum. The Department of Population Analysis and Monitoring conducts research, monitoring, and genetic analyses of marine and terrestrial mammals. The department consists of several working groups focusing on species monitoring, conservation, and genetic identification. Activities include monitoring harbour porpoises, seals, bears, golden eagles, and arctic foxes, as well as carrying out genetic analyses for a wide range of conservation and environmental applications through the Centre for Genentic Identification (CGI). The department currently hosts four postdoctoral researchers and several senior researchers with expertise in ecology, genetics, and environmental monitoring. Work tasks Management of large carnivores such as brown bears, wolves, and wolverines requires reliable, transparent, and spatially explicit estimates of population size and dynamics. Scandinavia hosts one of the worlds largest long-term genetic monitoring datasets for large carnivores. However, current statistical methods do not fully exploit the richness of these data. The BearKin project, funded by the Swedish Environmental Protection Agency, aims to develop scalable and ecologically realistic statistical methods for estimating spatio-temporal abundance of large carnivores, with a primary focus on the Scandinavian brown bear. The project integrates: - Open-Population Spatial Capture-Recapture (OPSCR) - Close-Kin Mark-Recapture (CKMR) - Advanced Bayesian computation and custom Markov-Chain Monte Carlo (MCMC) algorithms - Spatial models with heterogeneous detection processes - Web-based tools for transparent dissemination of abundance estimates All methods will be implemented in R using the NIMBLE framework and integrated into the open-source package nimbleSCR. As a postdoc within this project, you will play a central role in the methodological development, including: - Developing computationally efficient OPSCR models for large-scale monitoring data - Implementing custom MCMC samplers and reparameterisations in NIMBLE - Modelling spatially heterogeneous detection processes (e.g. Gaussian random fields) - Integrating ecological constraints and kinship information into dynamic population models - Publishing results in leading journals in statistical ecology and computational statistics - Contributing to open-source software development (nimbleSCR, rovquantR) - Participating in workshops and stakeholder communication. You will collaborate closely with Martin Skold (Swedish Museum of Natural History) and the RovQuant project (Applied Quantitative Ecology Group, Norwegian University of Life Sciences). Requirements: - PhD in statistics, computational mathematics or similar or PhD in ecology or similar, with exceptional quantitative and computational skills. It is considered an advantage if the doctoral degree was completed no more than three years prior to the application deadline. - Documented experience in several of the following areas: Bayesian statistics, hierarchical modelling, spatial statistics, Markov-Chain Monte Carlo methods and capture-recapture or population modelling. - Strong programming skills in R - Experience of preparing peer-reviewed scientific papers - Proficient in written and spoken English. Meritorious qualifications: - Experience with NIMBLE, Stan, or other probabilistic programming frameworks - Experience with spatial capture-recapture (SCR/OPSCR) - Experience with genetic or kinship-based population inference - Experience with development of R packages - Interest in applied wildlife management and conservation. We are looking for someone who takes initiative, is structured, and has strong collaborative skills. You initiate activities and achieve results. You plan, organise, and prioritise your work effectively, and you set and adhere to timelines. You work well with others and relate to people effectively, listening and communicating in a responsive and professional manner. Application deadline: 04/06/2026 23:59 Application link: `https://recruit.visma.com/spa/public/apply?guidAssignment=b176e481-9cc1-4756-9cb7-573d20d66b63&description=True`

Pierre Dupont Forsker — Researcher — Chercheur Norwegian University of Life Sciences AQEG group — PopFlow project — RovQuant project

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UCBerkeley EvolutionaryGenomics

The Nachman lab at the University of California, Berkeley is hiring a postdoc as part of an NIH-funded project to study the genomic basis of environmental adaptation in house mice. House mice are native to Western Europe and were introduced into the Americas in association with humans during the last few hundred years. In this short time, mice have adapted to different environments through changes in morphology, behavior, and physiology. We seek to understand the genetic basis of this variation using a variety of approaches, including whole-genome sequencing of wild-caught mice across North and South America, studies of gene expression and chromatin accessibility, and genetic crosses using wild-derived inbred strains of mice from different environments. We are also using long-read data to study the role of structural variation, including insertions of transposable elements, in adaptation. The successful candidate will work on existing projects in the lab and also have the opportunity to develop new projects in the context of our research program. Please direct questions about this position to Michael Nachman: mnachman@berkeley.edu. For complete details and to apply, please see https://aprecruit.berkeley.edu/JPF05376.Michael Nachman Director, Museum of Vertebrate Zoology Professor, Department of Integrative Biology

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U CollegeLondon MitochondrialEvolutionaryGenomics

We are seeking a talented and motivated researcher to lead computational work on our latest venture on mitochondrial heteroplasmy using bees. Candidate will generate and analyse single-cell datasets with the aim to explore heteroplasmy dynamics. This project represents a unique opportunity to work at the intersection of mitochondrial biology, evolutionary genetics and genomics. Position is a 2-year fixed term as a start, with possibility to extend dependent on milestone completions. Requirements: PhD in genetics/evolutioanry biology/molecular biology/genomics + expertise in NGS and bioinformatics Apply now via UCL careers or get in touch: f.camus@ucl.ac.uk https://www.ucl.ac.uk/work-at-ucl/search-ucl-jobs/details?nPostingId=18225&nPostingTargetId=44219&id=Q1KFK026203F3VBQBLO8M8M07&LG=UK&languageSelect=UK&mask=ext (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UC SanDiego Evolution of neural cell fate specification

The Perry Lab at UC San Diego is recruiting postdocs interested in the evolution of neural cell fate specification. We use a comparative approach to identify changes in gene regulatory networks that allow novel cell types to evolve. We use the insect visual system as a model to study the changes that gave rise to innovation in sensory systems and new visually guided behaviors. Study systems include butterflies, mosquitos, house flies, and Drosophila species. Research Focus & Projects We combine single-cell sequencing (10x Genomics) and tests of gene function (CRISPR, transgenesis) to explore: - The Evolution of Novelty: Identify how novel cell types and gene regulatory networks arise. - Convergent Evolution: Determine whether the same or different genes and regulatory regions are used in the convergent evolution of complex traits. - Evolutionary Constraints: Examine how the interconnected nature of neural circuits shapes or limits how the brain evolves. Qualifications - Required: Ph.D. in Biological Sciences with 3+ years of lab experience in molecular or developmental biology. - Preferred: Experience with Drosophila or other genetic model systems. Experience with single cell seq. -Interests: Comparative functional genomics, evo devo, genetic tool development, and gene regulation. Position Details This is a renewable position with full benefits and a competitive salary based on experience. Start date is flexible. To Apply: Please email a CV, a description of research interests, and contact information for three references to Prof. Perry (mwperry@ucsd.edu). Priority deadline: June 19th, 2026. Position remains open until filled.

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UEdinburgh AvianRecombinationGenomics

Dear EvolDir Community,

I am advertising a 2-year NERC-funded postdoc at the Institute of Ecology and Evolution at Edinburgh (Scotland, UK). The job advert and application portal is here, with a deadline of 3rd July 2026: https://elxw.fa.em3.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1001/job/14307?utm_medium=jobshare We are looking for a skilled and motivated postdoctoral researcher to investigate the causes and consequences of sex-differences in individual recombination rates and landscapes. The award holder will integrate whole-genome, single-cell, and gamete-sequencing approaches from house sparrows in Helgeland in Norway, to understand fine-scale individual variation in recombination, sex-specific genetic architectures and associations with functional variation, with scope to investigate impacts of recombination on individual fertility.

The award holder will join Susan Johnston's lab in the dynamic Institute of Ecology and Evolution, University of Edinburgh, as part of a project funded by the Natural Environmental Research Council (NERC). Applicants must have a PhD (or to be completed in 3 months) in population genetics, quantitative genetics, and/or bioinformatics. The post requires experience in genomic analyses, creativity in problem solving, and strong communication and organisational skills. An understanding of the biology of meiotic recombination and inference methods using sequence and/or pedigree-based approaches is desirable.

This post is full-time (35 hours per week).

An overview of the laboratory can be found at https://sejohnston.com/. We are a friendly group in a dynamic institute, with excellent support and career mentoring. This project is in collaboration with Henrik Jensen at NTNU (Norway), Simon Martin at Edinburgh (UK), and Alison Wright at Sheffield (UK). Informal enquiries are welcome: please contact Susan.Johnston@ed.ac.uk

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UFreiburg DE Molecular Ecology of Forest Trees

Postdoctoral Researcher in molecular ecology of forest trees (f/m/d/x) at the Excellence Cluster Future Forests, University of Freiburg Full-time/Part-time, fixed-term until September 2029 (third-party funded) Remuneration according to TV-L 13 Starting date: October 2026 https://uni-freiburg.de/stellenangebot/00005010/The Excellence Cluster Future Forests at the University of Freiburg invites applications for a Postdoctoral position to investigate the molecular basis of stress resilience and stress memory of forest trees. The successful applicant will coordinate controlled experiments and data collection in natural forests with Douglas fir and sessile oak that will be exposed to biotic and abiotic stressors (hot droughts and pathogenic fungi for Douglas fir and oak lace bugs for sessile oak). The postdoctoral researcher will be responsible for generating and analyzing data to investigate the molecular basis of priming and resilience of these trees. Specifically, we seek to study DNA methylation, histone marks, protein folding and gene expression. The Excellence Cluster Future Forests at the University of Freiburg is an interdisciplinary research center dedicated to questions of adaptation and transformation of forests and their societal use in the face of global change. Future-oriented research on the complex interactions between forests and society is conducted here with outstanding international visibility, supported by the German Research Foundation. Future Forests brings together more than 50 researchers from four faculties as well as non-university partner institutions. The position will be linked to the Professorship of Forest Genetics (https://uni-freiburg.de/enr-forgen/) and the project is planned in close collaboration with the Faculty of Biology groups Plant Environmental Signalling and Development (Jun. Prof. Sjon Hartman) and Molecular Plant Physiology (Prof. Jurgen Kleine-Vehn). Your Tasks - Independent scientific research in the field of forest genetics and plant molecular sciences - Wet lab work applying different methods (DNA/RNA extraction, CUT&Tag, RNA-seq, library preparation) - Bioinformatic analysis (analysis of NGS data including RNAseq, WGBS, etc.) - Collaboration with interdisciplinary and international research teams - Supervision/support of graduate and undergraduate students - Coordination of tasks and collaboration in our "Theme" within Future Forests, including the coordination of greenhouse and Ecotron experiments (involving 3 doctoral researchers) - Contribution to scientific publications and presentations at national and international conferences - Writing of progress reports and scientific publications and presentations at national and international conferences - Active involvement in and contributions to cluster activities, workshops, and outreach events (including engagement in social-ecological studies e.g. on acceptance of GMO in forestry) Your Profile - Completed university degree (M.Sc. or equivalent) in Biology, Forest Sciences, Environmental Sciences or related fields - PhD/doctoral degree in Forest Genetics or Plant Molecular Sciences - Proven experience in wet lab methods described above, and in bioinformatic analysis of sequencing data (preferably of the specific methods mentioned above) - Good skills in plant experimental work, - Ability to work independently and as part of an interdisciplinary team - Proficient written and spoken English - Experience in scientific writing (publications) is an advantage - Experience in project coordination We Offer - An exciting interdisciplinary environment within an internationally renowned researchers at a newly established Excellence Cluster - Structured support and supervision for your scientific and career development - A diverse, collaborative, and inclusive research community, including initial University and cluster-specific onboarding support - Opportunities for further training, attendance at conferences, and professional networking - Flexible working hours and support with work-life balance - Salary according to TV-L 13 - A 3-year contract - An individual financial budget for project-specific expenses as well as for career development activities The University of Freiburg is dedicated to the principles of equal opportunity and diversity and welcomes applications from all qualified candidates regardless of gender, nationality, ethnic and social background, religion/belief, disability, age, or sexual orientation. Application Please upload your application (including cover letter, CV, relevant certificates/transcripts, contact details for two scientific referees, and, if applicable, publication list) by June 30th, 2026 to the application portal of the University of Freiburg.

