
E v o l D i r

October 3, 2026

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

Foreword

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

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

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Breckenridge CO US Keystone Symposia Conference Transposable Elements-From Evolution to Engineering

Registration is now open for the Keystone Symposia Conference "Transposable Elements: From Evolution to Engineering" <https://www.keystonesymposia.org/conferences/conference-listing/meeting/C22027> to be held on March 15-18, 2027 at the Beaver Run Conference Center in Breckenridge, CO, USA. The meeting will cover all aspects of transposon biology, including but not limited to evolutionary comparative genomics and epigenomics, structural and mechanistic aspects of transposition and genome defense, interactions with the host under normal and pathological conditions, and applications in genome editing and engineering. The deadline for talk abstract submission and scholarship applications is November 17, 2026, and the discounted early registration deadline is January 13, 2027. We have over 30 available slots for short talks selected from submitted abstracts. Please share this information with interested colleagues and trainees who have a transposon story of any kind. Looking forward to welcoming you at the meeting! Your organizing team: Irina Arkhipova, Samuel Sternberg, Ting Wang, Phillip Zamore

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GordonResearchConference UrbanEvolutionAndEcology Jan31 2027 US

This is the second announcement for the inaugural Gordon Research Conference in Urban Evolution and Ecology (<https://www.grc.org/urban-evolution-and-ecology-conference/2027/>) Jan 31-Feb, 2027 in Ventura, California. Please note that for those that have already registered, the GRC system will soon allow us to accept the applications, and within a week or so you will also be able to check the final registration fees online and fully register. You can view online the full program, list of speakers and discussion leaders, and you can apply via the same website. The application portal will stay open until Jan 3, 2027, unless the conference is full before this deadline. For those of you less familiar with the Gordon Research conference format, please note that there is a strong requirement that only unpublished results can be presented. There is also one single presentation session at a time that everyone attends (all invited talks), and there is a 2/1 talk/discussion ratio with talks. The poster sessions are much richer at GRCs than other conferences. There is a small number of posters and everyone attends them, which makes them among the most enriching part of the meetings. We will also have many 'free time' slots to foster discussions inspired by the posters, talks and

discussions. Please forward this announcement to anyone who is interested in Urban Evolution, Urban Ecology, and/or Urban Evolutionary Ecology! Best wishes, Anne Charmantier (co-chair), Marc Johnson (co-chair), Kiyoko Gotanda (vice-chair), Brian Verrelli (vice-chair) (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

KarlstadU EvolutionInSweden 11-13Jan2027

The Evolution in Sweden conference will be held in Karlstad, Sweden, January 11-13 2027.

Evolution in Sweden is a biannual meeting, which broadly gathers evolutionary biologists working in Sweden.

The meeting is intended to be a broad meeting on every aspect of evolutionary biology and all forms of life on earth. However, please note that the meeting is primarily (though not exclusively) for scientists active in Swedish academic departments. We also actively encourage younger researchers active in Sweden to present their research in this forum. There are no registration fees.

The keynote speakers will be Johanna Mappes, Cameron Ghalambor, Josefin Stiller and Kjetil Lysne Vøje. More details: <https://sola.kau.se/evolutioninsweden2027/> Submissions for talks and abstracts are now open. Deadline for submission October 31st 2026. Valkomna! ————— Ted Morrow and Evolution in Sweden organising committee Department of Environmental and Life Sciences Karlstad University (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

KULeuven BE CfA Life As It Could Be Interdisciplinary Perspectives on Artificial Life 7-8Dec2026

Call for Abstracts:

"Life As It Could Be: Interdisciplinary Perspectives on Artificial Life"

7-8 December 2026

Mini-Symposium Aula Symbiosis, BioScience Center, KU Leuven, Celestijnenlaan 200R, 3001 Leuven, Belgium <https://hiw.kuleuven.be/clps/events/symposium-lifeasitcouldbe/home> Deadline: October 23rd 2026

KU Leuven Organizers: Lendert Gelens (Department of Cellular and Molecular Medicine), Bart Smeets (Department of Biosystems), Alejandro Fabregas-Tejeda (Institute of Philosophy), Grant Ramsey (Institute of Philosophy), and Sylvia Wenmackers (Institute of Philosophy)

Invited Speakers Mark Bedau (Reed College), Liedewij Laan (TU Delft), Andrea Loettgers (University of Vienna), Gry Oftedal (University of Oslo), Juli Pereto (University of Valencia), and Ricard Solé (Pompeu Fabra University)

This mini-symposium will provide a forum for discussion of A-Life's objectives, overarching theoretical frameworks, main achievements and shortcomings, and prospects for the coming decades of scientific inquiry into what life is and could be—in silicon, in laboratories, and perhaps beyond Earth.

We welcome contributions from theoretical and empirical researchers—philosophers and scientists alike—interested in fostering interdisciplinary dialogues on the past, present and future of A-Life as a scientific field. We invite submissions of abstracts (max. 500 words) for presentations. Abstracts must include affiliation and contact information. Please send the abstracts to Alejandro Fabregas-Tejeda via email (alejandro.fabregastejeda@kuleuven.be). Deadline: October 23rd 2026. Notifications of acceptance: October 30th 2026.

Some of the themes and topics that we will cover include (but are not restricted to): - What are the objectives of A-Life as an interdisciplinary field? What can the history of A-Life teach us about which questions to carry forward and which to retire? - What does the field of A-Life offer that is unique or of value to the philosophy of science? - What role does the study of self-organization play in research into artificial life? - What distinguishes strong A-Life (genuine instantiation of life) from weak A-Life (simulation and modeling)? How to determine the threshold between them? - When does a simulation or synthetic system constitute evidence of the general properties of life-as-it-could-be? - Which overarching conceptual/theoretical frameworks have proven most fruitful in A-Life investigations, and why? - What are A-Life's genuine successes, and by what criteria should they be judged? - What has A-Life contributed to adjacent disciplines (e.g., cell and de-

developmental biology, evolutionary biology, cognitive science, origins-of-life research, astrobiology, and artificial intelligence) that those fields could not have produced on their own? - Which empirical findings in A-Life defy the soundness of our extant theoretical frameworks, and how can our theories be better tested experimentally?

- What are the main empirical challenges currently facing the field of A-Life? - Whither A-Life research? What trajectories are in store for the field? More information is available on this website: <https://hiw.kuleuven.be/clps/events/symposium-lifeasitcouldbe/home> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Nantes France ERA2027 Evolutionary Responses to Anthropogenic 20-21Apr2027

Dear colleagues, We are pleased to announce the first edition of ERA 2027 - Evolutionary Responses to Anthropogenic Drivers, which will take place on 20-21 April 2027 at IFREMER Nantes, France. ERA 2027 will bring together researchers interested in understanding how human activities reshape evolutionary processes and biodiversity trajectories, across marine and terrestrial ecosystems. The conference will provide an opportunity to discuss recent advances, exchange perspectives across systems and disciplines, and explore the implications of anthropogenic change for the future of biodiversity. The call for abstracts is now open! We welcome contributions for oral and poster presentations. Abstract submission is open until 30 November 2026. A detailed description of the scientific scope of the conference, together with practical information and abstract submission guidelines, is available on the ERA 2027 website: <https://era2027.sciencesconf.org> Please feel free to circulate this announcement widely within your networks. We look forward to welcoming you to Nantes in April 2027! Best regards, The ERA 2027 Organising Committee

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Online ESEB PolyAdaptSTN September24

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 24th September, 2026, 3 pm CET/CEST (Germany). Our speaker for this seminar is Dr. Bonnie Fraser from the University of Exeter, UK.

Title: Genomic basis of local adaptation in guppies
Meeting details: Topic: STN seminar - Bonnie Fraser
Time: Sep 24, 2026 03:00 PM Amsterdam, Berlin, Rome, Stockholm, Vienna Join Zoom Meeting <https://eu02web.zoom-x.de/j/63442058916?pwd=ymBNOQr0EsKiZhLa7pW2rdsNYvUQSF.1> Meeting ID: 634 4205 8916 Passcode: 185267 If you would like to get on our mailing list and take part in our upcoming events, please visit our website (<https://polygenic-adaptation-network.org/>) for more information. Sincerely, Neda Barghi on behalf of the Special Topic Network Polygenic Adaptation (STN-PolyAdapt) organizing committee ESEB-funded Special Topic Network "Polygenic Adaptation" <https://polygenic-adaptation-network.org/https://eseb.org/prizes-funding/special-topic-networks/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online InternalConflictsAsiaOceania 15Oct2026

Internal Conflicts and Organismal Adaptation Across Asia-Oceania Virtual symposium: 15th of October 2026 This free virtual symposium will bring together evolutionary biologists studying genetic and other internal conflicts, including meiotic drive, transposable elements, gene drives, transmissible cancers and feminising endosymbionts. The meeting will encompass both fundamental research and potential applications, with a particular focus on work from Asia and Oceania. Invited speakers: Beata Ujvari – Deakin University, Australia Jun Kitano – National Institute of

Genetics, Japan Jackson Champer – Peking University, China Stephen Frankenberg – University of Melbourne, Australia The programme will also include contributed short talks, discussion sessions and opportunities for informal networking. Registration is free and open to all. We are still accepting abstracts for a small number of contributed short-talk slots. Registration and abstract submission: <https://forms.gle/dBaKg6NKfq27rfJP7> Further details: <https://internalconflictsstn.wordpress.com/asia-oceania-virtual-symposium/> We would be grateful if you could circulate this announcement to anyone who may be interested. With best wishes, Thomas Hitchcock, Nina Wedell, Arvid Agren, Manus Patten and Martijn Schenkel ESEB Special Topic Network "Internal Conflicts and Organismal Adaptation" <https://internalconflictsstn.wordpress.com/> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Young Systematists Forum Nov13th2026

Dear all, We are pleased to announce this year's edition of the Young Systematists' Forum. This is a free, online conference for students and early career researchers working on any aspect of phylogenetics, taxonomy or systematics. It is a friendly environment that aims to support young (in experience!) researchers giving some of their earliest international presentations and to encourage them to forge lasting networks. When: Friday, November 13 9:30-17:30 UTC+0 Where: Online Abstract submission deadline: Saturday, October 24 23:59 UTC+1 Registration deadline: Wednesday, November 11 11:59 UTC+0 Registration and abstract submission: <https://tinyurl.com/bdzxt2ht> We hope you will join us for this event. The YSF Organising Committee (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

SanDiego PAG34 January 8-12 2027

CALL FOR ABSTRACTS: PAG 34 We invite abstracts for five interconnected sessions at PAG 34, to be held

in San Diego, California, January 8-12, 2027: Domestication Genomics Ancient DNA Comparative Genomics - Animals One Health Hologenomics Wildlife Genomics Abstract submission deadline: October 9, 2026. Submit your abstract using the following Google Form: <https://forms.gle/EgwFCVyxaf7RcKBF7> Notification of submission outcomes will be sent by the end of October 2026. Thanks to our sponsors, registration fee support may be available for early-career researchers. Please feel free to distribute this announcement widely. More information about PAG 34: <https://www.intlpag.org/PAG/> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Vienna PopGenSeminarSeries winter2026-27

Dear colleagues,

The Vienna Graduate School of Population Genetics runs a weekly seminar series featuring talks by leading experts in population genetics. The talks are open to interested audience via online streaming. Please find the following schedule for the upcoming winter semester.

Details are found on our website: <https://www.popgen-vienna.at/news/seminars/> To receive weekly updates and streaming links, please sign up here: <https://forms.gle/eaWbQEWvEN9A1z4CA> Many talks are recorded and can be found on our YouTube channel: <https://www.youtube.com/@popgenvienna8051> Winter semester schedule:

All Tuesdays, starting at 17:00 CET/CEST

06.10.26 - Dan Nussey (Univ. Edinburgh, UK) The evolutionary ecology of senescence in wild animals
13.10.26 - Howard Rundle (Univ. Ottawa, CA) The population genetic consequences of mate competition: Empirical insights from *Drosophila*
20.10.26 - Josephine Pemberton (Univ. Edinburgh, UK) Evolutionary genetic studies in long term, individually-monitored wild animal populations
27.10.26 - Richard Benton (Univ. Lausanne, CH) Niche specialisation in nervous systems and beyond
03.11.26 - Thomas Bataillon (Aarhus Univ., DK) How to find a "Ruby in the Rubbish?": On using population genomics to make inference about beneficial mutations, deleterious mutations and their impact on adaptation
24.11.26 - John Welch (Univ. Cambridge, UK) When will hybridization be beneficial?
01.12.26 - Thomas Flatt (Univ. Fribourg, CH) Inversions and

the hunt for the genomic targets of selection 15.12.26
 - Andreas Futschik (Vetmeduni, AT) Frequentist and Bayesian inference for population genetic data 12.01.27
 - Leif Andersson (Uppsala Univ., SW) On the origin of Baltic herring by means of natural selection 19.01.27
 - Mikkel Schierup (Aarhus Univ., DK) De novo mutations, cross-overs and gene conversions across primate species inferred from HiFi sequencing of sperm and testis tissue 26.01.27 - Thomas Wiehe (Univ. Cologne, DE) Looking at (some) plant genes with a joint LLM-population genetics lens

Sincerely, Junya Watanabe

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We are committed to making the conference as inclusive as possible. If you have any questions regarding accessibility, we encourage you to reach out to us at conference@sortee.org or complete this anonymous accessibility form (https://docs.google.com/forms/d/e/1FAIpQLSez9gVh0UufxjLI4g_GULvtTaj0Iv7ESpNs4aZJUMqdaT9ZDA/viewform). We share responses only with the SORTEE Conference Committee and Board of Directors.

The conference is free for SORTEE members, and becoming a member can be free too. Join us (<https://sortee.org/join>)!

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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. We are thrilled to announce that the full program is now available online through the SORTEE Shiny app at <https://conf-sortee.shinyapps.io/2026-program-app>. We have two fantastic plenary talks lined up: - Dr. Lauren Cadwallader: "Code Sharing in Practice: Lessons from Expanding a Publisher's Policy" - Dr. Tatsuya Amano: "Is science open across languages?"

The program also features Workshops on GitHub workflows, test-driven development, and Docker; Unconferences exploring FAIR data, preregistration, and open scholarship; and Hackathons focusing on data and code transparency, research contributions, and equity. Come ready to learn, connect, and participate as much as you would like!

This year, we are introducing microgrants. Do you experience any barriers to attending the SORTEE Conference in October? Would a small financial contribution help you overcome this? Apply at https://docs.google.com/forms/d/e/1FAIpQLSe8gQ_GB_91j97rnh-ektwan_TD4-u2DWjKnwd2V8TqnjREFg/viewform. Deadline: September 6, 2026.

WashingtonDC Species Interactions and Evolution Oct24

Conference: George Washington U, DC. Species Interactions & Evolution. Oct24

Species Interactions & Evolution Meeting: A regional meeting to be held at George Washington University, DC, on Saturday October 24th, 2026. Registration is free here: <https://forms.gle/mwXxeVFzmqykRXNj6>. The goal of this meeting is to bring together researchers working at the intersection of species interactions and evolution, broadly defined. We hope to provide a low-cost opportunity to share research and ideas around this topic, and to meet others working in the field. All are welcome, and we plan to emphasize presentations by students and postdocs as much as possible. The meeting is only "regional" in the sense that we hope many will be able to attend by traveling relatively short distances via carpooling and public transportation. The meeting format will be a day of short talks with afternoon posters and evening social. Overnight stay is encouraged, to make the most of the afternoon and evening program, but not necessary. Organized by the Powell Lab (GW) and the Hembry Lab (JMU). Questions? Contact scottpowell@gwu.edu.

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GradStudentPositions

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AuburnUniversity PhD in UndergradBiologyEdResearch

Two PhD Positions: NSF-Funded Biology Education Research at Auburn University

Position Description. The Auburn University Center for Discipline-Based Education Research (DBER) is recruiting a cohort of nine STEM PhD students through the NSF EPSCoR Graduate Fellowship Program. Fellows will gain a unique multidisciplinary research experience through Auburn's College of Science and Mathematics (COSAM) and College of Engineering, where established DBER faculty across Biological Sciences, Engineering, Geosciences, Mathematics & Statistics,

and Physics collaborate to address challenges in STEM teaching and learning. Fellows will earn PhDs in their home disciplinary departments while joining a collaborative cohort that integrates disciplinary STEM expertise with rigorous education research. They will receive mentorship, training, and professional development to prepare them for careers advancing STEM education, research, and innovation.