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UHaifa EvolutionaryBiology

Molecular Biology Ph.D., postdoctoral and researcher positions open - University of Haifa The Sagol Lab for Evolution Research at the University of Haifa, directed by Prof. Adi Livnat, studies fundamental questions about how evolution occurs, focusing on the mechanisms of mutation. For more than a century, it has been thought that mutations are random with respect to fitness; namely, that while mutation rates vary across the genome, the causes of individual mutations bear no meaningful relationship to their biological consequences. Recently, however, a new methodology that enabled the measurement of de novo origination rates of individual mutations for the first time uncovered empirical patterns that were unexpected under this view. Our lab studies a range of exciting questions that follow from this new evidence, with potentially fundamental implications for our understanding of evolution. We are currently looking for highly motivated individuals with a strong background in molecular biology and a record of academic excellence for empirical studies on the origin of mutations. Ph.D., postdoctoral and researcher positions are available. For more information, read about our recent work (`https://www.pnas.org/doi/10.1073/pnas.2424538122`) or see our website. Requirements: Background in molecular biology/molecular genetics, high motivation and a record of excellence. To apply: Send a CV and a cover letter to `adi.livnat@sci.haifa.ac.il`, and arrange for 2-3 referees to send a letter of recommendation to the same address.

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UKansas PlantMolecularEvolution

The Choi lab (`https://jychoilab.github.io/`) at the University of Kansas is seeking for a postdoctoral scholar to join an interdisciplinary project that combines plant genetics, chromosome biology, and evolution. This is a NIH funded position to understand the genetics and function of telomere variation in plants, and the evolutionary forces that shapes plant telomeres.

The primary question of our lab asks why the telomeres of plants are so variable between and within species. To answer this question our lab has developed Mimulus (common name monkeyflower) as a model for studying the evolutionary genetics of plant telomeres. The postdoc will use M. guttatus to understand the genetic basis of telomeric variation and the evolutionary forces that shapes the telomere. The project will combine quantitative genetics with CRISPR and functional genomics including single cell approaches and population genomics. Our ultimate goal is to establish the genetic mechanism and evolution underlying telomeric variation.

Basic Qualifications: *Applicant should have a Ph.D. in the following or related fields: genetics, molecular biology, or evolution. *Demonstrated experience in plant biology, especially plant genetics or plant molecular biology is required. *A strong interest in evolutionary biology is necessary.

Preferred (but not necessary) Qualifications: *Experience with high-throughput sequencing and genomic data analysis is desired but not necessary. This can be taught to the candidate.

The lab is looking for someone who is personable and enthusiastic about working in a collaborative environment. Responsibilities will include contributing to ongoing research in the lab, developing independent research projects, and mentoring graduate/undergraduate students. This is a 1 year appointment with possibility of an extension. The preferred start date is summer 2026 but it is also negotiable.

Application instructions: Applicants can email PI Jae Young Choi (jaeyoung.choi@ku.edu) that includes: (1) a curriculum vitae (2) a cover letter - letter of application that summarizes your qualifications and interest in the position (3) contact information for three references

Applications will be reviewed as they are submitted and the position will remain open until filled.

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ULausanne CH Biogeography Phylogenetic Comparative Analysis of Sociality

Postdoc position Biogeography/ Phylogenetic Comparative Analysis of Sociality Link:

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UmeaUniv ConiferGenomics

The Department of Ecology, Environment and Geosciences at Umea University (Sweden) announces a two-year postdoctoral fellowship in conifer genomics. The project focuses on developing GWAS strategies to better understand fungal pathogen resistance in Scots pine. The application deadline is 20th June. For further details, please refer to the official announcement available on the Umea University website: https://www.umu.se/en/work-with-us/postdoctoral-scholarships/postdoctoral-fellowship-2-years-in-conifer-genomics_934908/Best regards, Xiao-Ru Wang

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Xiao-Ru Wang, Prof. Dept. Ecology, Environment and Geoscience Umea University SE-901 87 Umea, Sweden

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UMichigan PopulationGenetics

UMichigan US DepStatistics Statistical genetices and computational genomics

The Terhorst Lab in the Department of Statistics at the University of Michigan is recruiting a postdoctoral research fellow in statistical genetics and computational genomics. The position is part of a collaborative project with the University of Edinburgh and the University of Oxford focused on developing scalable methods for complex trait analysis using ancestral recombination graphs (ARGs). Research areas include statistical/quantitative/population genetics, genealogical inference, machine learning, genetic prediction, genome-wide association studies, scalable linear mixed models, and efficient algorithms for large-scale genomic data analysis. This is a one-year appointment starting as early as possible, with renewal possible based on the availability of funds, availability of work, and satisfactory performance. Responsibilities - Develop novel statistical and computational methods for ARG-based quantitative genetics - Analyze large-scale genetic and phenotypic datasets - Implement scalable software and algorithms for genomic inference - Collaborate with researchers across statistics, genetics, and computational biology - Contribute to manuscripts, presentations, and open-source software development - Participate in interdisciplinary collaborations related to predictive breeding and genome editing - Travel to the United Kingdom to collaborate with project partners at the University of Edinburgh and the University of Oxford Required Qualifications - PhD in statistics, computer science, computational biology, genetics, applied mathematics, or a related quantitative field is required - Proof of degree completion must be in hand on or before the start date - Strong programming and computational skills - Experience with statistical modeling, machine learning, or large-scale data analysis Desired Qualifications - Experience with population genetics or statistical genetics - Familiarity with Bayesian methods, probabilistic modeling, or graphical models - Experience with scientific computing in Python, JAX, Torch, Julia, C++, or related languages - Experience with high-performance computing or scalable algorithms - Interest in interdisciplinary research spanning genomics and evolutionary biology Modes of Work The position is on-site in Ann Arbor, Michigan. Salary and Benefits Salary will be commensurate with experience and is expected to be in the range of $65,000-80,000 per year, plus benefits and a $3,000 *relocationassistancebonus.HowtoApplyToapply,pleasesubmitthefollowingmaterials* : *−Acoverlettersummarizingresearchexperienceandinterests−Curriculumvitae,includingpublicationsand/orpreprints−* *ContactinformationforthreereferencesApplicationswillbereviewedonarollingbasisuntilthepositionisfilled.BackgroundScre* *partyadministratortoconductbackgroundchecks.BackgroundchecksareperformedincompliancewiththeFairCreditReporting* U-M EEO/AA Statement The University of Michigan is an equal opportunity/affirmative action employer. - Regards, Jonathan Terhorst Associate Professor of Statistics University of Michigan

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UNorthCarolina PopulationGenomics

The Schrider Lab (https://www.schriderlab.org/) in the Department of Genetics at the University of North Carolina at Chapel Hill is hiring a postdoc in population genetics and/or phylogenetics. The successful candidate will help design and carry out projects related to one or more of the following: 1) the development and application of computational methods to interrogate the impacts of (and interplay between) adaptation, recombination, introgression, and demographic changes on genetic diversity within and between species; 2) elucidating the phylogenetic relationships among species and/or the genealogical relationships of individuals of the same species; 3) the study of these or other evolutionary questions in mosquito genomes; 4) examining the dynamics of evolutionary models (e.g. the evolution of therapeutic resistance in cancer) via simulation and/or analytical theory. This a multidisciplinary position and candidates from a variety of backgrounds will be considered and receive training to address deficits as needed. A PhD in Evolution, Genetics, Bioinformatics, Computer Science, or a related field must be completed prior to the postdoc's hire. Those interested should email Dan Schrider (drs@unc.edu) and include their CV as an attachment. The University is an equal opportunity employer and welcomes all to apply without regard to age, color, gender, gender expression, gender identity, genetic information, national origin, race, religion, sex, or sexual orientation. We encourage all qualified applicants to apply, including protected veterans and individuals with disabilities.

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Uppsala SWE Genomics of adaptation

Postdoctoral researcher: Genomics of local adaptation and mal-adaptation in agricultural landscapes The Department of Ecology, SLU, Uppsala We are seeking a postdoctoral fellow to a project focusing on the genomic footprints of demographic and evolutionary responses to changed agricultural practises and climate in northern wheatears (Oenanthe oenanthe). You will be part of a strong international research team with competence ranging from evolutionary ecology, genomics, population dynamics to statistical modeling. Read more and apply: https://www.slu.se/en/about-slu/work-at-slu/jobs-and-vacancies/genomik-av-lokala-anpassningar-i-jordbrukslandskap--institutionen-for-ekologi-/Submit your application before deadline June 5, 2026

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UppsalaU MolecularEvolution

Postdoctoral position in Molecular Evolution Are you interested in conducting evolutionary biology research, with the support of competent and friendly colleagues in an international environment? Are you looking for an employer that invests in sustainable employeeship and offers safe, favourable working conditions? We welcome you to apply for a Postdoctoral position at Uppsala University.

The Department of Cell and Molecular Biology is divided into seven research programs, each focusing on different areas within cell and molecular biology: computational biology and bioinformatics, microbiology and immunology, molecular biology, molecular biophysics, molecular evolution, molecular systems biology, and structural biology. The scientific foundation of what we do lies in biology, but our research overlaps with other fields such as medicine, computer science, mathematics, chemistry, engineering, and physics. The department has over 200 employees, including around 50 doctoral students. Please read more about our work at https://icm.uu.se.The position is placed in the Molecular Evolution program, with main supervisor Jennifer James. The applicant will become a member of a newly established research group working at the intersection of population genetics, phylogenetic analysis, and proteomics. If you are interested in using bioinformatics and computational biology to address big questions in evolutionary biology, please get in touch! Duties This is a VR-funded postdoctoral research position. The proposed work will be entirely computational, focussing on analysing existing proteomic and genomic datasets. The postdoctoral researcher will therefore be responsible for writing code, conducting statistical analyses, and for writing and publishing scientific articles.The project aims understand how protein domains come to be combined and arranged in protein coding genes, in order to address the following three research questions: 1) How do protein domains become associated over evolutionary time, and do any domain properties predict having a high number of interaction partners? 2) Where does selection tend to act in multidomain proteins? 3) Is variation in the rate of association of protein domains, or variation in rates of rearrangement, driven by selection? Are particular domain combinations associated with certain clades of organisms, and could this be an informative character to understand phylogenies, or to infer genome rearrangement events? The successful applicant will be expected to spearhead the project work and to develop upon these ideas, with flexibility to shape the precise direction of the research to their own interests. Requirements We are looking for a highly motivated and creative individual with a PhD degree in the field of biology, or a foreign degree equivalent to a PhD degree in the field of biology. The degree needs to be obtained by the time of the decision of employment. Priority will be given to applicants who have completed their degree no more than three years before the deadline for applications. Due to special circumstances, the degree may have been obtained earlier. The three-year period can be extended due to circumstances such as sick leave, parental leave, duties in labour unions, etc. Candidates must be able to express themselves fluently in spoken and written English. An ability to code (e.g., in Python) is a valuable skill for this post. Experience working with a high-performance computer cluster is also important, as is an ability to use command line tools, and to conduct statistical analyses using programmes such as R. Additional qualifications An evolutionary biology background will be considered beneficial for this position. Experience with computational biology, bioinformatics or mathematics is desired, as are good communication skills and an ability to work collaboratively and independently. An interest in developing research ideas and exploring new methods will also be advantageous. The ideal candidate is comfortable with bioinformatics and population genetics, and is excited to make this project their own! About the employment The employment is a temporary position of 2 years according to central collective agreement. Full time position. Starting date 2026-09-07 or as agreed. Placement: Uppsala Application Please submit your application by 29th of June 2026, UFV-PA 2026/1828. Please submit your application through Uppsala University's recruitment system, Varbi: `https://uu.varbi.com/what:job/jobID:940581/` The application (in English) should include: 1) A letter of intent describing yourself, your research interests and motivation of why you are applying for this position 2) CV 3) Name and contact information to at least two reference persons (e-mail address and phone no.) 4) Relevant publications 5) PhD exam

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USA Ohio State InsectMicrobeInteractions

The Short Lab at Ohio State is recruiting a Postdoctoral researcher to study mosquito-microbe interactions

Job Description: This Postdoctoral researcher will contribute to an NIH-funded study (R01AI189572, `https://reporter.nih.gov/search/wk0CzbUpwE69AxJ0uTlPBQ/project-details/11296317`) which focuses on the interplay between the microbiota and life history traits in male Aedes aegypti mosquitoes. The position will be in the lab of Dr. Sarah Short. To learn more about the lab, go to https://shortlab.cfaes.ohio-state.edu/. Dr. Short's lab is housed in the Department of Entomology and in affiliation with the Infectious Diseases Institute. In collaboration with their scientific mentor (the P.I.), the successful candidate will design and execute experiments, analyze data, and publish findings in competitive scientific journals. They will develop new methodologies and troubleshoot as necessary. They will also mentor junior members of the laboratory to hone their instructional and mentoring skills. They will apply for appropriate grant and fellowship funding to support their research. They will also enrich their training by attending relevant seminars and colloquia and by developing independent projects that build upon the laboratory's ongoing work. The position is renewable for up to five years, pending satisfactory performance and availability of funds.

Responsibilities: 955Salary: $61,008.00-63$,480.00/annual Minimum Education Required: Doctorate (Academic) with a Major in the life sciences Required Qualifications: Required: The successful candidate must have a Ph.D. in the life sciences and must show a strong record of publication and success in research. They must have a strong background in experimental design, bioinformatics, and data analysis. Preferred Qualifications: The preferred candidate will have experience in vector biology and microbiology, as well as insect-microbe interactions, bacterial community profiling, microbial ecology, metagenomics, and/or metabolomics. Experience working with teams and conducting field work is a plus, as is experience performing molecular and organismal experiments in insect systems. Location: Howlett Hall, Columbus Ohio, 43210, USA Contact: email Sarah Short: short.343@osu.edu To apply: Go to OSU Careers (https://hr.osu.edu/careers/) and search for R149804 or use the link: https://osu.wd1.myworkdayjobs.com/OSUCareers/job/Columbus-Campus/Postdoctoral-Researcher$_R149804-1PleaseprovideaStatementofInterestandaCVwhenapplying.$

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USaoPaulo Brazil CoevolutionInEcologicalNetworks

A postdoctoral position is available in the laboratory led by Paulo R. Guimaraes Jr. at the University of Sao Paulo to develop studies on evolutionary dynamics, cascading effects, and information flow in networks formed by plants and frugivores in altered landscapes. This postdoctoral fellowship will be part of the project "Evolutionary dynamics in networks formed by plants and frugivores in altered landscapes" (FAPESP Grant 2025/24923-8). The application deadline is June 10, 2026. Essential qualifications: - A PhD in Ecology, - A strong background in Ecology, Mathematical Modelling, Boolean networks, and R Desirable qualifications: - Information Theory Mandatory documents for application: - Updated CV - A recommendation letter - PhD certificate - A short letter explaining why the candidate would like to work with coevolutionary dynamics of ecological interactions The positions are open to Brazilian and foreign citizens. The selected candidates will receive a FAPESP postdoc fellowship - current salary of R12570.00$permonth.Thecandidatewillalsoreceive15Application:$ $Candidatesshouldsendthemandatorydocumentslistedabovetobye-mail$() indicating as e-mail subject: Post-doc [candidate name]

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USaoPaulo Brazil Genomics

We have a postdoc position open at the University of Sao Paulo, Brazil, with a total duration of 2 years. The fellowship recipient will be responsible for (1) preparing parasite DNA samples and generating genome-wide sequencing data on Illumina MiSeq and NextSeq500 platforms, (2) performing bioinformatic and population genetic analysis, including estimates of genetic diversity, multiplicity of infection, gene flow, and genetic divergence between geographic subpopulations, and (3) writing reports and scientific articles describing the main findings. The supervisor is Prof. Marcelo U. Ferreira, PhD (https://sites.usp.br/moalab/).

Skills/Qualifications PhD in the biomedical field obtained within the last 7 years, mastery of population genetics concepts, experience with DNA sequencing on Illumina-type platforms, experience with genetic and genomic sequencing data analysis in R, and proficiency in English (written and spoken) are requested.

Specific Requirements Experience with Python programming, experience with sequencing and genetic analysis of protozoa, and proficiency in Portuguese or Spanish are desirable, although not mandatory.

Benefits R$12,570(approximatelyUS$ 2514) per month

Eligibility criteria PhD in the biomedical field obtained within the last 7 years, mastery of population genetics concepts, experience with DNA sequencing on Illumina-type platforms, experience with genetic and genomic sequencing data analysis in R, and proficiency in English (written and spoken).

How to apply Please send your CV, motivation letter, and two names for references to muferrei@usp.br . Email subject: 'PostDoc Genomics'

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US ChicagoBotanicGarden FieldMuseum eDNA PlantPollinatorInteractions

The Chicago Botanic Garden, in partnership with the Field Museum (Chicago, Illinois, USA), is seeking a Postdoctoral Research Associate to develop and apply eDNA approaches to study plant-pollinator interactions using biological collections and living plant systems. This is a two-year, full-time position (with possibility of extension). The project combines collections-based research, pollinator ecology, molecular methods, and bioinformatics, with substantial flexibility for the successful applicant to shape the research direction in line with their interests and expertise. Opportunities include working with extensive insect collections, developing novel metabarcoding and target-capture approaches, integrating molecular and ecological datasets, and contributing to pollinator conservation and collections-based science. We seek candidates with interests spanning ecology, evolution, entomology, molecular biology, bioinformatics, conservation, and/or biological collections. Application deadline: June 22, 2026. Full posting and application: https://workforcenow.adp.com/mascsr/default/mdf/recruitment/recruitment.html?cid=21ef98a3-d325-4110-a85a-7729320b6f80&ccId=19000101_000001&lang=en_US&jobId=9205873536598_1&&source=ENApplicants are encouraged to contact the PIs to discuss the position and potential project ideas: Bruno de Medeiros (bdemedeiros@fieldmuseum.org), Paul Caradonna (pcaradonna@chicagobotanic.org), or Jeremie Fant (jfant@chicagobotanic.org).

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US UniversityPuertoRico SpiderPhylogenomics

University of Puerto Rico: Postdoctoral Assistant Researcher in Spider Phylogeography and Phylogenomics The Ortiz Lab of Arthropod Evolution (OLAE) at the University of Puerto Rico-Rio Piedras Campus (UPRRP) is seeking a Postdoctoral Assistant Researcher to participate in ongoing and new projects on spider phylogeography, phylogenomics, and evolution. The appointment will involve approximately 75The position is initially for one year, with the possibility of extension to a second year based on satisfactory progress and institutional approval. The preferred start date is September 1, 2026, or as soon as possible thereafter. Research environment and project The OLAE is a newly established research group focused on arachnid evolution, systematics, phylogeography, and biodiversity, with particular emphasis on Caribbean and Mediterranean spiders. The successful candidate will play a leading role in analyzing existing genome-wide ddRADseq datasets and completing manuscripts on the phylogeography, systematics and evolution of Zodarion ant-eating spiders, a highly specialized and diverse spider lineage. Initial research will focus on genomic datasets comparable to those used in previous studies, including: - Ortiz D, Pekar S, Dianat M. 2024. A consequential one-night stand: Episodic historical hybridization leads to mitochondrial takeover in sympatric desert ant-eating spiders. Molecular Phylogenetics and Evolution 199: 108167. - Ortiz D, Pekar S, Bilat J, Alvarez N. 2021. Poor performance of DNA barcoding and the impact of RAD loci filtering on the species delimitation of an Iberian ant-eating spider. Molecular Phylogenetics and Evolution 154: 106997. Potential lines of research include how historical, ecological, and environmental factors shaped the diversification, survival, adaptation, and distribution of ant-eating spiders across Mediterranean peninsulas. These regions experienced major environmental changes during the Pleistocene glaciations while also serving as important glacial refugia. The selected candidate will also contribute to the development of new projects on the phylogeography and evolution of Caribbean arachnids. These projects may involve fieldwork, specimen curation, DNA barcoding, genomic data generation, and phylogenomic analyses. Candidate profile We are looking for a highly motivated and independent researcher with strong experience in evolutionary biology, phylogenomics, phylogeography, and/or population genomics, and an interest in using highly diverse terrestrial invertebrates to address evolutionary and biogeographic questions. The position is especially suitable for a researcher who wants to further develop expertise in genomic data analysis, manuscript preparation, field-based biodiversity research, museum-associated work, and university teaching while building an independent research profile. Qualifications Required qualifications: - Ph.D. in Biology or a related field - Strong background in evolutionary biology, phylogenomics, phylogeography, and/or population genomics - Experience analyzing genome-wide datasets - Proficiency in bioinformatics and data analysis, especially using tools such as R, Python, and Unix/Linux environments - Relevant publication record in peer-reviewed journals - Experience with DNA isolation and DNA barcoding - Excellent written and verbal communication skills - Ability to work independently and as part of a collaborative team - Proficiency in English Additional desirable qualifications: - Experience with genomic library preparation, especially ddRADseq and/or UCEs - Experience with arachnids or other terrestrial arthropods - Experience with fieldwork and biodiversity collections - Spanish-language ability Responsibilities Research responsibilities will include: - Analyze genome-wide ddRADseq and UCE datasets of Mediterranean and Caribbean spiders - Lead or contribute to manuscripts for publication in peer-reviewed journals - Participate in fieldwork and specimen-based research - Perform DNA isolation, DNA barcoding, and potentially genome-wide library preparation - Contribute to setting up the laboratory infrastructure and protocols of the newly established OLAE - Collaborate with members of the OLAE, the Department of Biology, and the Museum of Zoology of UPRRP - Present research findings at conferences, seminars, and other academic venues - Assist with grant writing, project coordination, and student mentoring Teaching responsibilities will include: - Contribute to undergraduate and/or graduate teaching in the Department of Biology, equivalent to approximately 25Location The position is based at the University of Puerto Rico-Rio Piedras Campus (UPRRP), in San Juan, Puerto Rico.