Fellows pursuing BIOLOGY EDUCATION RESEARCH will participate in research exploring how students learn biology and how evidence-based teaching practices can improve STEM education across varied learning environments. Our research group has broad interests, and fellows may investigate topics such as social models in STEM education, effective instructional practices, quantitative literacy, and the intersection of biology and society. Research approaches may include experimental and quasi-experimental designs,

survey development and validation, qualitative and mixed-methods approaches, and analysis of large-scale quantitative data. Research will address grand challenges in undergraduate biology education, drawing on knowledge from disciplinary biology and learning sciences, to develop evidence-based recommendations with applications across all undergraduate classrooms.

PREFERRED QUALIFICATIONS:

-BS or MS in biology, evolutionary biology, computational biology, or related field

-Interest in broad questions in biology education (e.g., social models in STEM education, effective instructional practices, quantitative literacy, and the intersection of biology and society)

-Experience or strong interest to learn quantitative and qualitative analysis

-Collaborative, team player, independent, and highly motivated

NSF-SPECIFIC QUALIFICATIONS (see submission portal for additional requirements):

-Named a GRFP Honorable Mention no more than three calendar years prior to this application (e.g., for 2027, applicants must have been named a GRFP Honorable Mention no earlier than Spring 2024).

-U.S. citizen, U.S. national, or permanent resident.

-Intend to enroll or be enrolled full-time in an Auburn University PhD program at the start of the fellowship.

FUNDING PROGRAM:

Two PhD positions will be fully supported (stipend, health care, tuition waiver) for three years with a stipend of \$37,000 per year and \$16,000 additionally available to enhance your education and research. You would be a PhD student within the Department of Biological Sciences graduate program at Auburn University.

Before applying to the program, I encourage potential students to contact Dr. Cissy Ballen at mjb0100@auburn.edu.

In this email, please include:

-a brief statement describing your research interests, their alignment with the lab's work/expertise, any relevant research experience, and motivation for joining the lab;

-a CV with college GPA and information for 2-3 references.

The application deadline for the EGFP program at Auburn University is May 15, 2027.

Here is more info about the program: <https://ballenlab.com/apply-egfp-bio-ed-research-multidisciplinary-opportunities-in-discipline-based-education-research/> Here is a bit more about my research group: ballenlab.com

You can apply here! <https://etap.nsf.gov/award/8537/opportunity/12045> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

BinghamtonU lizard organismal ecology

The Swierk Organismal Ecology Lab in the Department of Biological Sciences at Binghamton University (SUNY) is seeking 1-2 PhD students to join the lab starting Fall 2027 or Spring 2028. Our lab is broadly interested in the function, evolution, and underlying mechanisms of traits associated with animal communication, reproduction, and predator avoidance. We study how selection and phenotypic plasticity shape these traits in heterogeneous environments. Much of our lab's work is addressed using reptiles (primarily anoles) and amphibians in the Neotropics and in the Northeastern USA. The Swierk Lab seeks PhD students who are interested in developing questions that build upon our existing work in either of two research areas: 1) animal body coloration as a dynamic signal in conspecific and heterospecific communication, with an emphasis on visual modeling with respect to animal visual systems; and 2) specialized adaptations facilitating antipredator strategies, specifically the morphology, behavior, and respiratory physiology of rebreathing in semi-aquatic anoles. These projects will be developed using Neotropical anoles as a study system. Qualifications: - BA/BS in related field - Motivated, independent, collaborative - Relevant research experience - Demonstrated scientific writing and communication skills - Willing to spend 2-3 summer months/year conducting research at Neotropical field stations

Preferred candidates will also have: - Strong statistical / quantitative skills - Prior experience with tropical field research, animal behavior, and/or herpetology - Completion of MS degree (though any candidate is welcome to apply) - Interest in applying for external grants/fellowships (e.g., NSF GRFP)

Binghamton University (BU) is the top-ranked institution in the SUNY system and is consistently rated as

one of the premier public universities in the Northeast. BU is included in the Carnegie Classification system's "very high research activity" (R1) category. PhD students are supported by tuition-waived teaching assistantships. Our 930-acre campus is located in the Southern Tier of New York, between the Catskills and Finger Lakes, about a 3-hour drive from NYC. The region features abundant opportunities for outdoor recreation and a very reasonable cost of living.

To indicate interest: Please email LSwierk@binghamton.edu with a subject line "Prospective PhD 2027". In the email, please include which of the two research areas (outlined above) you are interested in, a brief description of past research experience, your GPA and relevant coursework, and your CV with references. You may also send reprints of published papers or writing samples, if you wish. Qualified applicants will later be invited to send in a formal application to BU's Graduate School.

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EasternNewMexicoU Portales NM USA Testing the microbial role in metazoan macroevolution ENMU Spring2027

Subject: Funded M.S. position: the microbial role in host macroevolution (ENMU, Spring 2027) What: A funded M.S. project on how microbes contribute to evolutionary novelties and constraints in turtles and amphibians. Where: The Microbial Ecology and Macroevolution Group in the Department of Biology at Eastern New Mexico University (Portales, NM, USA) is offering a funded M.S. position beginning Spring 2027. Fieldwork opportunities in Panama and Ecuador.

The student will study how microbes shape the evolution of their metazoan hosts, working with turtles and amphibians and combining summer fieldwork in Panama (with the Smithsonian Tropical Research Institute) and potentially the Ecuadorian Amazon (Tiputini Biodiversity Station) with shotgun and long-read metagenomics and computational analysis. Thesis questions are developed with the PI within the group's research program. Funding: the selected student will be offered a graduate assistantship (about \$11,000 per 9-month academic year, plus in-state tuition), with a summer stipend of up to \$5,000 for each field season and

support for field costs. The student will be the first graduate student in the group. Requirements: B.S. in a biological field. Tropical field experience and working Spanish are preferred. Full consideration for applications received by 2 November 2026. Full ad and how to apply: https://kvasir7.github.io/ENMU_MS_ad_2026.pdf Questions: Joseph Madison at joseph.madison@enmu.edu (subject line: "ENMU MS Position")

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GraduatePosition UppsalaU Evolutionary Ecological Genomics

PhD-student in Evolutionary and Ecological Genomics ### Do you want to conduct frontier research in an outstanding environment within evolutionary biology at Sweden's largest faculty of science and technology? The Department of Ecology and Genetics at Uppsala University conducts world-leading research in biology, spanning from molecules to ecosystems and global biodiversity patterns. We are now looking to recruit a PhD student who wishes to develop their research career together with us. The Department of Ecology and Genetics (IEG) at the Evolutionary Biology Center (EBC) is an international environment with staff that conducts research to understand ecological and evolutionary processes across all levels of biological organization. IEG provides access to advanced national and local research infrastructures, including free super computing resources (NAISS) and the latest molecular technologies and sequencing platforms (SciLifeLab platforms). IEG hosts a Climate Lab with controlled environmental chambers and greenhouses, a state-of-the-art molecular lab, and animal rearing facilities. PhD-students at IEG take courses free of charge to further their development with general academia and the specific research field. They can also join the PhD school which provides ample opportunities for networking on and off campus with PhD-students from the other two biology departments at Uppsala University (Organismal Biology, Cellular and Molecular Biology). The position is offered by the research program in Animal Ecology at IEG. The program's current research spans population genomics and quantitative genetics, local adaptation, biotic interactions, the evolution of life histories, speciation, sexual selection, conservation genomics, as well as macro-ecology. ### Duties ### A central

question in evolutionary biology is whether evolution is repeatable, and whether the same genes contribute to repeated phenotypic adaptations. This question has important implications for predicting genetic responses to changing environments. Recent studies show that while phenotypic evolution is often repeatable, the underlying genes involved can be less predictable. This poses a challenge for using genomic data to predict a species' evolutionary potential. This project will address this challenge by integrating mechanistic insights about phenotypic adaptation with genomic data to understand how species evolve adaptations to changes in their environment. The PhD candidate will work with the main supervisor David Berger and with the co-supervisor, SciLifeLab fellow Gabriela Montejó-Kovacevich, both at IEG. The project will leverage data from a large-scale Evolve-and-Resequencing experiment in a cosmopolitan insect pest, the seed beetle *Callosobruchus maculatus*. This system allows us to study the roles of determinism and chance in the evolution of an organism's environmental tolerance and ecological niche breadth. Extensive phenotypic, RNA-seq, and DNA pool-seq data are available from multiple time points in the experiment, which is still ongoing. The Berger lab maintains several other *C. maculatus* strains sampled across its global distribution and closely related seed beetle species. This provides opportunities for comparative genomics and additional experiments and data collection if the candidate wishes to further develop the project. The PhD project will involve a combination of experimental work and bioinformatic analysis, with emphasis on the latter. The exact balance between tasks may depend on the candidate's interests and the project's development. The successful candidate is expected to collaborate with other researchers in the Berger and Montejó-Kovacevich groups, as well as researchers from two other groups working on seed beetles at IEG. PhD students at the Institute of Ecology and Genetics (IEG) have the option to engage in teaching and to develop their pedagogic CV by taking courses. The type and level of teaching will depend on availability and the student's interests but cannot exceed 20

Further Reading ### Rego A, Baur J, Girard-Tercieux C, de la Paz Celorio-Mancera M, Stelkens R, & Berger D. 2025. "Repeatability of Evolution and Genomic Predictions of Temperature Adaptation in Seed Beetles". *Nature Ecology & Evolution*, 1-14. <https://doi.org/10.1038/s41559-025-02716-5>. Burc E, Girard-Tercieux C, Metz M, Cazaux E, Baur J, Kopik M, Rego A, Hart AF & Berger D. 2025. "Life-History Adaptation under Climate Warming Magnifies the Agricultural Footprint of a Cosmopolitan Insect Pest". *Nature Communications* 16, (2025): 827.

<https://doi.org/10.1038/s41467-025-56177-2>.

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ImperialCollege London PhD opportunities Insect responses to global change factors

Imperial College London PhD opportunities - insect responses to global change factors.

The Gill research group is looking for PhD candidates to join their research group studying insect ecology and evolution. Namely, understanding insect responses to environmental change and pollution and the impacts on ecological function.

Taking a genes-2-ecosystem approach, we adopt a variety of approaches spanning biological levels: molecular-physiology-behaviour-population-community_interactions. Our focal insect system typically being studied are bees (along with their host plants), and the PhD candidate would have access to a variety of molecular tools, experimental setups, field sites and large datasets.

For chosen candidates, we will fully support the application. Whilst proposed projects can be flexible (desk-, lab- and field-based options), we have a set of projects outlined that fall under the following topics: 1. Thermal trait-based approaches for understanding adaptive behaviours of Arctic plant-pollinator responses to climate change

2. Leveraging entomological museum specimens for understanding how different dimensions of biodiversity are responding to environmental change 3. Determining how changes to climate alter the impacts of pollution (e.g. pesticides) on the health and function of beneficial insects (and microbiomes) 4. Automated sensing for understanding insect distributions and dispersal across urban matrices. 5. Polli-markers: cueing honest plant pollination signals for mapping pollinator function across landscapes at scale.

A variety of competitive scholarships are available, including: # Life Sciences Department PhD - Link: <https://www.imperial.ac.uk/life-sciences/>

<https://www.imperial.ac.uk/study/fees-and-funding/postgraduate-doctoral/grants-scholarships/presidents-phd/> Deadline: 23:59 BST on 08 Jan 2027 / Eligibility: UK nationals (including EU candidates with UK settled status) # Imperial President's PhD Link: <https://www.imperial.ac.uk/study/fees-and-funding/postgraduate-taught/grants-scholarships/international-scholarship-collaborations/ics/> Deadline: 16:00 hours BST on 20 October 2026 / Eligibility: please see: <https://cscuk.fcdo.gov.uk/scholarships/commonwealth-phd-scholarships-for-least-developed-countries-and-vulnerable-states/> If interested: please email Richard Gill (r.gill@imperial.ac.uk) with your CV, the topic(s) of interest, and any supporting text, ASAP. Dr Gill will assess the candidates on a rolling basis and he will contact you if you are a suitable candidate. Emails will stop being assessed no later than Dec 21st.

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IndianaU ChemicalSignalEvolution

The Darragh lab (<https://kathydarragh.com/>) at Indiana University, Bloomington is recruiting PhD students to start in Fall 2027. Our research focuses on the evolution of chemical signals. We take a range of approaches including studying the behavioral function of chemical signals as well as investigating the underlying genetic and molecular mechanisms of biosynthesis of the chemical compounds. To do this, we combine techniques such as protein expression, enzyme assays, RNAseq, behavioral trials, gene family analyses and comparative studies, mainly in insects. We are currently particularly interested in the convergent evolution of insect biosynthetic pathways. However, students will have the opportunity to develop their own projects combining evolutionary biology with mechanistic molecular studies. We encourage students with diverse interests in evolutionary biology, chemical ecology, and molecular evolution to apply.

Interested candidates should email kdarrag@iu.edu with a CV and a cover letter. In the cover letter,

please include any previous research experience, future research interests, and what types of projects you would like to do in the Darragh lab. I will meet with candidates by zoom before applications are due for the graduate program deadline (December 1st 2026). Candidates would apply to be part of the EEB (Evolution, Ecology, and Behavior) graduate program at IU, a vibrant and interdisciplinary community with ample opportunity for collaboration. Candidates will have 5 years of guaranteed funding through TAs/ships/RAs/hips and will be encouraged to apply for independent fellowships.

Details about admissions to IU Biology: <https://biology.indiana.edu/graduate/how-to-apply/phd-apply.html> More details about EEB specifically: <https://biology.indiana.edu/graduate/evolution-ecology-behavior/steps.html> For more information contact kdarrag@iu.edu

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McGill U CA Fish Ecology and Genomics

Position: PhD Graduate position in Fish Ecology and Genomics - Sept 2027 Where: McGill University Macdonald Campus (Ste Anne-de-Bellevue) Type of Work: Fish genomics and bioinformatics of sunfish, Transcriptomics of Arctic cod and/or Greenland halibut from the Beaufort Sea and Baffin Bay, Whole Genome development and Annotation, etc,... Description: The fish population and conservation genomics lab at McGill is looking for a PhD student to continue projects related to, but not exclusively, on Arctic marine fishes. The lab specialises in using morphology, ecological tracers, and genomics (among others) to generate critically needed information on the ecology of these poorly understood fishes. We work extensively with collaborators all over the Arctic and beyond, including in Canada (Fisheries and Oceans Canada), Greenland (Greenland Institute for Natural Resources), and Norway (Institute for Marine Research). The work involves some sampling opportunities (Beaufort Sea, Baffin Bay, Norwegian slope), lab work (extracting and preparing DNA/RNA for whole genome sequencing), and analytical analyses using (sometimes also developing) bioinformatics (depending on the project). Because funding is related to bioinformatics - this is expected to be an important part of the students work. Lab work will be performed

in a newly renovated lab with state-of-the-art equipment for DNA/RNA manipulation and library preparation. McGill Mac campus also has ecological tracers and other supporting lab facilities. The selected student will have partial funding already set-up through a CREATE grant and be topped up with graduate entrance assistantships, lab funding, or external scholarships (e.g., FRQNT/NSERC or other). The student will become part of the Mac Campus McGill Graduate Student community which is a vibrant community of graduate students working in the Faculty of Agriculture and Environmental Sciences at McGill. Priority will be given to Quebec residents, Canadian citizens, and French Nationals. To apply, please provide a 1-page (1.5 spaced, 12pt font) motivation letter, a CV, and transcripts of both graduate and undergraduate marks, and email contact for two referees to: Denis Roy Natural Resource Sciences FAES - Macdonald Campus, McGill University 21111 rue Lakeshore, Ste-Anne-de-Bellevue, QC, H9X 3V9 denis.roy5@mcgill.ca

FRENCH VERSION

Poste : Doctorat en ecologie et genomique des poisons - Sept 2027

Lieu : Campus Macdonald de l'Universite McGill (Sainte-Anne-de-Bellevue)

Nature du travail : Genomique et bio-informatique des crapets (sunfish) ; transcriptomique de la morue arctique et/ou du fletan du Groenland (mer de Beaufort et baie de Baffin) ; assemblage et annotation de genomes complets, etc

Description : Le laboratoire de genomique des populations et de conservation des poissons de McGill recherche un etudiant au doctorat pour travailler sur les poissons marins de l'Arctique. Le laboratoire utilise la morphologie, des traceurs ecologiques et la genomique pour produire des informations essentielles sur l'ecologie de ces poissons encore mal connus.

Nous collaborons avec des partenaires dans l'Arctique et au-dela, notamment au Canada (Peches et Oceans Canada), au Groenland (Institut des ressources naturelles du Groenland) et en Norvege (Institut de recherche marine).

Le travail comprend des opportunités d'échantillonnage (mer de Beaufort, baie de Baffin, talus continental norvégien), du travail en laboratoire (préparation d'ADN/ARN pour le séquençage de genomes complets) et des analyses bio-informatiques (incluant le développement d'outils). Le financement étant lié à la bio-informatique, cette composante représentera une part importante du travail de l'étudiant. Les activités de laboratoire se dérouleront dans un laboratoire récem-

ment renové et bien équipé pour la manipulation de l'ADN/ARN et la préparation de banques génomiques. Le campus offre également d'installations pour l'analyse des traceurs écologiques et d'autres ressources de soutien.

L'étudiant sélectionné bénéficiera d'un financement partiel déjà établi via une subvention CREATE, complété par des bourses d'admission aux cycles supérieurs, des fonds du laboratoire et/ou des bourses externes (ex. : FRQNT, CRSNG). L'étudiant rejoindra la communauté dynamique des cycles supérieurs du campus Macdonald de McGill, au sein de la Faculté des sciences de l'agriculture et de l'environnement. La priorité sera accordée aux résidents du Québec, aux citoyens canadiens et aux ressortissants français. Pour postuler, veuillez soumettre une lettre de motivation d'une page (interligne 1,5, police taille 12), un CV, les relevés de notes des cycles supérieurs et du premier cycle, ainsi que les coordonnées (adresse courriel) de deux personnes de référence, à l'adresse suivante :

Denis Roy Département des Sciences des Ressources Naturelles FAES - Campus Macdonald Université McGill 21111, rue Lakeshore

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MOILAB UC Berkeley HHMI Rapid evolutionary genomics in plants

PhD POSITIONS: RAPID EVOLUTIONARY GENOMICS IN PLANTS Exposito-Alonso Lab, University of California, Berkeley www.moilab.science Moi Exposito-Alonso, Assistant Professor, Freeman Hrabowski Scholar (HHMI) Department of Integrative Biology / Innovative Genomics Institute / Center for Computational Biology / Center for Theoretical & Evolutionary Genomics / UC Berkeley

OVERVIEW We are recruiting a motivated PhD student with a background in evolutionary genomics. Research experience is a plus but not required. We are an interactive, interdisciplinary, and diverse lab, aiming for scientific excellence alongside a positive environment for growth (our lab values: moilab.science/our-values).

PhD students design their thesis with input from their advisor and peers.

RESEARCH FOCUS To address this, we have expanded classic reciprocal common garden approaches in plants with temporal genomics data that permits us to "see" evolution and adaptation in action. This project builds on our GrENE-net.org consortium project transplanting seeds from over 200 native *Arabidopsis thaliana* plant populations across continents, and whole-genome sequenced populations for up to 5 years (Wu, Bellagio, Peng et al. 2026, Science). To better understand the dynamics and function of genes involved in rapid adaptation from warm to cold climates, we are establishing experiments in California from low elevation at Berkeley to high elevation in the Sierra Nevadas. PhD projects can involve field experiments, whole-genome sequencing, and population-genomics data analysis.

DETAILS - Lab located in the Valley Life Sciences Building, UC Berkeley campus, CA 94720, USA - Guaranteed minimum salary \$52,000/year, with yearly rises, for 5 years (direct admit program) - Research-focused PhD; only two semesters required as teaching assistant - National and international applicants welcome - Application deadline: Nov 19, 2026 - Start date: Fall 2027

HOW TO APPLY - Berkeley graduate admissions (all programs) and how to apply: <https://www.google.com/url?q=https://grad.berkeley.edu/admissions/steps-to-apply/apply/&source=gmail&ust=1790349850946000&sa=E> Informal MOILAB pre-submission interest form (recommended before applying): <https://www.google.com/url?q=https://forms.gle/T1MN75iYn8MKdnBZA&source=gmail&ust=1790349850946000&sa=E> Questions? Email the lab at moiexpositoalonso@berkeley.edu – happy to talk before you apply.

Flyer: <https://tinyurl.com/flyerphdmoilab> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

MSc EastTennesseeStateU EcoEvo EcoGenomics

M.S. Student Opportunity in Ecological Genomics and Evolutionary Ecology We are seeking a motivated M.S. student to join our research in ecological genomics and evolutionary ecology using *Daphnia* as a model organism in the Department of Biological Sciences at East

Tennessee State University (ETSU), starting in Spring, 2027. Potential research projects include the evolution and genomics of salinity tolerance and the effects of dietary and biochemical interventions on longevity, with opportunities to develop related projects based on the student's interests. Our department has several active research labs and provides excellent opportunities for collaboration and training across evolutionary biology, ecology, genetics, and genomics. ETSU is located in Johnson City, Tennessee, in a beautiful region surrounded by the Appalachian Mountains, lakes, and extensive natural areas. For questions about research projects, contact Lev Yampolsky at yampolsk@etsu.edu. For questions about the M.S. program, contact Tianhu Sun at sunt02@etsu.edu. Application: <https://www.etsu.edu/gradschool/Deadlines>: October 1 for international applicants; January 1 for domestic applicants.

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NTNU Norway Marine Dispersal and Spatial Population Genetics

PhD Position in Modelling Marine Larval Dispersal and Spatial Population Genetics and Demography Location: Norwegian University of Science and Technology (NTNU) in Trondheim, Norway. Supervisor: Dr. Scott Burgess (<https://www.ntnu.edu/employees/scott.c.burgess>) Application due date: 20 October 2026. Topic: The overall aim is to provide new understanding of the processes that affect marine larval dispersal and gene flow, how we measure it with genetic data, and how we use that information to predict the genetic and demographic responses of spatially structured marine populations to environmental variation and change. Specifically, the primary focus of the PhD will be to understand how complex coastlines, ocean circulation, and biology (e.g., reproductive systems and phenology, larval behavior and survival) interact to affect the spatial structure of the genetic and demographic properties of marine populations. There is flexibility, and an expectation, for candidates to develop their own line of research within this broad scope. For example, projects could focus on combining simulations using spatial-genetic-demographic individual based models (e.g., using the software SLiM), machine learning approaches, and genomic data to estimate larval dispersal distances from the spatial structure of ge-

netic genealogies across the genome, and the genetic relatedness among individuals; or develop and use biophysical models (hydrodynamics + particle tracking) to understand the demographic and genetic dynamics of marine metapopulations and adaptation to environmental change. The PhD position provides an exciting opportunity to gain broad experience and expertise working at the interface of population genetics and demography, oceanography, and computer science. It will provide broad training in research skills, and will suit a candidate who is curious and is motivated to undertake high-level research to gain skills in computational methods and software tools to understand large, complex biological data.

The candidate must have: - a relevant background in evolution or ecology - quantitative and computational skills.

The candidate should also meet at least some of these points: - Experience with computer coding, such as R, Python, or MATLAB, and Linux command-line tools including Bash scripting and running analyses on high-performance computing systems. - Experience with, or ability to learn, the evolutionary simulation software SLiM (Selection on Linked Mutations), or similar. - Experience applying machine learning techniques, or the ability to learn them. - Experience using biophysical dispersal models, or the ability to learn to use them. - Experience working with geospatial data and spatial analysis, or the ability to learn. - Experience analysing whole genome libraries, including quality control, sequence alignment, and calculating population genetic summaries.

NTNU's Department of Biology hosts internationally leading research activity in ecology, evolutionary biology, physiology, marine science and technology, and cell & molecular biology. The position will be hosted within a dynamic international research group based at NTNU, with strong links to local and international collaborators. NTNU is a broad-based university with a technical-scientific profile and a focus in professional education. The city of Trondheim is a modern European city with a rich cultural scene. Trondheim is the tech capital of Norway with a population of roughly 200,000. The Norwegian welfare, including healthcare, schools, kindergartens and overall equality, is probably the best of its kind in the world. Professional subsidized day-care for children is easily available. Furthermore, Trondheim offers great opportunities to enjoy nature, culture and family life and has low crime rates and clean air quality. Trondheim has excellent bicycling and public transport options, making it easy to get around town without a car.

For more information, including how to apply, please visit: <https://www.jobbnorge.no/en/available-jobs/job/308848/phd-candidate-in-modelling-marine-larval-dispersal-and-spatial-population-genetics-and-demography> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

OhioStateU GraduateStudentPosition FreshwaterMolluskEvolutionConservation

The Whelan Lab at The Ohio State University is seeking graduate students to join the lab in August 2027. The lab is part of the Department of Evolution, Ecology, and Organismal Biology and is recruiting up to two graduate students at either the masters or PhD level. Potential masters and PhD projects include conservation genetics and molecular ecology of freshwater mollusks, phylogenetics and systematics of freshwater gastropods, and genomics of freshwater mollusks. Students interested in freshwater gastropods or those that have bioinformatics experience are especially encouraged to apply. Students will work in museum, lab, and field environments. The Whelan Lab is located at the Museum of Biological Diversity on the main campus of The Ohio State University. The lab's research includes both basic and applied science, and students work in an academic and museum research environment while collaborating with government researchers and on-the-ground conservation scientists. Students will have the opportunity to work directly with conservation practitioners and perform cutting-edge research. Current research projects in the lab include (1) phylogenomics and biogeography of freshwater gastropods, with an emphasis on Pleuroceridae, (2) conservation genomics and molecular ecology of freshwater mollusks, including threatened and endangered mussels and snails, (3) taxonomy of terrestrial snails, freshwater mussels, and freshwater snails, (4) freshwater mollusk life history evolution, and (5) computational research on phylogenetic methods. The Ohio State University is a public land grant institution with internationally recognized research and academics. Columbus, Ohio is a vibrant town with an excellent quality of life. Stipends and Start Dates: Students will receive a stipend of at least \$2,897/month and a tuition waiver. Students will likely serve as Graduate Teaching Assistants for their stipend, but competitive fellowships may be available. Health insurance, includ-

ing vision and dental, are provided to graduate students at no cost. Available start dates are August 2027. To apply: All potential graduate students will need to apply to The Ohio State University and be accepted by the Department of Evolution, Ecology, and Organismal Biology. The deadline for applicants is November 15, 2026. Before applying to OSU, students interested in working in the Whelan lab should contact Dr. Nathan Whelan to discuss potential graduate student projects. If you are interested in joining the Whelan Lab, please send a letter of interest, current CV, contact information for 2-3 references, and unofficial transcripts to: Dr. Nathan Whelan, Whelan.105@osu.edu

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PhD DonanaBiologicalStation ChromosomalInversions Quail

PhD Position in Evolutionary Biology We invite applications for a 4 year PhD position to work on the project: "The role of chromosomal inversions in the diversification of common quail across a heterogeneous landscape" (PID2025-175880NB-I00). The PhD candidate will be supervised by Carles Vila and Carlos Leiva, and will join a research environment focused on understanding the evolutionary processes shaping biodiversity as member of the "Conservation and Evolutionary Genetics Group" (<https://www.consevol.org/>).

The project Chromosomal inversions are structural variants that can profoundly influence genome evolution, population differentiation, and adaptation. This PhD project will combine genomic data with ecological and evolutionary perspectives to understand how chromosomal variation interacts with landscape heterogeneity and gene flow, particularly in island environments, using a migratory bird, the common quail *Coturnix coturnix*, as the model organism.

The successful candidate will have the opportunity to address questions at the interface of evolutionary genomics, population biology, landscape genomics, and adaptation. The project as a whole is inherently multidisciplinary and combines field and laboratory work with bioinformatic analyses.

Candidate profile We are looking for a highly motivated researcher with a strong interest in evolutionary biology, population genomics, and/or molecular ecology and a

Master's degree (or equivalent) in evolutionary biology, genomics, ecology, bioinformatics, zoology, or a related discipline.

Ideally, the candidate should also have: Previous experience with bioinformatic or genomic data analysis. Programming experience, particularly in R and/or Python, and familiarity with command-line environments. Willingness to acquire and develop laboratory skills in molecular genetics/ genomics and fieldwork and animal handling. Good analytical and problem-solving abilities. Ability to work independently while contributing positively to a collaborative research environment. Good written and spoken English. A strong motivation to learn is more important than having experience in every technique used in the project.

Why join the Estacion Biologica de Donana (EBD-CSIC)? The Estacion Biologica de Donana (EBD-CSIC) is one of Spain's leading centers for research in ecology, evolution, biodiversity, and conservation. Located in Seville and closely connected to the exceptional natural laboratory provided by the Donana region, EBD-CSIC offers an outstanding environment in which to investigate fundamental questions about biodiversity and its evolution.

One of EBD's major strengths is its research-oriented training environment. PhD researchers become part of a broad scientific community encompassing evolutionary biology, ecology, genetics, animal behavior, conservation biology, and environmental sciences. This provides opportunities to interact with researchers working on complementary questions and approaches, facilitating collaborations that extend beyond the immediate PhD project. PhD students are exposed not only to their own research projects but also to seminars, scientific discussions, collaborations, field activities, methodological training, and an international research community. The combination of fundamental and applied research creates opportunities to understand biodiversity from molecular and genomic processes through to populations, species, and ecosystems.

How to apply Candidates should submit a CV by email, including a brief explanation on their motivation and relevant experience. The text should also provide contact information for one or two researchers that could provide references. Applications should highlight, where applicable, experience in genomic laboratory techniques, bioinformatics, population genetics, R/Python programming, and analysis of high-throughput sequencing data as well as experience in the study of natural populations. Applications and requests for additional information should be addressed to Carles Vila (carles.vila@ebd.csic.es) and Car-

los Leiva (carlos.leiva@ebd.csic.es) by September 15, 2026.

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PhDposition U Miami OXPHOSFunctionAndGenom

PhD Student Position Available - OXPHOS Function & Genomics A highly motivated PhD student is sought to investigate the multiomics of oxidative phosphorylation (OXPHOS) within the mitochondria of high-altitude adapted birds and other animals. Advanced training on the Oroboros O2k and analysis of genomic, transcriptomic, proteomic, and other integrative data will be possible. The position will be based at the University of Miami in Coral Gables, Florida, with Dr. Kevin McCracken and a team of collaborating investigators, many affiliated with universities in South America. Travel to high-altitude sites in the Andes will be required. Spanish speaking skills are essential. As most fieldwork will be remote, a driver's license and ability to drive a manual transmission will be necessary. Students from the Andean Community are especially encouraged to apply. Biology PhD students at the University of Miami are guaranteed 5 years of support with annual stipends of ~\$35,000/year, including a full tuition waiver and health benefits with expected increases for cost of living each year. Both university fellowships and departmental teaching assistantships are available, as well as summer support. Applications to the PhD program at UM are due 1 December 2026 for fall 2027 admission (<https://biology.as.miami.edu/graduate/index.html>). Interested individuals should send a statement including background and research interests and curriculum vitae to: Dr. Kevin McCracken Professor & Kushlan Chair in Waterbird Biology and Conservation Department of Biology University of Miami Coral Gables, FL 33146, U.S.A. kevin.g.mccracken@gmail.com +1 (907) 378-2100 www.duckdna.org (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

PhDProject U Valencia EvolutionThermalTolerance

PhD Project: Evolution of thermal tolerance in human-modified habitats PhD position available at the University of Valencia, Spain, working on the evolution of thermal limits in response to human-modified landscapes in soil-dwelling animals. Using springtails (Collembola) as a model system, the project combines fieldwork and experimental physiology to measure thermal tolerance, reproductive success, and rapid adaptive plasticity across natural habitats and anthropogenic plantations. Ideal for candidates with a background in ecology, evolutionary biology, or physiology. Note that the project involves fieldwork and long-stays in Spain, Brazil, and Australia. Supervisors: Dr. Maider Iglesias-Carrasco and Prof. Pau Carazo. Deadline: 30-10-2026 Any questions: maider.iglesias@uv.es. More information here: <https://maideriglesias.weebly.com/people.html> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

PhD UC SanDiego EvolutionaryMorphology DevelopmentalBias

PhD Position in Evolutionary Morphology and Developmental Bias at UCSD The Rohner Lab at the University of California San Diego is recruiting a PhD student interested in understanding how developmental variability shapes morphological evolution. The student will join the Ecology, Behavior and Evolution (EBE) track in the Biological Sciences PhD program. The project will investigate the role of developmental bias in shaping the direction and predictability of phenotypic evolution. A central goal will be to determine whether patterns of developmental variation within species predict evolutionary diversification across populations and species. The research will primarily use insect morphology, particularly sepsid flies and horned dung beetles, as a model system and will combine geometric morphometrics with experimental and comparative approaches. Depending on the student's interests, the project will

involve: - Quantifying developmental variation using geometric morphometrics and experimental approaches - Testing how genetic and environmental variation influence morphology - Comparing patterns of morphological variation within and among populations and species - Integrating morphometric data with phylogenetic, ecological, or genomic information - Developing or applying automated image-analysis and machine-learning pipelines for large-scale phenotyping

The student will have considerable freedom to develop their own questions within the broader research interests of the Rohner Lab. The position would be particularly well suited to someone interested in evo-devo, evolutionary ecology, quantitative genetics, geometric morphometrics, or the evolution of morphological diversity. Applicants should have a bachelor's or master's degree in biology or a related field and a strong interest in evolutionary biology. Previous experience with geometric morphometrics, quantitative analysis, R, insect biology, or image analysis would be valuable but is not required. More important are intellectual curiosity, enthusiasm for quantitative and experimental research, and a willingness to learn new approaches. The Rohner Lab is part of the Department of Ecology, Behavior and Evolution at UC San Diego. Our research integrates evolutionary ecology, quantitative genetics, evo-devo, comparative biology, and emerging approaches for automated phenotyping. The student will join a social and collaborative research environment with consistent interaction among researchers working across evolutionary biology, ecology, and evo-devo. Prospective applicants are encouraged to contact Patrick Rohner at prohner@ucsd.edu before applying. Please include a brief description of your research interests and your CV. Applications to the UC San Diego Biological Sciences PhD program are due December 2, 2026 and can be submitted at <https://connect.grad.ucsd.edu/apply/>. More information about the Rohner Lab can be found at <https://rohnerlab.biosci.ucsd.edu/>. (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

StellenboschU SouthAfrica
Plio-Pleistocene sea level change
effects on plant diversification in the
Cape Floristic Regio

The Department of Botany and Zoology at Stellenbosch

University, South Africa (<https://www.su.ac.za/en/faculties/science/departments/botany-and-zoology>) and the South African National Biodiversity Institute are seeking applicants for a full-time PhD in Botany for research on Plio-Pleistocene sea level change effects on coastal plant diversification in the mega-diverse Cape Floristic Region. The project, supervised by Dr Zaynab Shaik, Prof. Allan G. Ellis and Dr Thaabet Parker, will use next-generation sequencing to investigate whether edaphic specialisation to spatially fragmented limestone and deep coastal sand habitats has been a primary driver of allopatric divergence among Cape coastal endemic lineages. Study commences in January 2027 and is based at Stellenbosch University in the Western Cape Province of South Africa, with a field and laboratory work component.