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UTennessee Evolution of acoustic communication

Job Description The Tanner Lab (Department of Ecology and Evolutionary Biology and Department of Psychology & Neuroscience) at the University of Tennessee, Knoxville (UTK) is seeking up to two motivated postdoctoral research associates to conduct acoustic communication research in non-human animals.

The successful candidate will contribute to broad research themes in the lab, including the evolution of acoustic signals by sexual selection and decision-making in complex natural contexts. Current efforts in the lab explore how pre- and post-copulatory sexual selection shape sexual signals; choice overload and its consequences for decision making in animals; constraints to the expression of mating preferences, especially the effects of noise; and the causes and consequences of within-individual variation in acoustic signaling. The Tanner lab has two large (3.9 m length x 3.4 m width x 2.6 m height) state-of-the-art, temperature-controlled, semi-anechoic chambers available for studies of acoustic communication behaviors. We work primarily in frogs native to our location in East Tennessee, especially gray and green treefrogs (Hyla chrysoscelis and H. cinerea; Hyla = Dryophytes), but also with field crickets (Gryllidae). We are open to candidates excited about working in any of these systems, and potentially in more than one.

The preferred start date for this position is June 1, 2026 or as soon as possible. Funding is available for up to two years, contingent upon start date, performance, and the availability of funding. Extensions beyond June 2028 would require the acquisition of additional external funding. Salary will be competitive, commensurate with experience, and inclusive of benefits.

Responsibilities The postdoctoral research position will involve collaborative experimental design, data collection and analysis, manuscript preparation, and participation in the development of external funding proposals. The postdoc will provide mentorship to undergraduate and graduate researchers in the lab and contribute to maintaining a collaborative, productive, and positive research environment.

Research in the Tanner Lab combines controlled laboratory and field experiments with frequent field collection of wild animals; interest in and availability to work outdoors at night is essential. This position requires full-time, in-person work. Seasonal but regularly-occurring night and weekend research effort is necessary during experiments because we work on nocturnal animals with seasonal communication behaviors. Willingness and ability (i.e., a valid driver's license) to drive a vehicle to and from field sites at night is a requirement.

UTK is home to a vibrant interdisciplinary community of behavioral scholars called the Collaborative for Animal Behavior (`https://artsci.utk.edu/research-and-creative-activity/research-centers-and-institutes/colab/`), which will provide many opportunities for mentorship, collaboration and networking to early career scholars. Located in proximity to Great Smoky Mountains National Park and many other natural areas, Knoxville offers excellent access to nature as well as incredible access to a local and national music scene.

Application Instructions

In addition to the online application, please send the following materials to Dr. Jessie Tanner (`tanner@utk.edu`):

1. Curriculum vitae

2. A cover letter that includes:

a. the candidate's educational background and prior research experience,

b. current research focus and future research goals, including what topic(s) they hope to pursue as a postdoc in the Tanner Lab

c. perceived competencies and experience in relevant skills, including scientific writing, coding, statistical analysis, and experimental methods,

d. what they hope to gain from this position and how it will support their long-term development as a scientist.

3. Two letters of recommendation emailed by your recommender directly to Dr. Jessie Tanner (`tanner@utk.edu`).

4. A PDF of a first-author publication (published or in press)

About The Department

EEB is in the top 10

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UTennessee PlantEcophysiologyandEvolution

Postdoc: Plant Ecophysiology and Evolution

Description: The Suissa lab in the Department of Ecology and Evolutionary Biology at the University of Tennessee, Knoxville (UTK) is seeking a highly motivated Postdoctoral Research Fellow to join the lab (https://www.botaneelab.com/). This 2-year, full-time position will focus on the hydraulics of seed-free plants, with an emphasis on mechanisms of drought tolerance.

The successful candidate will take a leading role in advancing research on vulnerability to drought-induced embolism and vascular architecture in seed-free plants. This work will integrate physiological and anatomical approaches to address fundamental questions in plant function and evolution. The fellow will be expected to drive projects toward publication, contribute to grant development, and actively engage with the broader EEB community.

Responsibilities and opportunities: Lead research on vulnerability to embolism in seed-free plants Conduct anatomical analyses on vascular structure. Publish findings in peer-reviewed journals. Present research at national and international conferences. Mentoring graduate and undergraduate students.

Qualifications: PhD in plant physiology, ecophysiology, evolutionary biology, or related field. Strong background in physiology, hydraulics, and anatomy. Experience with estimating vulnerability to drought-induced embolism (preferred using the optical vulnerability method). Proficient in statistical analyses and data visualization, using R or a related language. Excellent written and oral communication skills.

Position details: Salary: $62,000, plusbenefits.Startdate : August2026.Location : InpersonTheUniversityofTennessee, Knoxville.Benefits : Healthcare, 401kbenefitplans.Opportunitiesforoutreachandscie$

How to apply: Submit your CV, a summary of research interests and experiences, and the contact information of three references to Jacob Suissa (jsuissa@utk.edu). Review of applications will begin immediately and continue until the position is filled. The University of Tennessee is an equal opportunity employer. The Suissa Lab is committed to fostering an inclusive, intellectually rigorous research environment grounded in curiosity, collaboration, and continuous learning.

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U Warsaw Poland StemCellEvol Bioinformatics

Application deadline: 31.08.2026 Publication of the results of the competition: 31.09.2026 Salary: Around 8700 PLN gross/month plus a 13th salary and seniority allowance Period of employment: 24 months, starting on 1.11.2026 or later Position: Post-doctoral researcher (Bioinformatician) in the project "Evolutionary perspective on irradiation resistance of stem cells" funded by the Polish National Science Centre (Sonata 20) Project leader: Dr. Ludwik Gasiorowski Research group: Comparative Invertebrate Zoology (https://ibe.biol.uw.edu.pl/en/835-2/research-groups/comparative-invertebrate-zoology/)

Project description: The project is focused on the evolution of stem cells in non-model invertebrates. In particular, we want to study how stem cells evolved resistance to ionizing radiation and what mechanisms are employed during the repair of double-stranded breaks across different groups of animals. The project comprises experiments on irradiation resistance, comparative transcriptomics, functional analyses, and advanced microscopy techniques. The person hired in the current call will be responsible for bioinformatic analyses, focused on the evolution of genes active in the stem cells of various animals.

Eligibility criteria: Candidates must: * Meet the requirements specified in Article 113 of the Law on Higher Education and Science (Journal of Laws 2024, item 1571, consolidated text). * Hold a Ph.D. degree in biological sciences or a related field obtained before the application deadline. * Have significant scientific achievements documented by well-cited publications in renowned international journals, invitations to deliver lectures or seminars, etc. * Have international experience, e.g.: participation in international conferences, engagement in international research projects, international collaborations documented by joint publications. * Submit a research plan outlining personal scientific development. * The position may be filled by a person who has earned a doctoral degree from an institution other than the University of Warsaw or has completed at least 9-month, continuous, and documented research internship, completed during doctoral school, doctoral studies, or after obtaining a doctoral degree, at an institution other than the University of Warsaw and in a country other than the country where the doctoral degree was obtained. * Only individuals who obtained their doctoral degree within 12 years prior to the start of employment are eligible to apply

Research competencies: * experience in one or more of the following fields: comparative transcriptomics, single-cell transcriptomics, phylostratigraphy, phylogenomics, transcriptome analyses * proficiency in spoken and written English * experience in preparing and publishing scientific articles * ability to work independently and as part of a team

Primary responsibilities: * In silico identification of new stem cell markers * Identification and characterization of genes involved in irradiation resistance in various animal clades * Phylostratigraphic analyses of identified genes * Routine bioinformatic work related with the project (e.g. transcriptomes assembly and annotation, differential gene expression analyses) * Preparation of scientific publications, presentation of results at international conferences, and supervision of students involved in the project * Fulfilling other academic teacher responsibilities as required by employment at the University of Warsaw.

Selection process Reference number of the announcement: WB-KG-7/2026 Application deadline: 31.08.2026 How to apply: Send applications via email to `ludwik.gasiorowski@uw.edu.pl` and the Faculty Dean's Office: `dziekanat.biol@uw.edu.pl`. Candidates will receive an email confirmation of document submission. If no confirmation is received, please contact the project leader. Required documents o Personal questionnaire - available on the Faculty of Biology UW website (`https://www.biol.uw.edu.pl/wp-content/uploads/sites/19/2025/03/Kwestionariusz-osobowy-ENG-250319.docx`). o Motivation letter including description of scientific interests and research activity plan (max. 2 pages A4). Ensure the completeness of your application and submit it by the deadline. Failure to meet these requirements will result in rejection on formal grounds.

Expected date and method of announcing the competition results Interviews will take place in the first half of September 2026. Candidates will be individually notified about their interview schedule with the selection committee. Candidates will be informed of the results via email by 31.09.2026.

Contact for inquiries

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U Warsaw Poland StemCellEvol Experimental

Application deadline: 31.08.2026 Publication of the results of the competition: 31.09.2026 Salary: Around 8700 PLN gross/month plus a 13th salary and seniority allowance Period of employment: 24 months, starting on 1.11.2026 or later Position: Post-doctoral researcher (Experimental) in the project "Evolutionary perspective on irradiation resistance of stem cells" funded by the Polish National Science Centre (Sonata 20) Project leader: Dr. Ludwik Gasiorowski Research group: Comparative Invertebrate Zoology (https://ibe.biol.uw.edu.pl/en/835-2/research-groups/comparative-invertebrate-zoology/)

Project description: The project is focused on the evolution of stem cells in non-model invertebrates. In particular, we want to study how stem cells evolved resistance to ionizing radiation and what mechanisms are employed during the repair of double-stranded breaks across different groups of animals. The project comprises experiments on irradiation resistance, comparative transcriptomics, functional analyses, and advanced microscopy techniques. The person hired in the current call will be responsible for experiments focused on differences in radiation tolerance between various groups of animals and on the characterization of their stem cell systems, with a special emphasis on gene expression.