Applicants should be in possession of an MSc in Biology, Botany, Evolutionary Biology or similar, have experience with molecular biology techniques, bioinformatics, and field work, and preferably possess a valid driver's license.

Applications will be accepted until a suitable candidate is secured. To apply, send your CV, full academic record, and letter of motivation to zshaik@sun.ac.za. Questions about this position may also be directed to zshaik@sun.ac.za.

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StockholmU EvolutionaryGenomics

PhD student position at Stockholm University

We have an open 4-year PhD student position to investigate genomic signatures of selection in association with pollination mode shifts across flowering plants.

This project will investigate the evolutionary drivers and genomic consequences of pollen evolution in association with shifts in pollination mode in flowering plants. The work will involve comparative genomic analyses in a phylogenetic framework, as well as population genomic and transcriptomic analyses in suitable plant systems.

For this position, we are looking for a person with a strong interest and training in evolutionary genetics.

The complete ad with information on qualification requirements and instructions on how to apply is at:

<https://su.varbi.com/what:job/jobID:966879/>
Application deadline: October 24, 2026. Please apply via the Stockholm University website linked from the ad.

The PhD student will join the research group of Prof. Tanja Slotte (<http://tanjaslottelab.se>) and will be enrolled in the research subject Ecology and Evolution at the Dept. of Ecology, Environment and Plant Sciences, Stockholm University. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both evolutionary geneticists, plant biologists, and ecologists. The city of Stockholm is known for its beauty, its buildings and architecture and its abundant open water.

The PhD project is part of a large interdisciplinary project "Harnessing evolutionary transitions, machine learning, and genomics to decode pollen evolution and unravel sexual selection mechanisms shared across kingdoms" led by Prof. Tanja Slotte in close collaboration with co-investigators Prof. John Fitzpatrick, Prof. Catarina Rydin, and Dr. Allison Hsiang at Stockholm University.

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Stockholm U Wetland Ecology

PhD-Position in Wetland Ecology at Stockholm University. If you are interested in wetland ecology and wetland restoration, this is a good opportunity to work in an interdisciplinary group involving ecologists, hydrologists and biogeochemists. The PhD-project will focus on arthropod ecology, but link their abundances to environmental factors such as water table fluctuations and soil moisture. A major part of the project will be to evaluate large scale restoration projects in a Before-After-Control-Impact design, but other parts will examine specific mechanisms such as soil properties. The work will involve extensive field work, species identifications and GIS-work. For further information (and for application details) see <https://su.varbi.com/en/what:job/jobID:969795/> For questions: peter.hamback@su.se

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StonyBrookUniversity PhD MicrobiomeTraitGenomicsModeling- Permafrost

The Microbial Genomes And Metagenomes to Unravel Traits Lab (mGAMUT Lab; PI: JL Weissman) at Stony Brook University (<https://microbialgamut.com/>) is recruiting a PhD student to work on an NSF-funded project developing microbial genomic trait prediction and microbiome modeling approaches in permafrost systems (we also have openings trait-based approaches for studying the human microbiome). Students with a strong background in theoretical ecology, population genetics, and/or statistics and mathematics will receive special consideration. We seek students interested in developing new bioinformatics and mathematical modeling approaches (not just an interest in applying bioinformatics tools or developing pipelines). We primarily recruit students through Ecology & Evolution, but can also support students via the Genetics, and potentially even other programs (e.g., AMS). We welcome a broad range of academic backgrounds to the lab, but we specifically look out for rigorous quantitative preparation.

You can read more here: <https://www.microbialgamut.com/join.html>

*Please note that our lab has a strong no-AI policy for academic writing and we do not expect each other to read AI-generated content (e.g., emails). With this in mind, AI-generated inquiries about this position will not be viewed positively. I would rather you send me a less polished but honest email expressing interest in the lab than a low-effort and/or generic one. The most successful applicants show a real engagement with the work we do and a familiarity with at least some of our published science.

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Switzerland Eawag 3 PhD opportunities EvolutionaryEcology EvolutionaryGenomics EcosystemScience

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is an internationally networked aquatic research institute within the ETH Domain (Swiss Federal Institutes of Technology). Eawag conducts research, education and expert consulting to achieve the dual goals of meeting direct human needs for water and maintaining the function and integrity of aquatic ecosystems.

The Department of Fish Ecology & Evolution (FishEc) has vacancies for 3 PhD positions in the fields of Evolutionary Ecology, Evolutionary Genomics, and Ecosystem Science

In a recently funded SNF project we propose to combine both comparative and experimental field studies in lakes of Southern Greenland to study how biotic and abiotic sources of natural selection can interactively shape species interactions during community assembly and impact the overall structure and functioning of lake ecosystems. Specifically, we will investigate the evolution of copepod populations in lakes with different abiotic (e.g., glacial vs non-glacial) and biotic (e.g., composition of fish predator communities) ecosystem properties, and the evolution of stickleback when they occur with and without species of Arctic char. We will also use an ongoing whole-lake manipulation to study how sticklebacks evolve following their release from predation by charrs, and how the establishment of these stickleback populations affects the evolution of copepods.

The overall goal of this project is to deepen our understanding about the interplay between (rapid) evolution and community assembly dynamics in lake ecosystems undergoing environmental change. This would involve studying the evolution of both threespine stickleback and diaptomus copepods, and how biotic and abiotic sources of selection affect evolution at different stages of community assembly in sub-arctic lakes.

We are looking for highly motivated candidates with a master's degree in Ecology, Evolutionary Biology, Organismal Biology, or Environmental Science. In this integrative project we are looking for candidates who enjoy working in a collaborative and international environment and are interested in integrating and synthesizing their work. We are planning three integrative PhD projects:

1. Evolutionary ecology of copepods - This PhD position will focus on the ecology and evolution of copepods studying phenotypic and genetic variation across lakes along a gradient of community assembly. Here we look for candidates with an interest in evolutionary ecology and/or molecular ecology. The project will include field work, lab raising of copepods, phenotyping of copepods, genomic work including molecular lab work and bioinformatics, and potentially evolutionary simulations.

2. Stickleback evolutionary genomics - This PhD position will investigate the adaptive capacity and genetic basis of evolvable traits in stickleback. Here we look for candidates with an interest in population and/or quantitative genetics. This project will include some field work and molecular lab work but will have a large genetic data analysis and bioinformatic component potentially including forward in-time genomic simulations.

3. Ecosystem ecology and evolution of stickleback - This PhD position will explore the causes and consequences of stickleback evolution in lakes of Southern Greenland. Here we look for candidates with an interest in evolutionary ecology and ecosystem sciences. The project will include field work surveying fish and invertebrate communities and quantifying lake ecosystem functioning, as well as lab work rearing and phenotyping stickleback.

The project is carried out by a consortium of researchers at Eawag and the University of Bern (Switzerland), as well as the Technical University of Zvolen (Slovakia) and the University of Edinburgh (UK). The successful candidates will be supervised by Dr Blake Matthews and/or Dr Philine Feulner, enrolled as doctoral students at the University of Bern, and co-supervised by either Prof. Catherine Peichel or Prof. Claudia Bank.

At Eawag, we have a working environment in which people with different experiences, strengths, and perspectives can fully contribute and further develop. Here, you can help us advance! We promote genuine participation, exchange, and mutual understanding. We create structures that enable the compatibility of work and other areas of life, such as care work, and continuously make efforts to reduce barriers.

Do you have specific requirements regarding the application process or the position, or do you need additional information? Talk to us about it – we will be happy to support you with possible flexible workplace, working hours, and job design solutions. For further information please visit our website about Eawag as well as our conditions of employment.

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U CambridgeUK Colour Polymorphisms Trumpetfish

PhD opportunity at the Department of Zoology, University of Cambridge, UK The mechanisms underlying colour polymorphisms in trumpetfish Supervisors: Dr James Herbert-Read, Dr Josefin Stiller, Dr Martin How & Dr Sam Matchette Project Background Some populations contain individuals with two or more distinct colour morphs. Understanding how different colour morphs are maintained, and whether they represent discrete genetic units or variations in phenotypic plasticity, provides opportunities to understand the adaptive value of colour variation within populations. Trumpetfish (*Aulostomus maculatus*) have three putative colour morphs; yellow, brown, and blue individuals. This project will investigate trumpetfish colouration at multiple biological levels. The project will quantify variation in colour and pattern among morphs, characterise pigment composition and chromatophores using histology and reflectance spectrophotometry, assess gene flow between putative morphs, and compare gene expression profiles using RNA-seq or qPCR. By integrating morphological, biochemical, and genetic data, this study will reveal whether these morphs represent distinct genetic lineages or flexible phenotypic states, advancing our understanding of how colour diversity is generated and maintained within populations. Type of Work The student will investigate trumpetfish colouration through a combination of field, laboratory, and data analysis. The project will begin with field surveys and specimen imaging to document and quantify colour and pattern variation across the putative yellow, brown, and blue morphs. This will involve diving under SCUBA, standardised photography, image analysis, and statistical comparisons to define morphs. In the laboratory, the student will conduct histological examinations and chromatophore identification to map the types and distributions of pigment cells in trumpetfish skin. They will use reflectance spectrophotometry to measure the spectral properties of intact skin, generating objective profiles of each morph's colouration. There is further scope to explore properties of the morphs' visual capabilities and relate this to their ecology and colouration. The student will also perform molecular analyses to explore genetic and transcriptomic differences between morphs. This may include extracting DNA and RNA,

preparing and processing samples for RNA-seq, conducting qPCR assays on candidate pigmentation genes, and analysing sequence or expression data to identify potential genetic drivers of colouration. Finally, the student will quantify gene flow between morphs using population genetic analyses, integrating these results with phenotypic and pigment data to assess whether morphs are genetically distinct or not. The project will be supported by four supervisors with different expertises; Dr Herbert-Read & Dr Sam Matchette (behavioural ecology), Dr Josefin Stiller (genetics of colouration) and Dr Martin How (visual ecology). By the end of the project, the student will have developed skills in marine fieldwork, microscopy, spectrophotometry, molecular biology, bioinformatics, and statistical analysis, while contributing to a novel, multidisciplinary investigation of colour polymorphisms. Applicants are encouraged to contact Dr James Herbert-Read jh2223@cam.ac.uk before applying. Applicants should send a copy of their CV, academic transcript and a brief cover letter outlining their interests and motivations for applying.

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UCologne 36 Months Plant Evol Genomics

A PhD position is available in the research group of Prof. Juliette de Meaux at the University of Cologne, Germany. The PhD student will investigate the Genetics of hybridization among Arabis Floodplain Species.

Several Arabis species interbreed, however hybridization is limited to a subset of genotypes in each species. For this project, the PhD candidate will investigate the genetic basis of differences in the ability to hybridize using a combination of formal genetics and pollen sequencing methods. The PhD candidate will acquire a broad array of skills ranging from genomics to molecular genetics and ecology, and develop a solid basis in experimental design, data management and analysis. The project is a collaboration with the Tellier Lab in Munich.

The position will be associated to TRR341, a Collaborative Research Center funded by the German Research Foundation (DFG). In a joint and interdisciplinary approach, combining Plant Molecular Biology and Ecology, we are investigating the genetic underpinnings of plant responses and adaptation to global environmental

change. Together, our aim is to provide new molecular and genetic data and tools to better understand the molecular basis of plant adaptation. We thereby hope to support current and future efforts for the preservation of plant biodiversity.

The applicant must hold a Master degree in Biology, with expertise in genomics, plant genetics, quantitative biology and/or ecology. This position is open to applicants of all nationalities but the usual language in the lab is English. Successful candidates should have a strong interest in generating knowledge on the ecological and genetic adaptation of plants to changing environments and thus contributing to the preservation of plant ecosystems/ diversity. Successful candidates will convince us that they are excellent team players, driven by curiosity and with an aptitude for interdisciplinary research. The position is available as soon as possible and are to be filled for three years. According to the applicant's personal qualification and the institution, employment payment will be based on 65The University of Cologne is an equal opportunity employer striving for gender equality and diversity. Applications from individuals with backgrounds that are underrepresented in MINT disciplines are expressly welcome. Women with comparable qualifications will be considered preferentially. Applications from suitably qualified severely disabled persons or people of equivalent status according to Book IX of the German Social Legal Code (SGB - Soziales Gesetzbuch) are encouraged. Severely disabled applicants of equal merit and qualifications will be given priority.

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UC Riverside Conservation genomics and insect biodiversity

The MacDonald Lab in the Department of Entomology at the University of California, Riverside is recruiting up to two PhD students for Fall 2027 interested in conservation genomics, landscape genomics, and insect biodiversity. We use chromosome-scale genome assemblies and whole-genome resequencing, often from hundreds of individuals sampled across species' entire ranges, to study population structure, connectivity, local adaptation, species limits, and conservation. Much of our work is associated with the California Conservation Genomics Project. We have several very large

preprocessed datasets available for immediate analysis. Students may develop projects from these existing datasets, contribute to ongoing collaborative studies, or establish their own landscape or conservation genomics projects on insect taxa of interest. The lab has numerous butterfly and damselfly projects at different stages of completion and strong collaborative networks across UCR's Department of Entomology, Department of Evolution, Ecology, and Organismal Biology, and universities and conservation agencies across the U.S. and Canada. Applicants with experience in bioinformatics, coding, statistics, population genomics, evolutionary genomics, or related fields will be prioritized. We increasingly outsource routine molecular lab work. Wet lab experience is welcome but is less important than analytical experience, natural history knowledge, and strong field skills. UC Riverside has one of the world's leading entomology departments and a strong community in evolutionary genomics. Riverside and nearby communities such as Redlands offer comparatively affordable living and exceptional access to the Transverse Ranges, Joshua Tree National Park, the Sierra Nevada, and the Southern California coast. Prospective students should send a CV, a brief description of their research interests and relevant experience, and contact information for two to three references to Zachary MacDonald at zmacdona@ucr.edu with the subject line "PhD inquiry: [Last Name]."