Eligibility criteria: Candidates must: * Meet the requirements specified in Article 113 of the Law on Higher Education and Science (Journal of Laws 2024, item 1571, consolidated text). * Hold a Ph.D. degree in biological sciences or a related field obtained before the application deadline. * Have significant scientific achievements documented by well-cited publications in renowned international journals, invitations to deliver lectures or seminars, etc. * Have international experience, e.g.: participation in international conferences, engagement in international research projects, international collaborations documented by joint publications. * Submit a research plan outlining personal scientific development. * The position may be filled by a person who has earned a doctoral degree from an institution other than the University of Warsaw or has completed at least 9-month, continuous, and documented research internship, completed during doctoral school, doctoral studies, or after obtaining a doctoral degree, at an institution other than the University of Warsaw and in a country other than the country where the doctoral degree was obtained. * Only individuals who obtained their doctoral degree within 12 years prior to the start of employment are eligible to apply

Research competencies: * experience in one or more of the following fields: evolutionary developmental biology, invertebrate zoology, molecular biology, stem cell biology, confocal microscopy * proficiency in spoken and written English * experience in preparing and publishing scientific articles

Primary responsibilities: * Organization and optimization of culturing methods for research organisms * Optimization of irradiation assays for selected species * Visualization of stem cells with the use of EdU stainings and RNA in situ hybridization * Extraction and preparation of RNA samples for transcriptome sequencing * Preparation of scientific publications, presentation of results at international conferences, and supervision of students involved in the project * Fulfilling other academic teacher responsibilities as required by employment at the University of Warsaw.

Selection process Reference number of the announcement: WB-KG-6/2026 Application deadline: 31.08.2026 How to apply: Send applications via email to ludwik.gasiorowski@uw.edu.pl and the Faculty Dean's Office: dziekanat.biol@uw.edu.pl. Candidates will receive an email confirmation of document submission. If no confirmation is received, please contact the project leader. Required documents o Personal questionnaire - available on the Faculty of Biology UW website (https://www.biol.uw.edu.pl/wp-content/uploads/sites/19/2025/03/Kwestionariusz-osobowy-ENG-250319.docx). o Motivation letter including description of scientific interests and research activity plan (max. 2 pages A4). Ensure the completeness of your application and submit it by the deadline. Failure to meet these requirements will result in rejection on formal grounds.

Expected date and method of announcing the competition results Interviews will take place in the first half of September 2026. Candidates will be individually notified about their interview schedule with the selection committee. Candidates will be informed of the results via email by 31.09.2026.

Contact for inquiries

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UWisconsinMadison PopulationGenetics

The Ragsdale lab at UW-Madison is recruiting one or more postdoctoral researchers. We have openings on NIH-funded (MIRA) projects on the development and/or application of population genetics approaches for evolutionary inference. There is quite a bit of flexibility in research focus. Possible projects include evolutionary inference in humans and hominins (in particular, the deep evolutionary history of both modern and archaic humans), inference of natural selection and selective interactions (such as dominance, epistasis, or background selection), and connecting selection on quantitative traits (e.g., stabilizing selection) to selection on trait-contributing variation in non-equilibrium demographic settings. Potential applicants with related interests in population genetics and evolution are encouraged to reach out via email with informal inquiries. UW-Madison offers a vibrant and interactive research community in evolution, genetics and genomics (`https://evolution.wisc.edu/`). Quality of life in Madison, Wisconsin, is high, with excellent public transit and biking infrastructure, affordability, and ready access to both outdoors and urban activities. Start date is flexible, and the position follows the NIH postdoc salary scale. Informal inquiries are welcome and should be emailed to Aaron Ragsdale (`apragsdale@wisc.edu`), and more information about our lab and research, including ongoing projects and recent publications, can be found on our webpage (`https://apragsdale.github.io/`). To apply, please email `apragsdale@wisc.edu` with your CV and briefly describing your past research experiences and interests in the Ragsdale lab. Reviews of applicants will begin on June 22 and continue until filled. Aaron Ragsdale

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UWisconsinMadison PopulationGenomics

The research group of John Pool at the University of Wisconsin - Madison invites applications for a postdoctoral research 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 focus of this postdoctoral position will depend on the intersection of interests between the candidate and the mentor. Examples of potential focus areas include: * Analyzing genomic variation within laboratory fly strains to uncover their cryptic history, and developing new cutting-edge population genomic resources. * The population genomics of admixture/introgression between partially isolated fly populations and species. * Using multi-omic data to investigate the evolution of maternal investment and reproductive tradeoffs in a challenging environment. Our lab currently includes 1 masters-level lab manager with a diverse skill set, 1 recently arrived postdoc, 2 advanced PhD students (with a couple rotating first year PhD students to in the fall), and several undergraduates. Lab alumni include 6 postdocs and 5 PhD recipients. Further lab info: http://www.johnpool.netUW-Madison offers a superb scientific environment with a vast biological research community and a supportive, collaborative, and egalitarian culture. Numerous labs focus on population genetics, evolutionary genomics, and Drosophila research: https://genetics.wisc.edu/evolutionary-and-population-genetics/https://evolution.wisc.edu/people/faculty/https://genetics.wisc.edu/drosophila-and-other-insects/Madison offers an exceptional quality of life in a beautiful landscape, and has been ranked as both the best US city for young adults and the best for raising a family. http://www.visitmadison.com/media/rankings/Downtown and campus are bordered by lakes, it's easy to get around by bike or bus, and Madison features diverse art, music, cultural, and culinary offerings. We welcome applicants from all backgrounds, including those poised to add unique or rare perspectives to our field and our community. Start dates are flexible. Salary follows the NIH scale. Benefits include individual or family health insurance. Applications are due by June 15. However, earlier applications are welcome, and later applications may still be considered. Informal inquiries are also welcome at any time. To apply, send a statement of research interests (up to 1 page) addressing the intersection between your own scientific interests and the Pool lab's research in terms of potential projects, along with a CV and contact info for 3 references. John Pool Professor of Genetics Director of Wisconsin Evolution (The J. F. Crow Institute) University of Wisconsin - Madison jpool@wisc.edu

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UZurich evolutionary genetics ecology

PostDoc position in evolutionary genetics/ecology I am looking for a PostDoc with a background in evolutionary- or ecological genetics or evolutionary ecology. You should have recently (within the last three years) obtained your PhD degree and have worked in any field of evolutionary genetics/genomics/ecology, such as coevolution, adaptation or speciation, natural selection, etc. in plants or plant-animal interactions. Skills in bioinformatics are welcome, too. Proficiency in English, both orally and written, and prior experience with scientific publishing is required. The job will be embedded in an SNF-funded project on plant-pollinating herbivore coadaptation in Raphanus raphanistrum and Pieris rapae, pursued together with two PhD students. The project consists of field work, greenhouse experimental work, and genomic analyses. The initial duration of the employment will be for three years but prolongation is possible. I offer a vibrant, collaborative work environment and a competitive salary; earliest starting date is 1st July 2026. Our department is located in the University Botanical Gardens and houses modern molecular and ecological labs, including greenhouses and climate chambers for plant cultivation. The University of Zurich has a broad research coverage of organismal and molecular biology. If you are interested in the job, please send me by e-mail (florian.schiestl@systbot.uzh.ch) a letter describing your motivation, CV including a list of publications, and e-mail addresses of two academic referees, by 15th of June 2026. Please send all documents in a single file. If you have any further questions, don‘t hesitate to contact me.

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WorkshopsCourses

Advanced Python for Bioinformatics APYB02-EvolutionaryBiologyApplications

Advanced Python for Bioinformatics (APYB02) - Evolutionary Biology Applications https://prstats.org/course/advanced-python-for-bioinformatics-apyb02/Delivered by experienced bioinformaticians and Python developers working in computational biology and data science. Take your Python skills further and build efficient, scalable workflows for advanced bioinformatics analysis. Modern bioinformatics increasingly requires robust, maintainable code capable of handling large and complex biological datasets. This hands-on course teaches advanced Python programming concepts for biological research, including object-oriented programming, testing, optimisation, and workflow development for real-world bioinformatics applications. What you'll gain - Advanced Python programming skills for bioinformatics research - Practical experience with object-oriented and functional programming - Skills to optimise and structure complex analysis workflows - Understanding of testing, debugging, and reproducible software practices - Confidence working with large biological and genomic datasets Course format - Live, instructor-led online training - Hands-on coding with biological and bioinformatics datasets - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Bioinformaticians and computational biologists - Researchers already familiar with basic Python - PhD students and quantitative life scientists - Anyone looking to build more advanced and scalable Python workflows Why take this course? Basic scripting is often not enough for modern biological research. As datasets become larger and analyses more complex, researchers need the ability to write efficient, reusable, and well-structured code. This course equips you with advanced Python skills used in professional bioinformatics workflows, helping you automate analyses, manage complex projects, and develop robust computational pipelines for modern biological research. Learn more & enrol PR Stats course page for Advanced Python for Bioinformatics (APYB02) Questions? Email: oliver@prstats.org

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AntCourse 2026Mexico

Dear colleagues, Applications are now open for the Ant Course, an intensive international field course focused on ant biology, systematics, and ecology. Information on location, dates, instructors, and how to apply, can be found here: https://www.antcourse.org/ The Ant Course is a globally recognized training program that brings together students, researchers, and professionals to learn directly from leading myrmecologists through a combination of lectures, laboratory work, and hands-on field experience. Participants gain practical skills in ant identification, sampling, specimen curation, and the study of ant diversity, behavior, and their roles in ecosystems. The course emphasizes: - Ant phylogeny, diversity, and classification - Social behavior and colony biology - Field collection and biodiversity sampling methods - Specimen preparation and identification techniques The program is designed for a broad audience, including students, postdocs, professors, researchers, and motivated participants from diverse backgrounds in biology; prior specialization in ants is not required. Please feel free to share this announcement widely with interested students and colleagues. Best regards, Marek Borowiec

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EvoDevoMec workshop Nov 2nd-5th 2026 Paris

Dear colleagues, We are happy to announce the forthcoming workshop entitled ”Roadmap for EvoDevoMec”, Nov. 2nd - 5th, 2026, Universite Paris Cite. The link with evolutionary history of an organism is key to understand embryonic development. Much of the focus has been so far on genetic circuitry. However, it has become increasingly clear that physical constraints are an essential aspect at the basis of morphogenetic processes. We have now reached an exciting stage where it becomes possible to integrate mechanical considerations in our view of how development has been shaped during evolution: EvoDevMec. This new approach has recently raised great interest, but biological questions still need to be reformulated with precision. In addition, due to its integrative nature, it poses a scientific and technical challenge: What type of experimental systems could be used? How could we define experimental proof of concepts? How can theoretical biophysical models help integrate various questions and approaches? We aim at discussing these questions in an informal context, i.e. with chalk talks. The workshop is limited to 30 persons, from PhD students to senior scientists from various countries. We will welcome biologists using a breadth of models (from unicellular organisms to animal and plant models), physicists (theoreticians, numericians, experimentalists), and mathematicians. For application and details see : https://evodevmec2026.sciencesconf.orgLooking forward to seeing you in Paris, Francois Fagotto, Francois Graner, Marie Manceau, Dennis Worthmuller

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HoodCollegeMD July13-17 IntroToConservationGenetics

WHERE: Hood College, Frederick, MD WHEN: July 13 - 17, 2026 WHAT: Introduction to Conservation Genetics Workshop Join us to discover the genetic foundations that sustain life on Earth - How to protect species, ecosystems, and our planet's biological heritage. What to Expect: . Hands-on laboratory sessions with cutting-edge genomic tools and datasets . Insightful lectures from leading scientists in conservation and genetics . Networking opportunities Lecture topics covered: Human evolution, DNA sequencing technologies, phylogenetics, wildlife forensics and ecology, de-extinction and conservation, and more! WHO: Excellent undergraduate and graduate students, early-career researchers, and anyone passionate about genetics, wildlife conservation, or environmental health. Registration: email Dr. Meredith Yeager (yeager@hood.edu) to reserve your spot. Fee: Because of a generous grant from the American Genetic Association, registration costs for this workshop will be just 25/*participant*!

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Introduction to Snakemake (SNKM03)

Introduction to Snakemake (SNKM03) https://prstats.org/course/introduction-to-snakemake-snkm03/Delivered by experienced bioinformaticians and workflow automation specialists. Learn how to build reproducible, scalable, and automated data analysis pipelines using Snakemake. Modern biological and ecological research often involves complex, multi-step analyses that can be difficult to reproduce and manage manually. This hands-on course introduces Snakemake, one of the most widely used workflow management systems in bioinformatics and computational science, helping you automate analyses and build robust research pipelines. What you'll gain - A strong understanding of workflow automation concepts - Practical experience building pipelines using Snakemake - Skills to manage complex multi-step analyses efficiently - Understanding of reproducible and scalable computational workflows - Confidence in automating research pipelines and data processing tasks Course format - Live, instructor-led online training - Hands-on coding with real-world datasets and workflows - Interactive practical exercises throughout - Strong focus on applied, research-ready workflows Who is this course for? - Bioinformaticians and computational biologists - Researchers working with large or complex datasets - Python and command-line users wanting to automate workflows - PhD students and quantitative researchers Why take this course? As datasets and analyses become increasingly complex, manually running scripts and managing files is no longer sustainable. Workflow management systems like Snakemake provide a powerful way to automate analyses, improve reproducibility, and scale research pipelines efficiently. This course equips you with the skills to design, manage, and execute reproducible workflows, helping you save time, reduce errors, and build robust computational pipelines for modern scientific research. Learn more & enrol PR Stats course page for Introduction to Snakemake (SNKM03) Questions? Email: oliver@prstats.org Oliver Hooker Managing Partner Advanced Training for Researchers in the Life Sciences oliver@prstats.org — www.prstats.org

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Lastchance-ExploratoryMultivariateAnalysisinR

Hello EVOLDIR members

Last chance - This seminar offers essential skills for analyzing complex datasets and deriving robust empirical insights. Exploratory Multivariate Analysis in R is a 2-day seminar livestreaming May 7 and 20 with SMCS (Universite Catholique de Louvain). This seminar introduces exploratory multivariate analysis with a focus on practical implementation in R for empirical research. Mastering techniques like principal component analysis and clustering enables researchers to reduce dimensionality, discover latent structures, and handle mixed data types in complex datasets. These methods can be applied to advance research in evolutionary biology and genetics, from analyzing genomic data to understanding complex ecological interactions.

Sign up today (https://instats.org/seminar/exploratory-multivariate-analysis-in-r) to reserve your place before it starts, and feel free to circulate this with colleagues and students!

Best wishes

Michael Zyphur Professor and Director Instats — instats.org

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Lastchance-ModellingandMappingTraitEvolution

Hello EVOLDIR members

Last chance - We invite you to explore advanced methods for understanding evolutionary processes and phenotypic change. Modelling and Mapping Trait Evolution is a 2-day seminar livestreaming May 11 and 13 with Renan Maestri (Department of Ecology, Universidade Federal do Rio Grande do Sul). This seminar provides statistical and computational methods for modelling and mapping phenotypic trait evolution on phylogenies, integrating theoretical foundations with practical R implementation. Researchers can apply these rigorous tools to infer evolutionary processes, test macroevolutionary hypotheses, and produce publication-ready visualisations and results in their own studies. Participants will acquire methodological clarity on continuous and categorical trait models, ancestral-state estimation, and parameter-rich extensions to strengthen inference and improve study design.

Sign up today (`https://instats.org/seminar/modelling-and-mapping-trait-evolution`) to reserve your place before it starts, and feel free to circulate this with colleagues and students!

Best wishes

Michael Zyphur Professor and Director Instats — instats.org

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Lastchance R Regression and rms Package Essentials

Hello EVOLDIR members Last chance - This seminar offers a practical introduction to essential statistical and computational methods. Introduction to R, Regression, and the rms Package is a 2-day seminar livestreaming May 11 with Frank Harrell (Department of Biostatistics, Vanderbilt University) and Drew Levy. This seminar provides a foundational introduction to the R programming environment, RStudio, linear and multiple regression principles, and the rms package for robust statistical modeling. Researchers in evolutionary biology can apply these skills to analyze complex genetic data, model evolutionary traits, and develop reproducible research workflows for transparent and verifiable findings. Mastering these tools will enable more rigorous quantitative analysis, enhance data visualization capabilities, and support the dissemination of reproducible results within their specialized fields. Sign up today (`https://instats.org/seminar/introduction-to-r-regression-and-the-rms`) to register now, and we'd appreciate you sharing this with colleagues and students who might benefit! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Last-chanceSeminarOnline WhatGrantReviewersSeek

Hello EVOLDIR members

Last chance - Discover practical strategies to enhance your research proposals and secure crucial funding. What Do Grant Reviewers Look For? (Free Seminar) is a 2-day seminar livestreaming May 13 with Phil Batterham (National Centre for Epidemiology and Population Health, Australian National University). Understanding grant reviewer expectations is crucial for advancing evolutionary and genetics research careers. This seminar helps researchers apply reviewer criteria to strengthen proposals, ensuring methodological rigor and clear articulation of significance for their evolutionary studies. Participants will learn to refine aims, justify methods, and address common critiques, directly improving funding prospects and publication success in their field.

Sign up today (`https://instats.org/seminar/what-do-grant-reviewers-look-for-free-se`) to secure your spot, and please share this opportunity with colleagues and students who might benefit!

Best wishes

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Online aDNAPopulationGenomics 21-25September

Dear all, the 4th edition of the online course "Population Genomics Using Ancient DNA Data" will take place from 21-25 September.

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

This 5-day course will provide participants with both theoretical background and practical training in the analysis of ancient DNA (aDNA) data for population genomics research. Topics include data processing and authentication, population structure analysis, coalescent-based demographic inference, D and F statistics, relatedness, simulations, and natural selection analyses.

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

We would be grateful if you could share this opportunity with colleagues and students who may be interested.

Best regards, Carlo ————————

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

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Online AdvancedRCodingSkills 1-4June

Dear all,

Are you already using R, but looking to write cleaner, more efficient, and fully reproducible code for your research projects?

There are a few last seats available for our upcoming online course, Beyond Beginner R: Advancing Your Coding Skills, taking place from 1-4 June (live sessions, 1:00 PM - 7:00 PM Berlin time).

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

This four-day course is designed for researchers and professionals who already use R and want to strengthen their programming practices for reproducible, efficient, and collaborative data analysis.

Participants will learn how to: - Write clean, robust, and reproducible R code - Build well-structured analytical workflows - Use GitHub and Quarto for collaboration and reporting - Create advanced visualisations with ggplot2 - Work efficiently with large datasets and SQL - Use AI tools responsibly in coding workflows The course combines practical exercises with real-world best practices tailored to modern ecological and biological 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 AI for Research End-to-End in 10 Hours Workflows

Hello EVOLDIR members Last chance - Modern empirical research increasingly relies on robust computational workflows and automated data analysis. AI for Research: End-to-End in 10 Hours is a 2-day seminar livestreaming May 28-29 with Evagoras Xydas (University of Limassol). Evolutionary biologists can leverage these end-to-end machine learning workflows to analyze complex genomic and phenotypic datasets more efficiently. By mastering Python-based data structures and neural networks, researchers can automate the classification of diverse evolutionary traits and track experimental models with high precision. This systematic computational approach enables more reproducible analyses of genetic variation and evolutionary patterns across diverse populations. Sign up today (https://instats.org/seminar/ai-for-research-end-to-end-in-10-hours) to reserve your place before it starts, and feel free to circulate this with colleagues and students! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online BayesianSpeciesDistributionModelsInR 1-3July

Dear all, We are pleased to announce the 2nd edition of the online course ”Species Distribution Modeling with Bayesian Additive Regression Tree (BART) methods”, taking place 1-3 July.

Course website: https://www.physalia-courses.org/courses-workshops/barts/ This hands-on course will introduce Bayesian Additive Regression Tree (BART) methods for species distribution modeling and ecological applications using R. Participants will learn how to select environmental predictors, train and evaluate BART models, visualize predictor effects, and project species distributions across regions or time periods using the embarcadero and dbarts packages.

Topics include: - SDM workflows and machine learning methods - Bayesian statistics and regression - BART theory and applications for SDMs - Predictor selection, model evaluation, and troubleshooting - Spatial partial effects and random-intercept BARTs 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 BEAST2BayesianPhylogenetics Nov30-Dec11

Dear evoldir colleagues, Transmitting Science is offering the live online course ”Bayesian phylogenetic inference with BEAST2” (5th edition). Registration and course information: https://www.transmittingscience.com/courses/evolution/bayesian-phylogenetic-inference-with-beast2/ Participants will learn the theoretical concepts underlying the different models involved in Bayesian phylogenetic inference and get hands-on experience using these models in BEAST2. Particular attention will be given to more complex tree models, such as the fossilized birth-death model used to integrate past information into phylogenies, as well as rate-heterogeneous models, which allow for variations in evolutionary dynamics across clades. Finally, the course will give practical information on setting up and troubleshooting analyses in BEAST2. If you have any questions, do not hesitate to contact us at courses@transmittingscience.com Best regards, Haris – Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Clustering High-Dimensional Data May26-27

Hello EVOLDIR members We invite you to a seminar exploring advanced methods for analyzing complex datasets and extracting meaningful scientific insights. Clustering High-Dimensional Data 3.0 is a 2-day seminar livestreaming May 26, led by Nikolay Oskolkov (Lund University). Effectively analyzing and interpreting high-dimensional data is crucial for researchers in evolutionary biology and genetics. This seminar provides practical skills in clustering methods using R and Python, enabling you to identify patterns and group similar data points within complex genetic or phenotypic datasets. Participants will gain hands-on experience with advanced techniques to extract meaningful insights and strengthen analytical workflows for their own research.

Sign up today (https://instats.org/seminar/clustering-high-dimensional-data-30) to secure your spot, and please share this opportunity with colleagues and students who might benefit! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online EnvironmentalMetagenomics 12-16October

Dear all,

registrations are open for the 4th edition of the Environmental Metagenomics course.

Dates: Online, 12-16 October

Course website: https://www.physalia-courses.org/courses-workshops/environmental-metagenomics/

Participants will learn how to explore microbial diversity and function in complex ecosystems, including those dominated by uncultured organisms. Special attention is given to recent advances that enable the reconstruction of genomes directly from environmental samples, providing unprecedented resolution of microbial communities.

Through a combination of lectures and guided practical sessions, participants will gain experience with both read-based and assembly-based analytical strategies. We will use data from both short-read (e.g. Illumina) and long-read (e.g. Nanopore) sequencing platforms, as this combination dramatically improves the assembly and binning of metagenome-assembled genomes (MAGs) compared to short-read-only methods.