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U Georgia FreshwaterMusselDiversity

The Odum School of Ecology (<https://ecology.uga.edu/>) is seeking applicants for a M.S. position in the research group of Dr. John Wares (www.wareslab.net) in partnership with US Forest Service Research & Development. Research project will be partially defined by funding source and region, with a focus on freshwater mussels in the Great Lakes region; the project may incorporate comparative work with freshwater mussels/habitats in the southeastern US. Pre-applications required by October 1, and candidates will be notified of suitability by October 16, 2026. To be considered for this position, please send a single PDF that includes (1) a cover letter highlighting your research background and field experience to date, goals as a scientist, knowledge of freshwater mussels, and what types of research

questions you hope to address with respect to freshwater mussel diversity; (2) a current CV highlighting relevant professional experience, educational background, and current GPA. The PDF filename should start with your last name, and the email subject line should read "2027 MS-ICAS pre-application".

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U Georgia USA Graduate position

The Odum School of Ecology (<http://ecology.uga.edu/>) is seeking applicants for a M.S. position in the research group of Dr. John Wares (www.wareslab.net) in partnership with US Forest Service Research & Development. Research project will be partially defined by funding source and region, with a focus on freshwater mussels in the Great Lakes region; the project may incorporate comparative work with freshwater mussels/habitats in the southeastern US. Pre-applications required by October 1, and candidates will be notified of suitability by October 16, 2026. To be considered for this position, please send a single PDF that includes (1) a cover letter highlighting your research background and field experience to date, goals as a scientist, knowledge of freshwater mussels, and what types of research questions you hope to address with respect to freshwater mussel diversity; (2) a current CV highlighting relevant professional experience, educational background, and current GPA. The PDF filename should start with your last name, and the email subject line should read "2027 MS-ICAS pre-application".

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UGeorgia US Disease Ecology and Coronavirus Modeling

PhD Position in Disease Ecology & Coronavirus Modeling University of Georgia — Department of Infectious Diseases Sundaram Laboratory The Sundaram Laboratory at the University of Georgia is seeking a PhD student to join the research group, with an intended

start date in January. Our lab investigates wildlife reservoirs, coronavirus dynamics, and the mechanisms driving zoonotic spillover using an interdisciplinary approach that combines disease ecology, spatial statistics, and machine learning. Position Details: - Focus: Research centers on animal reservoirs, host dynamics, and the predictive modeling of coronavirus spillover. Students are encouraged to tailor projects to align with their specific scientific interests within these broader themes. - Support: 5-year full graduate research assistantship, including a stipend, tuition waiver, and health insurance. - Location: Athens, Georgia.

Responsibilities: - Curate and manage global databases on wildlife reservoirs and disease outbreaks. - Process and integrate GIS environmental and socioeconomic data layers. - Apply spatial modeling and machine learning to evaluate pathogen persistence and spillover risk. - Author manuscripts for publication in scientific journals.

To Apply: Interested candidates with a background in ecology, epidemiology, data science, or related fields are invited to contact Mekala Sundaram at msundara@uga.edu. Please include a CV, references and a brief statement of research interests.

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UGoettingen Germany Moth Ecology

At the University of Gottingen, Department of Forest Entomology and Department of Forest Nature Conservation, there is a position as doctoral researcher to be filled. Starting date is 1 Dec 2026. The position is limited to 30 Nov 2030.

We are seeking a highly motivated person to conduct scientific research in the project „Environmental and physiological drivers of spring activity of moth communities in Central European forests“. In this project, we aim to study the effects of habitat features (e.g. forest structure) and abiotic factors (e.g. temperature) on overwintering processes and spring phenology of moths inhabiting Central European forest ecosystems. We want to understand the spatiotemporal occurrence of ecologically relevant species and to assess the effects of changing environmental conditions on communities. We will use field data (obtained from trapping) and link them

with environmental parameters to infer the effects of habitat conditions on moth activity. Eco-physiological experiments will be performed under controlled conditions with selected species to study the effects of temperature on terminating dormancy and energy budgets, as well as timing of spring flight. The results will allow to predict seasonal activity patterns of moth communities and improve our understanding of the underlying regulatory mechanisms.

Your tasks: - Realization and coordination of field work in Central Germany - Assessing the spring activity of moths in the context of environmental conditions - Performing eco-physiological experiments in the laboratory to understand temperature-dependent processes underlying spring phenology of moths - Publication of results in scientific journals and attendance at scientific conferences

Your profile: - A Master's degree in biology, ecology, forestry, agriculture or a related field - Experience and interest in ecological/entomological experiments in the field and the lab - Experience and interest in the identification of arthropods - Experience in statistics and data analysis using R - Fluent in English (German is a plus) - Driver's license class B

Please submit your application (as a single pdf file) including 1) a letter of motivation (1 page), 2) your CV including, if applicable, a list of publications and congress contributions, 3) a short summary of your Master's thesis (1 page), and 4) relevant certificates as well as contact information of two references to <http://obp.uni-goettingen.de/de-de/OBF/Index/76648>

For further information see <https://www.uni-goettingen.de/de/644546.html?details=76648> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

ULausanne Switzerland Heat-treated lipids vs cognitive performance *Drosophila*

A PhD student position is available in Tadeusz Kawecki's lab at the Department of Ecology and Evolution, University of Lausanne, Switzerland (<https://www.unil.ch/fbm/en/home/menuinst/recherche/ssf/dee/recherche/kawecki-lab.html>). The lab focuses on understanding short-term adaptive evolution using experimental approaches, with *Drosophila*

as the study system.

We are looking for a candidate for a project on direct and evolutionary consequences of consuming heat-treated lipids for cognitive performance of *Drosophila* flies. The project is part of a new international research program "Heat-treated dietary lipids: chemistry, physiology, evolution". This program is motivated by the fact that humans are unique in obtaining most of their dietary lipids from food that has been cooked, roasted or fried. This induces extensive modification of lipids, but their consequences for physiology and evolution are unknown. In this framework the candidate will study the consequences of feeding on heat-treated lipids for the performance of fruit flies in complex behavioral/cognitive tasks relying on learning and memory. This includes aversive olfactory learning, identifying a receptive mate or choosing oviposition sites. The project will also use experimental evolution to study the consequences of genetically-based adaptation to heat-treated dietary lipids for cognitive performance and study the associated changes in brain metabolome.

The student will join a doctoral program, which offers graduate courses and workshops, and will be embedded in the overall heat-treated lipids research program and thus expected to participate in the meetings with other researchers involved in it. She or he will also act as a teaching assistant for courses corresponding to your expertise and interest. However, at least 80

The candidates should have a Masters degree in biology (formally required for admission), a strong motivation for experimental research in insect behavior, solid understanding of statistics and experimental design, and aptitude for laboratory research. Some experience with experimental work with *Drosophila* or other insects or experience / aptitude to work with machine learning tools would be a plus. No-preexisting knowledge of French is required (research-related discussions, seminars etc. and a part of teaching are in English) but learning basic French would make living in Lausanne more enjoyable.

The PhD student will join a multicultural, diverse and dynamic academic environment, with opportunities for professional training and personal development. The Department of Ecology and Evolution in Lausanne University hosts research groups working on a broad range of topics, producing a rich intellectual and social life. A medium-sized city located on lake Geneva, Lausanne offers a wide cultural offer, while the proximity of the lake and the Alps offer diverse outdoor activities.

Annual gross salary: CHF 61,000, initial contract for 1 year, renewable for a maximum total of 4 years.

Expected starting date: ideally February or March 2027

For legal reasons, applications must be submitted via an online recruitment system (<https://tinyurl.com/5yh7eped>). You will have to first create an account. You can switch the language of the interface to English using a button in the upper right corner.

Applications should include: o A letter containing a description of your research interests, as well as your motivation and fit for this position o Your CV o A summary (ca. 1 page) of your master thesis and other research experience o A copy your of master certificate/diploma (or the expected date of obtaining it) o Names and contact details (email) of 2-3 referees

Deadline: 18 October 2026

For informal inquiries, contact tadeusz.kawecki@unil.ch

UNIL is committed to equal opportunities and diversity. www.unil.ch/egalite UNIL supports early career researchers. www.unil.ch/graduatecampus (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Uppsala U Eco Evolutionary Genomics

PhD-student in Evolutionary and Ecological Genetics

Do you want to conduct frontier research in an outstanding environment within evolutionary biology at Sweden's largest faculty of science and technology? The Department of Ecology and Genetics at Uppsala University conducts world-leading research in biology, spanning from molecules to ecosystems and global biodiversity patterns. We are now looking to recruit a PhD student who wishes to develop their research career together with us. The Department of Ecology and Genetics (IEG) at the Evolutionary Biology Center (EBC) is an international environment with staff that conducts research to understand ecological and evolutionary processes across all levels of biological organization. IEG provides access to advanced national and local research infrastructures, including free super computing resources (NAISS) and the latest molecular technologies and sequencing platforms (SciLifeLab platforms). IEG hosts a Climate Lab with controlled environmental chambers and greenhouses, a state-of-the-art molecular lab, and animal rearing facilities. PhD-students

at IEG take courses free of charge to further their development with general academia and the specific research field. They can also join the PhD school which provides ample opportunities for networking on and off campus with PhD-students from the other two biology departments at Uppsala University (Organismal Biology, Cellular and Molecular Biology). The position is offered by the research program in Animal Ecology at IEG. The program's current research spans population genomics and quantitative genetics, local adaptation, biotic interactions, the evolution of life histories, speciation, sexual selection, conservation genomics, as well as macro-ecology. ### Duties ### A central question in evolutionary biology is whether evolution is repeatable, and whether the same genes contribute to repeated phenotypic adaptations. This question has important implications for predicting genetic responses to changing environments. Recent studies show that while phenotypic evolution is often repeatable, the underlying genes involved can be less predictable. This poses a challenge for using genomic data to predict a species' evolutionary potential. This project will address this challenge by integrating mechanistic insights about phenotypic adaptation with genomic data to understand how species evolve adaptations to changes in their environment. The PhD candidate will work with the main supervisor David Berger and with the co-supervisor, SciLifeLab fellow Dr. Gabriela Montejó-Kovacevich, both at IEG. The project will leverage data from a large-scale Evolve-and-Resequencing experiment in a cosmopolitan insect pest, the seed beetle *Callosobruchus maculatus*. This system allows us to study the roles of determinism and chance in the evolution of an organism's environmental tolerance and ecological niche breadth. Extensive phenotypic, RNA-seq, and DNA pool-seq data are available from multiple time points in the experiment, which is still ongoing. The Berger lab maintains several other *C. maculatus* strains sampled across its global distribution and closely related seed beetle species. This provides opportunities for comparative genomics and additional experiments and data collection if the candidate wishes to further develop the project. The PhD project will involve a combination of experimental work and bioinformatic analysis, with emphasis on the latter. The exact balance between tasks may depend on the candidate's interests and the project's development. The successful candidate is expected to collaborate with other researchers in the Berger and Montejó-Kovacevich groups, as well as researchers from two other groups working on seed beetles at IEG. PhD students at the Institute of Ecology and Genetics (IEG) have the option to engage in teaching and to develop their pedagogic CV by taking courses. The type and level of teaching will depend

on availability and the student's interests but cannot exceed 20

Further Reading ### Rego A, Baur J, Girard-Tercieux C, de la Paz Celorio-Mancera M, Stelkens R, & Berger D. 2025. "Repeatability of Evolution and Genomic Predictions of Temperature Adaptation in Seed Beetles". *Nature Ecology & Evolution*, 1-14. <https://doi.org/10.1038/s41559-025-02716-5>.
 Burc E, Girard-Tercieux C, Metz M, Cazaux E, Baur J, Koppik M, Rego A, Hart AF & Berger D. 2025. "Life-History Adaptation under Climate Warming Magnifies the Agricultural Footprint of a Cosmopolitan Insect Pest". *Nature Communications* 16, (2025): 827. <https://doi.org/10.1038/s41467-025-56177-2>.

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UppsalaUSweden PhDStudent EvolutionOfIntracellularBacteria

A PhD student position in evolutionary microbiology, with focus on the evolution of intracellular bacteria, is available in my lab at Uppsala University, Sweden. The position is fully funded for four years.

Last day to apply: 29 October 2026 Start: November 2026-March 2027

Apply at: <https://www.uu.se/en/about-uu/join-us/jobs-and-vacancies/job-details?query=974072>

Project description

The ability to feed on other organisms through phagocytosis is a crucial step in the evolution of eukaryotes, a prerequisite for food webs, multicellularity and probably the acquisition of mitochondria. It also paved the way for intracellular parasitism, as some bacteria avoided digestion by their hosts and multiplied in the nutrient-rich cytoplasm. Here, we focus on the Deep-branching Intracellular Gammaproteobacteria (DIG), a large group of related bacteria (e.g. *Legionella* and *Francisella*) with a wide variety of host-adaptation strategies. We hypothesize that the last common ancestor of DIG appeared during eukaryogenesis, 2 billion years ago, and was among the first bacteria to infect eukaryotes. In this project, the PhD student will gather a

solid set of DIG genomes, including isolates belonging to 30 novel species of *Legionella*, reconstruct their evolutionary history, assess their metabolic potential, and identify their host-adaptation genes. They will screen genomes for horizontal gene transfers from early eukaryotes or Asgard archaea and specifically analyse the evolution of the *Legionella* genus. A better understanding of the relationships between the first eukaryotes and their early invaders will shed light on eukaryogenesis, and particularly on the role of phagocytosis.

Qualifications

Required qualifications: - A Master's degree or equivalent (240 ECTS credits) in bioinformatics, molecular biology, microbiology, microbial ecology or a similar field. The degree should be completed, or expected to be completed, before March 2027. - Documented coding skills in Python or R - Experience in using and/or developing methods in metagenomics and molecular evolution - Background understanding of, and interest in, microbial evolution - Proficiency in spoken and written English - Ability to plan, carry out and complete research projects independently - Creativity and good teamwork skills

Desirable qualifications: - Experience of building pipelines for high-performance computing (HPC) clusters - Competence in handling large datasets - Experience with DNA extraction and sequencing library preparation

For further details, please contact Lionel Guy, lionel.guy@imbim.uu.se

Apply at: <https://www.uu.se/en/about-uu/join-us/jobs-and-vacancies/job-details?query=974072>

Last day to apply: 29 October 2026 Start: November 2026-March 2027

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UQueensland MicrobialEcoEvo

PhD Opportunity: Eco-evolutionary dynamics of antimicrobial resistance in microbial communities

Applications are invited for a PhD position in the research group of Dr Andrew Letten at the School of the Environment, University of Queensland (UQ) in Brisbane, Australia. The successful candidate will join a newly funded ARC Future Fellowship project - Build-

ing resilience without resistance in microbial communities - which aims to understand how environmental fluctuations shape microbial community stability and the evolution of antimicrobial resistance. Using microbial communities associated with the fruit fly (*Drosophila melanogaster*), the research will combine laboratory experiments and modelling to investigate how fluctuations in nutrients and antimicrobial exposure influence community dynamics, pathogen invasion, and resistance evolution.

The PhD project can be tailored to the interests and background of the successful applicant and may emphasize: experimental microbial ecology and evolution, antimicrobial resistance, mathematical modelling, or genomics and bioinformatics. The student will join an interdisciplinary research group working across ecology, evolution, microbiology, mathematics, and bioinformatics, and will have opportunities to collaborate with leading researchers in Australia and internationally.

The successful candidate will be nominated by Dr Letten for a University of Queensland Research Training Program (RTP) Scholarship in the upcoming international scholarship round. The RTP provides a tax-free living stipend and associated benefits for highly ranked international PhD candidates. Scholarship awards are competitive and subject to University of Queensland selection processes; however, this project is supported by a funded ARC Future Fellowship and the successful applicant will receive Dr Letten's nomination for an RTP scholarship.

Applicants should have: a strong academic background in ecology, evolution, microbiology, mathematics, statistics, bioinformatics, or a related discipline; an Honours or Masters degree suitable for admission to a PhD at UQ; strong quantitative and/or experimental skills; and excellent written and verbal communication skills. Prior experience with microbial systems, programming (e.g. R or Python), mathematical modelling, genomics, or experimental evolution would be advantageous.

To apply, please email a CV, academic transcripts, referee contact details, and a brief statement of interest (200 words) to a.letten@uq.edu.au. Informal enquiries are welcome.

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USouthCarolina US PhD in evolutionary biology

*** PURSUE A PHD IN EVOLUTIONARY BIOLOGY ***

We invite applications from highly motivated individuals seeking to complete a PhD in evolutionary biology in the Gitschlag Laboratory at the University of South Carolina. We are an interdisciplinary team of biologists who use a combination of experimental and theoretical approaches to address fundamental questions in evolution, especially the evolution of complex systems. Our main focus is the evolution of molecular sequences that control animal physiology, development, and reproduction. Have a wet-lab background and want to add mathematical modeling to your skill set? Have a computational background and want to gain experience with hands-on experiments? In either case, we have a number of exciting projects... *****RESEARCH DESCRIPTION***** Project 1: modeling the molecular evolution of animal life-history traits. Animal life history is characterized by basic decisions, such as the investment of resources in germline development versus somatic tissue maintenance. These important decisions are mediated through small regulatory sequences, including protein phosphorylation motifs. This makes these sequences an exceptional source of fundamental insight on how evolutionary forces acting at the molecular level, such as interactions between specific amino acids, influence whole-organism characteristics such as animal fertility and lifespan. We will use a combination of theoretical modeling, molecular genetics experiments, and experimental evolution to understand the mapping from genotype to phenotype for these sequences, as well as the evolutionary dynamics that are induced by the genotype-phenotype map. Project 2: germline-soma coevolution and reproductive strategy. Most species in the nematode genus *Caenorhabditis* reproduce by relying on mating events between males and females, similar to most vertebrates. However, the transition to hermaphroditic reproduction (via autonomous self-fertilization) has occurred numerous times independently, making this genus an excellent model for a comparative approach, using phylogenomics and statistical analysis of molecular datasets, to address the question: how does the biology of the organism change when it no longer evolves under the pressure to find a mate? Beyond this, we are interested in a wide range of top-

ics in organismal physiology and behavior, which we seek to understand by studying the molecular details of their evolution, using theoretical modeling, molecular genetics, and experimental evolution. ***QUALIFICATIONS*** A bachelor's degree is required, preferably in biology, genetics, biostatistics, biochemistry, or a related field. Ideally, the candidate will also have experience with programming in Python or a willingness to learn, and laboratory experience in an area of life sci-

ence (preferably molecular biology, cell biology, model organism genetics, population genetics, biochemistry, or biostatistics). ***HOW TO APPLY*** Submit a CV by email to Bryan Gitschlag at gitschlab@sc.edu, along with a brief description of your interests and experience.

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AMNH Assistant Curator Vertebrate Zoology

Link <https://careers.amnh.org/postings/4925>

The Division of Vertebrate Zoology at the American Museum of Natural History (AMNH) seeks an outstanding tenure-track Assistant Curator/Assistant Professor in either the Department of Ichthyology or Mammalogy, to start on or after 1 July 2027.

We seek an innovative evolutionary biologist who will develop a world-leading, collections-based research program focused on fishes or mammals. The successful candidate will leverage museum collections to address fundamental questions in evolution, biodiversity, and environmental change, integrating approaches from genomics, imaging, computational biology, biodiversity informatics, and/or other emerging analytical approaches. We are particularly interested in scientists who view natural history collections not simply as repositories of specimens, but as dynamic research platforms that generate new insights into the origins, diversification, and conservation of life on Earth.

Research and Collections The ideal candidate will have a record of high-impact scholarship, strong potential for securing extramural funding, and the vision to establish an independent research program, mentor graduate students and postdoctoral scholars, and establish effective collaborations and partnerships within and outside the Museum. Research areas may include, but are not limited to, systematics, comparative genomics, morphology, population genetics, biogeography, or macroevolution. We welcome applicants who combine organismal biology with advanced molecular, imaging, machine learning, and other data-intensive approaches that advance the study of biodiversity and evolutionary change.

The successful candidate will conduct original research on fishes or mammals, provide intellectual leadership for the continued development of their department's collections, and enhance those collections through field expeditions and scientific collecting. Responsibilities include the stewardship, curation, and long-term growth of one of the world's premier vertebrate zoology collections.

Education and Public Engagement The successful candidate will serve as an Assistant Professor in the Richard Gilder Graduate School and must have an interest in teaching and advising PhD students and post-

docs in comparative biology. There is also the opportunity to build on existing relationships with nearby partner institutions to advise doctoral students, including Columbia University and the City University of New York.

The position will provide opportunities to contribute to exhibition development, collaborate with the Museum's education department, and participate in public engagement initiatives, especially on efforts aligned with AMNH's strategic priority to address the local and global impacts of climate change and biodiversity loss through collaboration across science, education, exhibitions, and external partners.

Research Environment The AMNH, an independent, non-governmental institution, is a recognized leader in scientific research, graduate education, and public education about science and the natural world. The Museum provides an exceptional environment for collections-based research with resources such as: world-class zoological and other collections, including a cryogenic collection; genomics labs and an ancient biomolecules lab; high performance computing research resources; a wide range of optical, electron beam, and X-ray analytical tools (including CT scanning); the Southwestern Research Station in the biodiverse Chiricahua mountains of southern Arizona; access to the 4000-acre Black Rock Forest approximately 1.5 hours north of NYC; and generous internal funding opportunities to support ambitious field research and other innovative scientific projects.

The expected salary range for the Assistant Curator/Assistant Professor is \$120,000 - 130,000.

Pay will be determined based on several factors. The hiring range for the position at commencement is based on the type of work and the scope of responsibilities. The salary and placement offered is based on a number of individualized factors, including, but not limited to, skills, knowledge, training, education, credentials, areas of specialization and depth and scope of experience.

Application materials should include - Cover letter (maximum one page) - Curriculum Vitae - Research statement, including goals, achievements, and future plans (maximum three pages) - Museum service statement addressing your experience and interests in collections, collecting, teaching, exhibitions, and public outreach (maximum three pages) - PDFs of up to 5 publications and/or preprints - Names and contact information for three people who will be contacted to provide letters of reference at the time of application submission.

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AMNH US Tenure Track Curator of Lepidoptera

The Division of Invertebrate Zoology at the American Museum of Natural History (AMNH) seeks an outstanding tenure-track Assistant Curator/Assistant Professor with expertise in the evolution of Lepidoptera, to start on or after July 1, 2027.

We seek an innovative evolutionary biologist who will develop a world-leading, collections-based research program in Lepidoptera. The successful candidate will integrate modern approaches in evolutionary biology with genomics, imaging, computational biology, biodiversity informatics, and/or other emerging computational approaches. We are particularly interested in scientists who envision natural-history collections not simply as repositories of specimens, but as powerful research platforms for addressing fundamental questions about evolution, biodiversity, and environmental change.

The ideal candidate will have a record of high-impact scholarship, strong potential for extramural funding, and the vision to establish an internationally recognized independent research program. Research interests may include, but are not limited to, systematics, morphology, comparative genomics, biogeography, and/or macroevolution. We are especially interested in candidates who combine organismal biology with emerging computational approaches, including machine learning, computer vision, automated specimen identification, large-scale image analysis, and other data-intensive methods for understanding biodiversity.

Excellent knowledge of moth and butterfly diversity is essential.

Research and Collections The successful candidate will conduct original scientific research on Lepidoptera; steward and develop the Museum's Lepidoptera collection; and expand the collection through fieldwork, strategic collecting, and other accessions.

AMNH's Lepidoptera collection comprises more than 3 million specimens, with particular strengths in New World macrolepidopterans. The collection is well organized and largely housed in compactors, including a

spacious new butterfly facility. Together, these holdings provide an exceptional foundation for research across evolutionary timescales and geographic regions. We envision the successful candidate playing a leadership role in advancing the next generation of collections-based research through integration of physical specimens with genomic, morphological, ecological, geographic, imaging, and other digital datasets.

Opportunities include developing methods to extract new information from historical specimens; applying machine learning and advanced analytical methods to specimen images and biodiversity data; integrating museum specimens with genomic and environmental datasets; and developing computational approaches that accelerate species discovery, identification, classification, and our understanding of evolutionary change.

Education and Public Engagement In addition, the successful candidate will serve as an Assistant Professor in the Richard Gilder Graduate School and should have an interest in teaching and advising PhD students and postdocs in comparative biology through this program. There is also the opportunity to build on existing relationships with nearby partner institutions to advise doctoral students, including Columbia University and the City University of New York.

The position will provide opportunities to contribute to exhibition development, collaborate with the Museum's education department, and participate in public engagement initiatives, especially on efforts aligned with AMNH's strategic priority to address the local and global impacts of climate change and biodiversity loss.

Research Environment The AMNH, an independent, non-governmental institution, is a recognized leader in scientific research, graduate education, and public education about science and the natural world. The Museum provides an exceptional environment for collections-based research with resources such as: world-class zoological and other collections, including a cryogenic collection (<https://www.amnh.org/research/institute-comparative-genomics/amcc>) and associated facility; genomics labs (<https://www.amnh.org/research/institute-comparative-genomics/molecular-labs>)

and an ancient biomolecules lab (<https://www.amnh.org/research/sicg/ancient-biomolecular-lab>); micro-CT scanning and scanning electron microscopy; advanced optical, electron-beam, and X-ray analytical technologies; high performance computing research resources; the Southwestern Research Station in the biodiverse Chiricahua mountains of southern Arizona, which has hosted the Lepidoptera field course for the past 18 years; access through

AMNH's consortium membership to the 4000-acre Black Rock Forest approximately 1.5 hours north of NYC; and generous internal funding opportunities to support ambitious field research and other innovative scientific projects.

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app deadline 1 week USFS WI 6-month full-time lab tech molecular genetics aquatics ecol-evol

Position: 6 month, full-time molecular genetics and aquatics lab tech Pay: GS-7 level (Pay starts at \$24.18/hr) Located in: Rhinelander, WI USDA Forest Service Research & Development Northern Research Station - Rhinelander, WI Unit Application open: 9/25/2026 - 10/05/2026 Start date: Winter 2026/2027 (please apply if interested and reach out for specifics of start date) Apply via USAJobs and select Location as Rhinelander, WI. <https://www.usajobs.gov/job/886148100> Job title will come up as: Forestry Technician (Recreation, Timber, Range) This position is part of a large, batch hire across USDA Forest Service Research & Development and is listed under the general job description for a Forestry Tech. Please address the job duties/qualifications listed for the position on USAJobs in your application to satisfy HR. For the Rhinelander location, the person in this position will work with multiple Unit scientists and science support staff to conduct laboratory work that involves molecular genetic techniques and culture maintenance of zooplankton and phytoplankton communities to support experiments to study aquatic ecosystem health, process, and function in relation to active forest management. Ideal candidate will be highly detail oriented, have a can-do attitude, be open to constructive feedback, and have experience with some or all of the following: working in labs where eliminating sample contamination is paramount, DNA extractions, DNA quantification, running gels, qPCR, PCR, aspects of (zooplankton and phytoplankton) culture maintenance and growth, microscope use with zooplankton and phytoplankton, careful collection, handling, and analysis of data. Reach out with questions! (Rachel.toczydlowski@usda.gov)

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Assistant Professor Biological Sciences Wellesley College deadline Fri Sept 11

Position: R0007818 - Assistant Professor of Biological Sciences External Job Posting Link: https://wd1.myworkdaysite.com/recruiting/wellesley/wellesley-faculty/job/Wellesley-College/Assistant-Professor-of-Biological-Sciences_R0007818 Job Description:

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

Applications are due Friday, September 11, 2026 and should be submitted via our application web site (<https://www.wellesley.edu/about-us/working-at-wellesley>). Materials must include 1) a cover letter (ca. 1-2 pages), 2) curriculum vitae, 3) a statement of teaching philosophy, experience, and interests, and how those inform your pedagogical practices (ca. 2-3 pages), 4) a statement of research accomplishments and plans for the future including the incorporation of undergraduates (ca. 2-4 pages), and 5) the names/email addresses of three references who will be asked to submit confidential letters of recommendation. Individually, the three letters of recommendation can be from any prior or current component of the candidate's education or ex-

perience, but collectively, they should explicitly speak to the candidate's promise for both successful teaching and research. First-round interviews will be held on Zoom in early to mid-October with campus visits in late October and November. Questions should be directed to the Biological Sciences search co-chairs, John Goss (jgoss@wellesley.edu) and Steven Biller (sbiller@wellesley.edu). The minimum salary for Assistant Professors is \$103,000.00 annually.

Company Description: Wellesley's mission is to provide an excellent liberal arts education to women who will make a difference in the world. We advance our mission by working together as a community—faculty, students, staff, and alumnae. Embark on a fulfilling career journey at Wellesley College, where we prioritize your well-being. For those roles that are half-time or greater, we offer a comprehensive array of benefits and resources designed to enhance both your work-life balance and long-term success. -**Exceptional Benefits Package:** Access a comprehensive benefits package, including health, dental, vision and pre-tax saving benefits, life insurance, disability coverage (for full-time Faculty), and more to safeguard your health and that of your loved ones. -**Retirement Savings:** Plan for the future with our retirement savings plan. Wellesley College contributes up to 10.5-Work/Life and Wellness: Caregiving support through Wellthy, legal plan insurance, pet insurance discount and a variety of other resources including retirement planning, and access to cultural and leisure activities throughout metro-Boston. -**Commuting and Transportation:** Enjoy the convenience of free parking on our picturesque campus, easily accessible from major roadways. We are also accessible via the MBTA commuter rail. -**Campus Privileges:** Enjoy free use of our state-of-the-art athletic and fitness facilities with onsite fitness classes, Library resources, and seize opportunities to attend diverse campus events that contribute to a vibrant community.

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

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AssistantProf StanfordU EvoBio

Assistant Professor in Evolutionary Biology The Department of Biology at Stanford University seeks applicants for a tenure-track Assistant Professor in Evolutionary Biology. A successful candidate will conduct research that asks fundamental questions relating to evolutionary processes and drivers of evolutionary patterns. Candidates can make use of any of the major techniques of evolutionary biology, including computational, experimental, field, mathematical, statistical, or theoretical methods, or any combination thereof. Conceptual and mathematical research or research involving any species will be considered. The successful candidate's research will answer broad questions about evolutionary processes and principles using specific models and/or systems. Applicants must have a demonstrated commitment to teaching and mentoring and the ability to build and maintain a world-class research program. The successful candidate must have a Ph.D. in a relevant field at the time of appointment and will be expected to teach and advise students at both the graduate and undergraduate levels. The term of appointment is expected to begin on September 1, 2027. Candidates should apply through <https://facultypositions.stanford.edu/jobs/assistant-professor-in-evolutionary-biology-stanford-university-california-united-states?lApplicationSubSourceID=> and submit -a cover letter -curriculum vitae (including a complete publication list) -a research statement (three single-spaced pages, not including references) -a teaching and mentorship statement (one single-spaced page) -contact information for at least three letters of recommendation The nine-month salary range for this position is \$136,454 - \$162,039 for the academic year 2026-2027. Stanford University has provided a pay range representing its good faith estimate of what the university reasonably expects to pay for the position upon hire. The pay offered to the selected candidate will be determined based on factors including (but not limited to) the qualifications of the selected candidate, budget availability, and internal equity. Further information about Stanford's Department of Biology may be found at <https://biology.stanford.edu/>. Inquiries may be directed to Elayna McCarty, Faculty Affairs Coordinator, emccarty@stanford.edu. The application process will close on October 31, 2026 Stanford is an equal employment opportunity and affirmative action

employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, protected veteran status, or any other characteristic protected by law. Stanford welcomes applications from all who would bring additional dimensions to the University's research, teaching and clinical missions. Consistent with its obligations under the law, the University will provide reasonable accommodations to applicants and employees with disabilities. Applicants requiring a reasonable accommodation for any part of the application or hiring process should contact disability.access@stanford.edu.

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BridgewaterStateU Three Tenure-track Positions

BRIDGEWATER STATE UNIVERSITY HIRING
THREE TENURE TRACK BIOLOGY FACULTY
Seeking Assistant Professor Candidates with Research
Specialties in the Following Fields Genetics Physiology
Evolutionary Developmental Biology

To apply for the GENETICS specialty, visit <https://jobs.bridgew.edu/postings/33634> To apply for the PHYSIOLOGY specialty, visit <https://jobs.bridgew.edu/postings/33635> To apply for the EVO-DEVO specialty, visit <https://jobs.bridgew.edu/postings/33033> GENETICS Close Date: 9/25/2026 PHYSIOLOGY Close Date: 9/30/2026 EVO-DEVO Close Date: 10/05/2026

Department Summary: The Department of Biological Sciences at Bridgewater State University is a dynamic community with over 400 undergraduate majors and a growing master's program. We aim to provide our students with a broad background in the biological sciences while also supporting subdisciplines of interest (e.g., we have concentrations in Cellular and Molecular Biology, Ecology and Evolutionary Biology, Biomedical Science and Pre-medicine, and Secondary Education). Given the number of positions in biotechnology, research, education and health care in the area, the mission of the department is to train students and support their placement into the workforce and advanced degree programs. Students are the central focus and an integral part of the Department, working side-by-side with faculty who are enthusiastically committed

to teaching and research. A strong sense of community is fostered through small class sizes and individualized research and career mentoring from faculty. Our department has a strong and well-supported undergraduate research program that supports student research projects and student travel to present their research at local, national, or international conferences. The candidate will join thirteen Full-Time Tenure-Track Faculty in the department and teach a diverse student population. In Fall 2025, 46

Bridgewater State University is an inclusive community dedicated to the lifelong success of all students; focused on the continuous improvement of its people; and is responsible for leading innovation that benefits Southeastern Massachusetts, the commonwealth, and the world. Bridgewater's accessible environment of teaching and learning stimulates critical thinking and the pursuit of new knowledge and deeper understanding. The teaching and learning environment at Bridgewater also cultivates meaningful and diverse interpersonal relationships and fosters an appreciation for global engagement aimed at transforming lives and improving the human condition. Our commitment is reflected in our institutional values (<https://www.bridgew.edu/bsuvalues>), which ensure that all students are supported and succeed.