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 GenomicDataVisualisationWithPython 22-24June

Dates: 22-24 June

Course website: https://www.physalia-courses.org/courses-workshops/genomic-data-viz-python/

Modern genomics generates complex, high-dimensional datasets, making clear and effective visualization essential. This intensive 3-day course offers a hands-on introduction to creating publication-quality figures using Python, while building a personal toolkit of reusable scripts for genomic data analysis.

Participants will explore a broad range of visualization approaches, including differential expression plots (e.g. volcano and Manhattan plots), dimensionality reduction (PCA, t-SNE, UMAP), heatmaps and pathway visualizations, as well as more advanced representations such as phylogenetic trees, multiple sequence alignments, circos plots, synteny, and genome tracks.

The course combines widely used libraries such as Matplotlib, Seaborn, and Plotly with specialised genomics tools (e.g. pyCirclize, Toytree, pyGenomeTracks, DashBio), with a strong emphasis on practical application.

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

Best regards, Carlo ———— Dear all, We are pleased to announce our upcoming online course: Genomic Data Visualisation with Python

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

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Online IntegratedPopulationModels

Hello EvolDir,

If you're an evolutionary biologist looking to work with integrated population models, check out this online course and learn at your own pace with instructor support.

TITLE: Integrated Population Models

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

DATES: Summer: June 1 - September 6, 2026

PRICE: Price starts at 525$forstudentsorunemployed$,625 for currently employed

LEARN MORE & REGISTER: https://www.center forwildlifestudies.org/courses/p/integrated-population-models Thanks for your time!

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Online IntroductionToBioinformatics 8-12June

Dear all, there are only a few seats left for the 9th edition of the upcoming Spring School in Bioinformatics (9th edition), which will take place online from 8-12 June.

Course website: https://www.physalia-courses.org/courses-workshops/course68/ This five-day course provides a comprehensive introduction to Next-Generation Sequencing (NGS) data analysis, combining essential theoretical concepts with extensive hands-on training. Participants will gain practical experience working with real genomic and transcriptomic datasets, following the complete workflow from raw sequencing data to biological interpretation. Throughout the course, participants will learn how to evaluate sequencing quality, assemble and annotate genomes, perform RNA-seq and differential gene expression analyses, and investigate evolutionary relationships through phylogenomic approaches. We will focus on Illumina sequencing data as well as on the rapidly expanding field of long-read sequencing, exploring the applications, advantages, and analytical considerations of Nanopore and PacBio technologies. In addition to NGS data analysis, participants will develop essential computational skills for modern bioinformatics. Dedicated practical sessions will introduce the Linux command line, workflow management, and the use of Docker containers, empowering researchers to build reproducible and portable analysis pipelines.

Designed specifically for researchers and students with a background in the life sciences, this course is ideal for anyone seeking to strengthen their bioinformatics expertise and gain confidence in analysing genomic and transcriptomic data independently.

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 Last-chance AI Agents for Scientific Researchers

Hello EVOLDIR members Last chance - Integrating advanced computational tools can significantly accelerate your evolutionary biology and genetics research workflows. AI Agents for Researchers is a 2-day seminar livestreaming June 5 with Martin Qiu (Lazaridis School of Business and Economics, Wilfrid Laurier University). Evolutionary biologists can leverage agentic AI workspaces to automate the processing of massive genomic datasets and streamline phylogenetic analysis pipelines. By establishing structured, file-based workflows, researchers can ensure that complex evolutionary modeling and data-preparation steps remain fully reproducible and auditable. This approach allows genetics labs to integrate automated coding support and evidence tracing directly into their ongoing research operations. Sign up today (https://instats.org/seminar/ai-agents-for-researchers) to join before enrollment closes, and please pass this to colleagues and students who may be interested! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online LastChance Handle Missing Data with Confidence

Hello EVOLDIR members

Last chance - Effectively managing incomplete datasets is crucial for maintaining the integrity of your research findings. Handle Missing Data with Confidence is a 2-day seminar livestreaming May 22 with Centre for Applied Statistics Courses (CASC) (University College London). Missing data is a pervasive challenge in evolutionary and genetics research, from phylogenetic tree construction to population genetics studies, often impacting the validity of conclusions. This seminar equips researchers with robust statistical techniques, including multiple imputation, to effectively address data gaps and minimize bias in their analyses. Applying these methods will enhance the integrity and credibility of your evolutionary research, ensuring more reliable interpretations of complex biological datasets. Sign up today (https://instats.org/seminar/handle-missing-data-with-confidence) to secure your spot, and please share this opportunity with colleagues and students who might benefit! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online Lastchance StatisticalModelsandLinearRegressionEssentials

Hello EVOLDIR members

Last chance - Discover powerful statistical techniques that can transform your approach to complex evolutionary and genetic data analysis. Foundations of Statistical Models and Linear Regression is a 2-day seminar livestreaming May 7 with Centre for Applied Statistics Courses (CASC) (University College London). This seminar on statistical models and linear regression offers powerful tools for evolutionary biologists and geneticists to analyze complex datasets. Participants will learn to quantify relationships between genetic variants and phenotypes, model evolutionary trajectories, or assess environmental impacts on species adaptation using practical regression techniques. Mastering these skills, including hands-on software application and model diagnostics, will significantly enhance your ability to conduct rigorous, data-driven research and publish impactful findings in your field.

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

Best wishes

Michael Zyphur Professor and Director Instats — instats.org

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Online MachineLearningForMultiOmics 21-23September

Dear all, We are pleased to announce the online Physalia course Machine Learning for Multi-Omics Integration, taking place from 21-23 September.

Course website: https://www.physalia-courses.org/courses-workshops/multiomics/

This course will introduce machine learning methodologies for integrating large-scale biological and biomedical data generated through Next-Generation Sequencing (NGS) and other Omics technologies. Through a combination of lectures and hands-on sessions, participants will explore supervised, unsupervised, deep learning, and single-cell Omics integration approaches.

Participants are expected to have basic familiarity with the UNIX environment and beginner-level experience in R and/or Python.

By the end of the course, participants will be able to: - Understand machine learning approaches for biological data analysis - Select appropriate tools for integrative Omics analysis - Design and implement integrative bioinformatics workflows - Apply suitable methodologies to specific biological research questions 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 MarineGenomics 25-29May

Dear all,

there are still a few seats left for the online Physalia course "Marine Genomics", taking place 25-29 May.

Course website: https://www.physalia-courses.org/courses-workshops/marine-genomics/

This five-day course introduces the theoretical foundations and practical applications of marine and population genomics. Participants will learn how to process and analyse genomic datasets, assess genome quality, and apply integrative approaches linking genetic variation with environmental data (seascape genomics). The program combines lectures, discussions, and hands-on sessions using real marine datasets.

Topics include: Genome assembly assessment and annotation NGS data processing and variant calling Population genomics analyses Seascape genomics and environmental data integration Genotype-environment association analyses Sessions will run daily from 13:00-18:00 (Berlin time).

For the full list of our courses and workshops, please have a look at: https://www.physalia-courses.org/courses-workshops/ Best regards, Carlo ——————— Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org

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OnlineSeminar Lastchance Exploratory Analysis of Complex Datasets-with-AI

Last chance: Exploratory Analysis of Complex Datasets with AI

Hello EVOLDIR members Last chance - Enhance your research capabilities by mastering advanced techniques for exploring intricate datasets effectively. Exploratory Analysis of Complex Datasets with AI 3.0 is a 2-day seminar livestreaming May 27 with Nikolay Oskolkov (Lund University). Researchers in evolutionary biology and genetics often encounter high-dimensional, complex datasets, from genomic sequences to population dynamics, where traditional analysis methods can obscure critical patterns. This seminar provides advanced techniques in dimensionality reduction and clustering, enabling you to uncover hidden structures, identify novel genetic variations, or trace evolutionary trajectories within your own intricate biological data. You will learn to apply modern AI tools like ChatGPT, R, and Python to streamline data interpretation and enhance analytical workflows, directly advancing your capacity to derive robust insights from complex evolutionary and genetic studies. Sign up today (https://instats.org/seminar/exploratory-analysis-of-complex-datasets-4) to reserve your place before it starts, and feel free to circulate this with colleagues and students! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online SexChromosomeEvolution 12-16October

Dear all,

We are pleased to announce the upcoming Physalia online course "Sex Chromosome Evolution", taking place from 12-16 October.

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

This course will introduce how genomic and transcriptomic data can be used to detect sex chromosomes and to study the cause and consequences of sex chromosome differentiation. Participants will explore study design, data collection, and analysis strategies, and will learn how to identify sex chromosomes and investigate their molecular evolution.

Key topics include: - Sex determination systems and sex chromosomes (X0, XY, ZW, UV) - Identification of sex chromosomes using genomic approaches - Recombination suppression, evolutionary strata, and genome divergence - Gene gain/loss and gene expression differentiation - Sex-biased gene expression and dosage compensation - Comparative analyses across species The course combines lectures, hands-on exercises, and interactive discussions using real datasets.

Participants will work in a Linux environment and use R for data analysis and visualization. The course is aimed at graduate students and researchers in evolutionary biology, genetics/genomics, and bioinformatics. Basic experience in UNIX command line and R is recommended.

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

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Online Single Cell Data Analysis 3 0 Applying Single-Cell Analysis

Hello EVOLDIR members Last chance - Discover how advanced single-cell data analysis techniques can significantly enhance your evolutionary and genetic research endeavors. Single Cell Data Analysis 3.0 is a 2-day seminar livestreaming May 25 with Nikolay Oskolkov (Lund University). This workshop equips evolutionary biologists and geneticists with advanced computational skills to analyze single-cell data, offering unprecedented insights into cellular heterogeneity. Mastering these techniques enables researchers to explore complex biological systems at the most granular scale, identifying genetic variations and expression patterns relevant to evolutionary processes. Participants will learn to perform comprehensive single-cell analysis pipelines, from raw data handling to biological interpretation, fostering innovative research in adaptation and speciation. Sign up today (https://instats.org/seminar/single-cell-data-analysis-30) to reserve your place before it starts, and feel free to circulate this with colleagues and students! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online SpatialOmicsWithBioconductor 18-20May

Dear all, If you are interested in Spatial Omics, there are a few seats available for the 3rd edition of the online Physalia course: Spatial Omics in R/Bioconductor

Dates: 18-20 May

Course website: https://www.physalia-courses.org/courses-workshops/spatial-omics-1

Spatial omics technologies are rapidly transforming biological and biomedical research, creating new opportunities to study tissue organisation, cell interactions, and spatial gene expression at unprecedented resolution. This hands-on course provides an introduction to both sequencing- and imaging-based spatial omics analyses using modern R/Bioconductor frameworks, including SpatialExperiment, MoleculeExperiment, tidySpatialExperiment, and Seurat.

Participants will learn how to: analyse spatial omics datasets in R/Bioconductor work with tidy spatial workflows perform spatial differential expression and cell-neighbour analyses integrate multi-modal spatial datasets For the full list of our courses and workshops, please have a look at: https://www.physalia-courses.org/courses-workshops/

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

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Online SpeciesDistributionModelsInR 14-18September

Dear all, We are pleased to announce the online Physalia course Species Distribution and Ecological Niche Modelling in R, taking place from 14-18 September.