Qualifications & Essential Duties:

To view Required Qualifications, Preferred Qualifications, and Essential Duties (including expected teaching requirements) please see each of the three individual job ads:

To apply for the GENETICS specialty, visit <https://jobs.bridgew.edu/postings/33634> To apply for the PHYSIOLOGY specialty, visit <https://jobs.bridgew.edu/postings/33635> To apply for the EVO-DEVO specialty, visit <https://jobs.bridgew.edu/postings/33033> GENETICS Close Date: 9/25/2026 PHYSIOLOGY Close Date: 9/30/2026 EVO-DEVO Close Date: 10/05/2026

Special Conditions for Eligibility:

Please be aware that employment at Bridgewater State University is contingent upon completion of a successful background check. Bridgewater State University is an E-Verify employer.

Salary is commensurate with experience in accordance with the Appendix O of the MSCA contract. A reasonable starting salary range to expect for a new faculty member appointed at the rank of Assistant Professor is \$75,000 to \$85,000.

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Cornell AsstProf Neuroethology Evolutionary Neuroscience

The Department of Neurobiology and Behavior (NBB) in the College of Agriculture and Life Sciences (CALS) at Cornell University welcomes applications for a full-time tenure-track position in The Neural Mechanisms of Natural Behaviors at the assistant professor level.

We seek an outstanding scientist whose research connects animal behavior to its underlying neural mechanisms. We are interested in candidates who study how the brain generates, controls, or is shaped by innate or learned behaviors that have evolved in natural contexts, for example communication, navigation, mating, foraging, or social interaction, and who integrate neural measurements with rigorous, quantitative analysis of animal behavior. Laboratory and/or field-based research programs that utilize experimental, physiological, genomic, developmental, computational, or comparative approaches to uncover the neural mechanisms of animal behavior are welcome. Candidates working across species (both model and non-model; vertebrate or invertebrate) are encouraged to apply.

<https://academicjobsonline.org/ajo/jobs/32592> Applications received by November 15, 2026, will be given full consideration. The job is not strictly limited to evolutionary approaches, but scientists using evolutionary approaches to neuroscientific questions are encouraged to apply! For more information you can contact the search chair, Michael Sheehan - msheehan@cornell.edu

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CuratorMarineInvertebrates NHM LosAngelesCounty

The Natural History Museum of Los Angeles County (NHMLAC) seeks a full-time Assistant OR Associate Curator, commensurate with experience, of Marine Invertebrates. The successful candidate will conduct collection-based research in integrative invertebrate biology, specifically overseeing the growth and stewardship of the Museum's echinoderm collection. We are particularly interested in candidates who can tackle big-picture questions in marine biodiversity science and are able to apply research findings to issues of global importance. This role offers a unique opportunity to conduct integrative, specimen-based research at a globally recognized natural history museum. NHMLAC's marine invertebrate collections are the largest in the western United States, with strengths in benthic macroscopic specimens from the Eastern Pacific as well as globally. These collections house approximately 12 million specimens of extant phyla, with strong emphasis on crustaceans, mollusks, annelids, and echinoderms.

The Curator is expected to have and expand an active, public facing, and externally funded research program that includes field work. While research interests should span the globe, the position should emphasize California and Southern California-based studies that address questions in biodiversity science, complementing existing strengths of NHMLAC. Additionally, the Curator will supervise staff and volunteers, mentor students, and develop working relationships with local colleges and universities. Active participation in museum activities - including exhibits, education, community science, public outreach and media interactions, and fundraising - is required. Applicants must hold a Ph.D. and have a strong track record of peer-reviewed publications and competitive external funding. Experience with the care and management of marine invertebrate wet collections is highly desirable. Candidates must demonstrate excellent communication skills and the ability to engage with culturally diverse audiences. NHMLAC deeply values diversity, equity, inclusion, and access, and enthusiastically encourages applications from all people, including those who identify as a minority in science, person of color, neurodivergent, a woman, a person with a disability, a veteran, and/or part of the LGBTQAI+ community. Salary (\$83,000-112,000) and title (Assistant/Associate) will

be commensurate with experience, with a proposed start date of July 1, 2027. The application deadline is October 15, 2026. Interested candidates should submit all materials as a single PDF to Ciel Ramon-Canas at cramoncanas@nhm.org, including "Marine Invertebrate Curator Search" in the subject line. The application must include the following: - Cover letter - 2-page statement of proposed research and collection development (including the application of modern methods and informatics to Museum collections) - 1-3 page statement of interest and experience in public engagement - 1-page statement of experience with and commitment to diversity, equity, inclusion, and access in the natural sciences - Curriculum vitae - Full contact information for at least three references.

NHMLAC's values - adventurous, inclusive, authentic, and intentional - guide our work and visitor experience, committing us to foster a welcoming, safe and respectful workplace environment where innovation and collaboration thrive and every team member can contribute their unique perspectives to advance our mission. NHMLAC seeks candidates who are aligned with our values and priorities, and are passionate about connecting science with the vibrant and diverse communities we serve throughout Los Angeles. NHMLAC is a nonprofit organization committed to fostering a workplace and public environment that uplifts Kindness, Fairness, Openness and Dignity. These values extend not only to our employees, but to our guests, local community, and organizational partners. If you are interested in this position, we encourage you to apply!

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GeorgiaTech ComputationalGenetics TenureTrack

Job Summary: The School of Biological Sciences (<https://biosciences.gatech.edu/>) at the Georgia Institute of Technology in Atlanta, Georgia invites applications for a tenure-track faculty position in Computational Genetics. Applicants will be considered at all ranks. We seek outstanding scientists developing and applying innovative statistical, computational, and data-science approaches to understand the genetic architecture of complex traits. We are particularly interested in candidates whose computationally-oriented research in evolution, behavior, and/or human biology,

addresses fundamental questions about genetic variation as well as its consequences. Appropriate programs may include population and quantitative genetics, statistical genetics, evolutionary genomics, computational biology, integrative omics, machine learning for genetic discovery, and approaches providing mechanistic insight into disease susceptibility. Candidates are expected to demonstrate an exceptional commitment to the teaching and mentoring of students.

Link to job posting (ID: 303632): https://careers.hprod.onehcm.usg.edu/psp/careers/CAREERS/HRMS/c/HRS_HRAM_FL.HRS_CG_SEARCH_FL.GBL?Page=HRS_APP_JBPST_FL&Action=U&FOCUS=Applicant&SiteId=3000&JobOpeningId=303632&PostingSeq=1 About Georgia Tech: Georgia Tech prides itself on its technological resources, collaborations, high-quality student body, and its commitment to building an outstanding and diverse community of learning, discovery, and creation. We strongly encourage applicants whose values align with our institutional values, as outlined in our strategic plan. These values include academic excellence, diversity of thought and experience, inquiry and innovation, collaboration and community, and ethical behavior and stewardship. Georgia Tech has policies to promote a healthy work-life balance and is aware that attracting faculty may require meeting the needs of two careers. Georgia Tech is a top-ranked public research university situated in the heart of Atlanta, a diverse and vibrant city with numerous economic and cultural strengths. The Institute serves more than 45,000 students through top-ranked undergraduate, graduate, and executive programs in engineering, computing, science, business, design, and liberal arts. Georgia Tech's faculty attracted more than \$1.4 billion in research awards this past year in fields ranging from biomedical technology to artificial intelligence, energy, sustainability, semiconductors, neuroscience, and national security. Georgia Tech ranks among the nation's top 20 universities for research and development spending and No. 1 among institutions without a medical school.

About the School of Biological Sciences: Graduate degree programs include: MS and PhD in Biology, MS and PhD in Bioinformatics, MS and PhD in Computational Science and Engineering, PhD in Neuroscience & Neurotechnology, as well as a PhD in Quantitative Biosciences, Ocean Sciences and Engineering, and Dual Doctor of Physical Therapy/Doctor of Philosophy. Undergraduate degree programs include 4 year BS and 5 year BS/MS programs in Biology and Bioinformatics. Research strengths include: Molecular and Cellular Biology, Computational Biology and Bioinformatics, Neuroscience, Microbial Dynamics and Infection, as well as Integrative Physiology, Evolution, and Ecology. The

School is home to the two largest and most diverse undergraduate majors in the College of Sciences: Biology and Neuroscience. Faculty members in the School of Biological Sciences have the opportunity to work with students and faculty from across campus, including the Molecular Biomedical research community comprised by members labs from the schools of Biological Sciences, Chemistry and Biochemistry, Physics, and Chemical and Biomolecular Engineering. Georgia Tech prides itself on its technological resources, collaborations, high-quality student body, and its commitment to building an outstanding community of learning, discovery, and creation. We strongly encourage applicants whose values align with our institutional values. These values include academic excellence, freedom of expression and inquiry, innovation, collaboration, ethical behavior and stewardship. Georgia Tech has policies to promote a healthy work-life balance and is aware that attracting faculty may require meeting the needs of two careers.

Responsibilities:

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HoldenArboretum OH US Conservation Biologist

Conservation Biologist Holden Arboretum (OH) - Leach Rhododendron Research Station

Holden Forests & Gardens is comprised of the Holden Arboretum and Cleveland Botanical Garden and is committed to advancing plant and environmental science through research, conservation, and public engagement. The Leach Rhododendron Research Station serves as a center for rhododendron research, conservation, breeding, and education.

Opportunity: Holden Forests & Gardens seeks a Conservation Biologist to lead research, conservation, and operations at the Leach Rhododendron Research Station. This position offers the opportunity to build a research program around a globally significant living collection while directly influencing its future through conservation and breeding.

The successful candidate will combine scientific research, collection stewardship, breeding program lead-

ership, and public engagement to advance understanding and conservation of rhododendrons and related taxa. Research can center on the ecology, evolution, or pathology of rhododendrons and other ericaceous plants. Working at the intersection of research, horticulture, and education, the Conservation Biologist will serve as an institutional expert, foster scientific discovery, support the continued development of the Leach collections, and manage station operations.

The Leach Rhododendron Research Station serves as a hub for rhododendron expertise within Holden Forests & Gardens. As a member of the Research Department, the Conservation Biologist will develop and conduct research that advances understanding of rhododendrons and other ericaceous plants while supporting conservation, breeding, education, and public engagement initiatives. The successful candidate will collaborate broadly across Holden Forests & Gardens and with external researchers, universities, public gardens, conservation organizations, and professional societies.

Key Responsibilities: Key responsibilities of the Conservation Biologist include, but are not limited to: **Research and Scholarship:** - Conduct research relevant to plant conservation, with a focus on rhododendrons and other ericaceous plants. - Publish findings in peer-reviewed scientific journals. - Present research at scientific conferences, professional meetings, and public forums. - Pursue and secure external funding to support research initiatives. - Collaborate with colleagues across Holden Forests & Gardens and with external academic, governmental, nonprofit, and professional partners. - Serve as a primary advisor or committee member for graduate students in support of research objectives. **Institutional Expertise, Outreach, and Teaching:** - Serve as an institutional expert on rhododendrons, ericaceous plants, and the Leach Rhododendron Research Station. - Share scientific and horticultural knowledge through classes, workshops, public tours, educational programming, interpretive materials, and direct engagement with visitors and stakeholders. - Represent Holden Forests & Gardens in professional organizations and scientific networks, including organizations such as Botanic Gardens Conservation International (BGCI), the American Rhododendron Society, and related professional associations. **Station Leadership and Operations:** - Provide leadership for the Leach Rhododendron Research Station. - Provide scientific leadership for the Leach Rhododendron breeding program, integrating research, horticultural evaluation, and conservation priorities to guide the development of new cultivars. - Collaborate closely with the Curation team to support stewardship and development of the rhododendron and azalea collections at Leach Research Station. -

Supervise station personnel, including the Field Station Specialist, interns, seasonal staff, and volunteers.

Qualifications and Skills: - Ph.D. in biology, ecology, horticulture, forestry, or a closely related field. - Demonstrated record of scientific research and publication. - Experience communicating science to professional and/or public audiences. - Evidence of professional service and scholarly engagement. - Strong quantitative, analytical, and problem-solving skills. - Ability to develop and manage research projects, including personnel and budget responsibilities. - Demonstrated capacity to pursue external funding opportunities. - Commitment to collaboration across disciplines and institutions. - Appreciation for the role of arboreta, public gardens, museums, and similar mission-driven organizations in advancing science and public understanding. - Knowledge of rhododendrons, ericaceous plants, or related taxa, or demonstrated willingness or interest to develop expertise in these taxa. - Supports Holden Forests & Gardens' mission, vision, and values

Holden Forests & Gardens (HF&G) is a great place to work!

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HoldenArboretum OH US Ecologist

Ecologist Holden Arboretum (OH)

Holden Forests & Gardens connects people with the wonder, beauty and value of trees and plants, to inspire action for healthy communities. When you join HF&G, you join a team of professionals who are passionate about improving Northeast Ohio's communities through our mission-driven programs.

Opportunity: The Holden Arboretum seeks an Ecologist to join its Research Department. This position offers an exceptional opportunity to develop an independent research program that advances scientific understanding of plants and their environments while contributing practical solutions to pressing environmental challenges affecting the Great Lakes region and beyond.

The successful candidate will combine rigorous scientific inquiry with public engagement, translating research

discoveries into meaningful action through collaboration, education, and outreach. We welcome applicants whose expertise aligns with a broad range of plant and environmental research areas, including urban ecology, forest health, plant pathology, forestry, forest management, climate resilience, and related inquiries centered on relationships between plants and their environments.

As a member of Holden Arboretum's research team, the Ecologist will lead an independent research program, while contributing to the institution's mission through science communication, public engagement, and organizational service. The position balances research excellence with applied impact, creating opportunities to connect scientific discovery with conservation, environmental stewardship, and community understanding. Researchers have opportunities to collaborate across disciplines and with universities, government agencies, nonprofit organizations, and community partners.

Key Responsibilities: Key responsibilities of the Ecologist include, but are not limited to: Research and Scholarship: - Develop and sustain an independent, externally recognized research program. - Conduct innovative research addressing environmental challenges, particularly those relevant to the Great Lakes region. - Publish findings in peer-reviewed scientific journals. - Present research at scientific conferences, professional meetings, and public forums. - Pursue and secure external funding to support research initiatives. - Collaborate with colleagues across Holden Forests & Gardens and with external academic, governmental, nonprofit, and professional partners. - Translate scientific findings into practical responses to environmental and conservation challenges. - Serve as a primary advisor or committee member for graduate students in support of research objectives. Science Communication and Public Engagement: - Communicate scientific discoveries to diverse audiences through presentations, educational programming, publications, and outreach activities. - Serve as a scientific ambassador for the Holden Arboretum. - Foster public understanding of plant science, ecology, forestry, and/or environmental issues. - Contribute expertise to institutional initiatives that connect research with community engagement and education.

Qualifications and Skills: - Ph.D. in biology, ecology, horticulture, forestry, or a closely related field. - Demonstrated record of scientific research and publication. - Experience communicating science to professional and/or public audiences. - Evidence of professional service and scholarly engagement. - Strong quantitative, analytical, and problem-solving skills. - Ability to develop and manage research projects, including personnel and budget responsibilities. - Demonstrated capacity to pursue external funding opportunities. - Com-

mitment to collaboration across disciplines and institutions. - Appreciation for the role of arboreta, public gardens, museums, and similar mission-driven organizations in advancing science and public understanding. - Supports Holden Forests & Gardens' mission, vision, and values

Holden Forests & Gardens (HF&G) is a great place to work! In addition to the salary range of \$75,000 - 85,000, we offer Medical, Dental and Vision Benefits — Paid Time Off — 8 Paid Holidays a year + 3 Floating Holidays — 403(b) — Employee sponsored life insurance, long term disability and short-term disability — Work in a beautiful environment within Greater Cleveland — Discounts in our stores & cafes — Free parking at both campuses anytime we are open — Free admission to many Northeast Ohio Museums — Free Employee Assistance Program — And Much More!