Course website: https://www.physalia-courses.org/courses-workshops/course45/

This course will provide both the theoretical foundations and practical applications of species distribution models (SDM) and ecological niche models (ENM), with a strong focus on reproducible and automated workflows in R. Participants will learn how to design, build, validate, and apply SDM and ENM using real species occurrence data.

The course is aimed at students, researchers, and practitioners interested in biodiversity, ecology, conservation, and spatial modelling. Previous basic experience with R is desirable (https://www.physalia-courses.org/courses-workshops/messy-data/) .

By the end of the course, participants will be able to: Understand the key concepts behind SDM and ENM Build and evaluate models in R Assess the strengths and limitations of different modelling approaches Predict and project species distributions across space and time For the full list of our courses and workshops, please visit: https://www.physalia-courses.org/courses-workshops/ We would greatly appreciate it if you could share this opportunity within your networks.

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

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Online WebScraping and Data Collection May13-15

Hello EVOLDIR members Last chance - This seminar offers advanced training in methods that can significantly enhance your empirical research capabilities. Web Scraping and Data Collection is a 2-day seminar livestreaming May 13 and 15 with Moses Boudourides (Data Science Graduate Program, School of Professional Studies, Northwestern University). This seminar offers a rigorous, research-focused introduction to web scraping and structured data collection, providing essential skills for researchers who rely on diverse online information. Participants will learn to transform heterogeneous web sources into analysis-ready datasets, enabling them to gather contemporary, fine-grained behavioral, institutional, or textual data for evolutionary studies, such as genetic sequence metadata or species interaction records. The hands-on methods for data extraction, parsing, and reproducible pipeline integration will empower researchers to build robust datasets for large-scale comparative analyses or longitudinal studies in evolutionary biology and genetics.

Sign up today (https://instats.org/seminar/web-scraping-and-data-collection) to reserve your place before it starts, and feel free to circulate this with colleagues and students! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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Online Workshops Multivariate Ecology Community Structure and Evolutionary Processes

Dear Colleagues, Modern evolutionary biology increasingly depends on our ability to analyse ecological communities as complex, multidimensional systems. From adaptive radiation and niche evolution to community assembly and species coexistence, many of the central questions in evolutionary ecology now require sophisticated multivariate analytical approaches. As ecological and evolutionary datasets continue to grow in scale and complexity, tools for analysing community structure, species associations, and environmental gradients have become essential across biodiversity science, macroecology, conservation biology, and evolutionary research. One of the most widely used frameworks for this work is the VEGAN package in R, which provides a powerful suite of methods for multivariate ecological analysis, ordination, diversity analysis, and community modelling. *Why Multivariate Analysis Matters in Evolutionary Biology* Evolution rarely occurs in isolation. Species evolve within ecological communities shaped by competition, environmental filtering, dispersal, adaptation, and co-evolutionary interactions. Multivariate ecological methods allow researchers to investigate: - Patterns of community assembly across environmental gradients - Ecological niche differentiation and trait divergence - Beta diversity and evolutionary turnover - Relationships between species composition and environmental selection pressures - Functional and phylogenetic structure of communities - Large-scale biodiversity and macroecological patterns Methods such as PCA, NMDS, PCoA, CCA, RDA, PERMANOVA, and hierarchical clustering are now widely used throughout evolutionary ecology and ecological genetics to understand how ecological and evolutionary processes shape biodiversity. The VEGAN package has become one of the core analytical tools for these workflows, supporting reproducible, statistically robust analyses of ecological and evolutionary datasets. *Upcoming Course: Multivariate Analysis of Ecological Communities Using VEGAN* We are pleased to announce our course: Multivariate Analysis of Ecological Communities Using VEGAN (VGNR10) https://prstats.org/course/multivariate-analysis-of-ecological-communities-using-vegan-vgnr10/?utm_source=chatgpt.com This course provides a practical introduction to multivariate ecological analysis using the VEGAN package in R, with applications highly relevant to evolutionary biology, biodiversity science, and community ecology. Participants will explore: Community data preparation and transformation Ordination methods (PCA, NMDS, PCoA) Constrained ordination (CCA and RDA) Diversity and dissimilarity metrics PERMANOVA and ecological hypothesis testing Community structure and ecological gradients Visualisation and interpretation of multivariate analyses Reproducible ecological workflows in R The course is designed for evolutionary biologists, ecologists, conservation scientists, postgraduate researchers, and anyone working with ecological or biodiversity datasets. ——————- *Related Course: Joint Species Distribution Modelling* Researchers interested in extending multivariate community analyses into hierarchical and multi-species frameworks may also be interested in: Joint Species Distribution Modelling (JSDM01) https://prstats.org/course/joint-species-distribution-modelling-jsdm01/?utm_source=chatgpt.com Joint Species Distribution Models (JSDMs) provide a powerful framework for modelling multiple species simultaneously, allowing researchers to investigate co-occurrence patterns, environmental filtering, and latent ecological structure within communities. These approaches are increasingly important in evolutionary ecology because they help researchers move beyond single-species analyses toward understanding how ecological interactions, evolutionary history, and environmental change jointly shape biodiversity patterns across spatial and temporal scales. JSDMs are now widely applied in studies of community assembly, macroecology, niche evolution, and biodiversity responses to global change. ——————- *Suggested Reading* For those interested in multivariate ecology and evolutionary community analysis, we recommend: - Legendre P & Legendre L. Numerical Ecology - Borcard D, Gillet F & Legendre P. Numerical Ecology with R - Oksanen J et al. VEGAN: Community Ecology Package - Anderson MJ. A new method for non-parametric multivariate analysis of variance - Pollock LJ et al. Understanding co-occurrence by modelling species simultaneously with a Joint Species Distribution Model We look forward to welcoming you to one of our upcoming ecology and evolutionary biology courses. Best wishes, PR Stats Oliver Hooker Managing Partner

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

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Oslo TDWG-Multimodel-Biodiversity-Data-Symposium Sep21-25

For the 2026 Biodiversity Information Standards (TDWG) Conference, to be held Sep 21-25 in Oslo (Norway), we are organizing the following symposium: ”From Mobilizing Data to AI-Ready Knowledge: Infrastructure for Multimodal Biodiversity Data” (SYM25)

The organizers are Rob Guralnick (U. Florida), Hilmar Lapp (Neuromatch Inc.), Kelsey Huelsman (ERT, NASA), Eric Sokol (NEON, Battelle), and David Bloom (VertNet, UNC Greensboro). The symposium is motivated by the recognition that even as biodiversity data become increasingly multimodal and AI-driven analyses more common, major challenges nonetheless remain, especially in transforming fragmented observational records, images, sensor streams, and metadata into interoperable, research-ready knowledge. The symposium aims to explore how standards, ontology integration, uncertainty representation, and human-AI collaboration can support provenance-aware, fitness-for-use biodiversity data pipelines. Full symposium abstract: https://www.tdwg.org/conferences/2026/program/sessions-list/#sym25We greatly welcome submissions from the EvolDir community, in particular on addressing how community-aligned infrastructure and governance frameworks can enable AI-enabled research while respecting provider expectations and improving data quality, interoperability, and reproducibility. The abstract submission deadline is approaching fast on May 20 (AoE). Instructions for abstract submission: https://www.tdwg.org/conferences/2026/submissions/abstract-instructions/Hilmar Lapp, On behalf of the organizers.

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UCL LastChance SurvivalAndTime-to-EventDataAnalysis

Last chance - We invite you to explore a comprehensive introduction to survival and time-to-event data analysis. Introduction to Survival and Time-to-Event Data Analysis is a 2-day seminar livestreaming May 21 with Centre for Applied Statistics Courses (CASC) (University College London). This seminar introduces comprehensive methods for analyzing time-to-event data, crucial for understanding the timing and predictors of various biological and evolutionary phenomena. Researchers can apply these techniques, including Kaplan-Meier and Cox regression, to model events such as speciation, disease progression, or genetic mutation accumulation within populations. Participants will learn to prepare data, interpret hazard ratios, and evaluate model fit, directly enhancing their ability to publish robust findings in evolutionary and genetic research. Sign up today (https://instats.org/seminar/introduction-to-survival-and-time-to-eve-1) to register now, and we'd appreciate you sharing this with colleagues and students who might benefit! Best wishes Michael Zyphur Professor and Director Instats — instats.org

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UK LJMU Liverpool DNA Metabarcoding OxfordNanoporeSequencing 7to10July2026

Dear EvolDir community, We are advertising two training options in DNA metabarcoding and Oxford Nanopore sequencing for environmental, biodiversity, ecology, conservation, molecular ecology and molecular biology applications. Option 1: In person hands on course Course title: DNA Metabarcoding and Oxford Nanopore Sequencing Location: Liverpool John Moores University, Liverpool, UK Dates: 7 to 10 July 2026 Time: 09:00 to 17:00 each day Format: 4 full days in person Capacity: Up to 20 participants Fee: GBP750 Included: Lunch and tea or coffee each day, plus a live 2 day online bioinformatics course on 15 and 16 July 2026 This intensive hands on course covers the complete DNA metabarcoding and Oxford Nanopore sequencing workflow for environmental and biodiversity applications. Participants will work in small teams and carry out the critical wet lab steps, including DNA extraction, column based methods, an automation demonstration using the KingFisher Apex, COI metabarcoding PCR set up with controls, gel electrophoresis, bead clean up and QC, nanopore library preparation, barcoding, ligation, flow cell loading and live sequencing run monitoring. The final in person day includes a bioinformatics taster using a subset of sequencing data. Participants will demultiplex data, run quality control, build a simple taxonomy table and discuss interpretation issues such as controls and contamination. All in person delegates are also included in a live tutor led 2 day online bioinformatics course on 15 and 16 July 2026, from 10:00 to 14:00 UK time each day. These sessions complete the analysis workflow and help participants move from sequencing output to interpretable results. No separate booking is needed for this online component.

Option 2: Online bioinformatics only Course title: DNA Metabarcoding Bioinformatics Location: Online Dates: 14 to 16 July 2026 Time: 10:00 to 14:00 UK time each day Format: 3 live online sessions Fee: GBP350 This option is for participants who want the bioinformatics training only, without the in person wet lab course. Day 1 provides background on the laboratory workflow that generated the sequencing data. Days 2 and 3 focus on the practical analysis steps, including demultiplexing, quality control, taxonomy assignment, simple result summaries and interpretation using example Oxford Nanopore metabarcoding datasets. Who should attend These courses are suitable for researchers, technicians, students and environmental professionals working in ecology, conservation, environmental monitoring, biodiversity genomics, molecular ecology and molecular laboratories. Some familiarity with pipetting, PCR or molecular biology concepts is helpful, but the courses are designed to support mixed experience levels. Booking links In person hands on course: https://buyonline.ljmu.ac.uk/product-catalogue/faculty-of-health-innovation-technology-and-science/faculty-shop/dna-metabarcoding-oxford-nanopore-sequencing-hands-onOnline bioinformatics only: https://buyonline.ljmu.ac.uk/product-catalogue/faculty-of-health-innovation-technology-and-science/faculty-shop/dna-metabarcoding-bioinformatics-online-only-3-daysFor enquiries, please contact: Peter Shum Liverpool John

Moores University P.Shum@ljmu.ac.uk

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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 notifcation 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 LaTeX files, Excel files, etc. …plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be 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 preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.