Apply: <https://holdenfg.org/career-and-internships/?gnk=job&gni=8a78839ea06420ea01a09bc5d71a67ca> To be considered for this position, applicants must submit the following materials: - Cover Letter - Curriculum Vitae (CV) - Research Statement - Contact Information for Three References Application review begins: October 9.

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iCatch Bozeman Montana US Molecular Applications Scientist

About iCatch iCatch, Inc. is a new biotechnology company building field-deployable tools to revolutionize fisheries monitoring, enhance seafood traceability, and strengthen supply chain transparency. Learn more about us at <https://icatch.app/> The Role We're hiring 1-2 Molecular Applications Scientists to lead the design, optimization, and validation of field-ready molecular diagnostic assays. In this role, you will drive core R&D activities, supervise technical staff, and bridge lab-based assay development with practical field deployment. This position is ideal for recent PhD graduates to established scientists eager to build commercial diagnostic solutions from the ground up in a fast-paced biotechnology startup. If you are a detail-oriented, self-

motivated scientist driven by real-world applications, we encourage you to apply.

What You'll Do - Generate high-throughput genomic sequence datasets based on whole genome sequencing, reduced representation sequencing, and analogous methods. - Implement and manage bioinformatic pipelines to process and analyze complex genetic and genomic datasets. - Design, optimize, and validate field-deployable molecular assays for detecting nucleic acid targets. - Maintain rigorous quality control standards, laboratory notebooks, and field documentation. - Supervise, mentor, and train technical support staff. - Prepare technical data packages, validation reports, and executive summaries for regulatory partners and external review. - Support field testing and pilot deployment during field operations. Required Skills - PhD or Master's degree (the latter only with relevant research and supervisory experience) in molecular biology, genetics/genomics, bioinformatics, biochemistry, fisheries/wildlife science or a closely related field. - Hands-on experience developing and troubleshooting molecular assays (e.g., PCR/qPCR, isothermal amplification techniques, primer/probe design). - Experience with DNA/RNA extraction, NGS library preparation, and high-throughput sequencing workflows (e.g., species barcoding, eDNA, or target capture). - Strong proficiency in bioinformatic pipelines for analyzing complex genomic datasets, with specific expertise in variant discovery, sequence alignment, and target locus identification. - Experience supervising, mentoring, and managing laboratory technicians, research assistants, or junior scientific staff. - Robust organizational skills with a track record of maintaining detailed laboratory records, protocols, and digital workflows. - Adaptable, proactive, and comfortable thriving on a small startup team. - Able to work on-site in Bozeman, MT in a hands-on lab environment. - Eligible to work in the United States.

Preferred Skills - Experience translating lab assays into field-ready formats (e.g., lateral flow, lyophilization). - Experience with seafood, fisheries, or other aquatic species. - Background in forensic-grade testing, regulatory validation, or agency workflows. - Proven track record of drafting high quality scientific manuscripts or technical reports.

Additional Requirements Employment is contingent on: - Must be legally authorized to work in the United States. - Successful completion of a background check. - Successful verification of education credentials and relevant professional experience. - Signing a confidentiality/non-disclosure agreement.

Compensation, Location, & Timeline The initial hire

is for one year with additional years possible given satisfactory performance and available funding. Full-time, on-site employment in Bozeman, Montana; remote work options are not feasible. Competitive industry compensation commensurate with experience and generous benefits package. Start date is as soon as possible, but no later than December 1, 2026.

To Apply Submit the following items as a single PDF document to jobs@icatch.app with "Molecular Applications Scientist" in the subject line:

1. CV (up to 6 pages)
 2. Cover letter (up to 2 pages)
 3. Contact information for 3 professional references
- Applications will be reviewed immediately. Positions are open until filled, apply as soon as possible for full consideration.

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iCatch Bozeman Montana US Molecular Lab Technician

About iCatch iCatch, Inc. is a new biotechnology company building field-deployable tools to revolutionize fisheries monitoring, enhance seafood traceability, and strengthen supply chain transparency. Learn more about us at <https://icatch.app/> The Role We're hiring a Molecular Lab Technician to provide hands-on support in technical benchtop skills to our science team leads. Molecular Lab Technicians work in a fully equipped molecular lab setting. This position is ideal for recent graduates eager to launch their careers in applied biotechnology, as well as experienced technicians looking to contribute to fisheries technology development. If you are detail-oriented, self-motivated, and excited to help build field-ready diagnostic solutions from the ground up, we encourage you to apply.

What You'll Do - Catalog, process, and prepare tissue samples for DNA/RNA extraction and downstream molecular work. - Execute established molecular protocols including DNA/RNA isolation, PCR/qPCR amplification, library preparation for high-throughput sequencing, assay testing and validation, and lateral flow. - Prepare samples and materials for field sampling and testing. - Work efficiently and independently under the direction of the science team leads. - Maintain rigorous lab documentation and sample chain-of-custody. - Support lab operations by tracking inventory, maintaining equipment, and ordering supplies. - Assist with general

lab organization and safety compliance.

Required Skills - Master's or Bachelor's degree (the latter with relevant coursework and research experience) in biology, molecular biology, genetics/genomics, biochemistry, fisheries/wildlife science, or closely related field. - Hands-on experience with basic molecular biology techniques. - Careful worker who is diligent, organized, and able to work independently. - Exceptional organization skills with expertise in spreadsheet management and structured file management in Google Drive or similar collaborative platforms. - Adaptable, proactive, and comfortable thriving on a small startup team. - Able to work on-site in Bozeman, MT in a hands-on lab environment. - Eligible to work in the United States.

Preferred Skills - Experience in molecular assay development and testing. - Familiarity with bioinformatic and/or quantitative data analyses. - Familiarity with chain-of-custody and forensic protocols. - Experience with lab inventory and LIMS software.

Additional Requirements Employment is contingent on: - Must be legally authorized to work in the United States. - Successful completion of a background check. - Successful verification of education credentials and relevant professional experience. - Signing a confidentiality/non-disclosure agreement.

Compensation, Location, & Timeline The initial hire is for one year with additional years possible given satisfactory performance and available funding. Full-time, on-site employment in Bozeman, Montana; remote work options are not feasible. Competitive industry compensation commensurate with experience and generous benefits package. Start date is as soon as possible, but no later than December 1, 2026.

To Apply Submit the following items as a single PDF document to jobs@icatch.app with "Lab Technician" in the subject line: 1. CV (up to 3 pages) 2. Cover letter (up to 2 pages) 3. Contact information for 3 professional references Applications will be reviewed immediately. Position is open until filled, apply as soon as possible for full consideration.

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Job Faculty WuTsaiInstituteYaleU Neurocognition

The Wu Tsai Institute (WTI) at Yale University seeks candidates for an endowed tenure-track faculty position with a focus on researchers with an integrative approach, driving experimental or conceptual innovations to advance our understanding of cognition within its broader ecological, biological, or societal contexts, including interactions with technology. Applicants from a broad range of disciplines, models, and approaches are encouraged to apply. Successful candidates will receive a tenure-track appointment in one or more departments in the Yale Faculty of Arts and Sciences, School of Engineering and Applied Science, and/or School of Medicine. Faculty identified through this search will receive an attractive start-up package, join a growing community of ~220 faculty across Yale, and have access to state-of-the-art lab space and core facilities in our new research building, as well as special funding mechanisms, fellowships for postdocs and students, and other events and programs. Founded by a historic gift, WTI is dedicated to advancing our understanding of human cognition and human potential by sparking interdisciplinary inquiry. We are building a vibrant community where experimentalists and theorists work together to integrate approaches across disciplines through common mathematical, statistical, and computational frameworks. We foster a welcoming environment that provides equal opportunity to people of a broad range of backgrounds and perspectives. For more information and to apply, please visit <https://apply.interfolio.com/189343>. The deadline is October 15, 2026.

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JobMarineInvertsCurator NaturalHistoryMuseum LosAngelesCounty

The Natural History Museum of Los Angeles County (NHMLAC) seeks a full-time Assistant OR Associate

Curator, commensurate with experience, of Marine Invertebrates. The successful candidate will conduct collection-based research in integrative invertebrate biology, specifically overseeing the growth and stewardship of the Museum's echinoderm collection. We are particularly interested in candidates who can tackle big-picture questions in marine biodiversity science and are able to apply research findings to issues of global importance. This role offers a unique opportunity to conduct integrative, specimen-based research at a globally recognized natural history museum. NHMLAC's marine invertebrate collections are the largest in the western United States, with strengths in benthic macroscopic specimens from the Eastern Pacific as well as globally. These collections house approximately 12 million specimens of extant phyla, with strong emphasis on crustaceans, mollusks, annelids, and echinoderms. The Curator is expected to have and expand an active, public facing, and externally funded research program that includes field work. While research interests should span the globe, the position should emphasize California and Southern California-based studies that address questions in biodiversity science, complementing existing strengths of NHMLAC. Additionally, the Curator will supervise staff and volunteers, mentor students, and develop working relationships with local colleges and universities. Active participation in museum activities including exhibits, education, community science, public outreach and media interactions, and fundraising is required. Applicants must hold a Ph.D. and have a strong track record of peer-reviewed publications and competitive external funding. Experience with the care and management of marine invertebrate wet collections is highly desirable. Candidates must demonstrate excellent communication skills and the ability to engage with culturally diverse audiences. NHMLAC deeply values diversity, equity, inclusion, and access, and enthusiastically encourages applications from all people, including those who identify as a minority in science, person of color, neurodivergent, a woman, a person with a disability, a veteran, and/or part of the LGBTQAI+ community. Salary (\$83,000-112,000) and title (Assistant/Associate) will be commensurate with experience, with a proposed start date of July 1, 2027. The application deadline is October 15, 2026. Interested candidates should apply here: https://workforcenow.adp.com/mascsr/default/mdf/recruitment/recruitment.html?cid/c0a355-012e-4bef-9c85-724ae074a06a&ccId3000101_000001&lang=en_US&source=EN&selectedMenuKeyEreerCenter&jobId73150 and submit all materials as a single PDF to Ciel Ramon-Canas at cramoncanas@nhm.org, including a Marine Invertebrate Curator Search in the subject line. The application must include the fol-

lowing: - Cover letter - 2a??3 page statement of proposed research and collection development (including the application of modern methods and informatics to Museum collections) - 1a??3 page statement of interest and experience in public engagement - 1-page statement of experience with and commitment to diversity, equity, inclusion, and access in the natural sciences - Curriculum vitae - Full contact information for at least three references. NHMLACa??s valuesa??adventurous, inclusive, authentic, and intentionala??guide our work and visitor experience, committing us to foster a welcoming, safe and respectful workplace environment where innovation and collaboration thrive and every team member can contribute their unique perspectives to advance our mission. NHMLAC seeks candidates who are aligned with our values and priorities, and are passionate about connecting science with the vibrant and diverse communities we serve throughout Los Angeles. NHMLAC is a nonprofit organization committed to fostering a workplace and public environment that uplifts Kindness, Fairness, Openness and Dignity. These values extend not only to our employees, but to our guests, local community, and organizational partners. If you are interested in this position, we encourage you to apply!

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Job TenureTrack U GothenburgSweden EcologyEvolu- tionTerrestrialArthropods

Open call for a tenure-track position in ecology and evolution of terrestrial arthropods at the University of Gothenburg in Gothenburg Sweden. Application deadline October 30 Full details on position can be found here https://web103.reachmee.com/ext/I005/1035/job?site=7&lang=UK&validator=9b89bead79bb7258ad55c8d75228e5b7&job_id=41287 You are welcome to ask me if you have any questions regarding the position, (soren.faurby@bioenv.gu.se) Soren Faurby

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JobWheatonCollege IL AssistantProfessor Plant-Fungal Ecology

Job Title: Assistant Professor in Biological and Health Sciences (Expertise in Botany and Ecology who will contribute to the Biology and Conservation and Ecological Health Majors) Overview: Wheaton College (IL) is seeking a dedicated and passionate Assistant Professor to join the faculty in a tenure-track position in the Biological and Health Sciences Department. The successful candidate will be responsible for teaching courses in general biology, botany, ecology, and evolution. The candidate is also expected to participate in ongoing research (laboratory or field) in their area of expertise and involve undergraduate students in the research program. This individual will contribute to the intellectual and spiritual growth of our students, upholding academic excellence with a commitment to integration of Christian faith and learning. Start Date: Full-Time - Fall 2027 Application deadline: Until Filled The budgeted salary range for an Assistant Professor is \$62,000 - 68,000 Wheaton College, located in a suburban community in the Chicago metropolitan area, is a Christ-centered community whose faculty and staff must affirm the College's Statement of Faith as expressing their own theological convictions. They also agree to live by the moral standards in Wheaton's Community Covenant, modeling these commitments for the Christian formation of our students. Wheaton College faculty and staff also support the Christ-Centered Diversity Commitment, which highlights our desire to treat all individuals as equal image-bearers of Jesus Christ. We encourage applications from candidates who will work to deepen Christ-centered diversity by fostering a campus climate where all faculty, staff, students, and alumni feel welcomed, respected, valued, and supported. For more information about Wheaton College, visit www.wheaton.edu. Additionally, Wheaton College aspires to provide a physically safe environment for students, staff, and faculty to learn and work. In support of this objective, the College requires background checks for final candidates after an employment offer is extended. Employment is contingent upon successful completion of a background check. Responsibilities: - Develop and deliver engaging and comprehensive courses in general biology, course-based undergraduate research, botany, ecology, and evolution at the under-

graduate level. - Utilize diverse teaching methods, including lectures, laboratory sessions, discussions, and innovative educational technologies, to promote active learning and critical thinking. - Develop and sustain an active research program that involves undergraduate students. - Mentor and advise students in the Biological and Health Sciences Department. - Participate in faculty governance and service to the College and community. - Opportunities to contribute to the teaching of courses and/or the development of research activities at the Wheaton College Field Station in the Black Hills of South Dakota. Qualifications: - A Ph.D. in Biology, Botany, Ecology or a related field. - Demonstrated commitment to Protestant Christian faith and the ability to integrate faith and learning in the field of biological sciences. - Prior teaching experience at the university level is preferred, with a strong record of effective and innovative pedagogy. - An ongoing research (laboratory, field, and/or computational) program. - Excellent communication skills, both written and verbal, with the ability to engage and inspire students. Attributes: - Dedication to the integration of faith and learning in a liberal arts higher education setting. - Passion for teaching and mentoring students from diverse backgrounds. - Commitment to the institution's Christian mission and values. - Collaborative and enthusiastic about contributing to a vibrant academic community. Our institution is dedicated to providing a supportive and intellectually stimulating environment where students are challenged to grow academically, spiritually, and personally. We are committed to fostering an inclusive community that embraces diversity and equality. Application Process: Interested individuals should submit a curriculum vitae and a letter of interest, which should articulate the candidate's qualifications in terms of teaching and scholarship. Additionally, candidates should describe their interest in mentoring students in the integration of Christian faith and learning by drawing from their Christian faith background. Additional application materials will be requested from promising candidates. Please see the link below to submit your application. <https://www.wheaton.edu/about-wheaton/offices-and-services/human-resources/apply-for-positions-at-wheaton-college>

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Massachusetts US Visiting Assistant Professor

Hi there, we have a 2-year VAP position in Massachusetts, USA at a small liberal arts college. Can you please post to your job section. We're looking for someone beginning in January 2027 which is an unusual time here in the US to be posting academic jobs. So I'm trying to get this out to as many of my community as possible.

Here is the full listing:

Position title: Visiting Assistant Professor (FULL TIME) Academic Year: (Spring 2027, AY2027-2028 and Fall 2028) Position Type: Faculty Department: Biological, Chemical and Environmental Sciences Description of Position: The Biological, Chemical, and Environmental Sciences (BCES) Department at Wheaton College is seeking applicants for a two-year Visiting Assistant Professor position starting Spring 2027 (Jan 18th) and continuing for Fall 2027, Spring 2028, and Fall 2028. The 3/3 teaching responsibilities will include upper-level courses in the candidate's area of expertise in the Spring, and Genetics and a course in data analysis using R or Python geared towards bioscience majors in the Fall. We are particularly interested in candidates with expertise and teaching experience in evolution, genetics, or bioinformatics.

Job Summary/Basic Responsibilities:

- o Teaching effectively in an in-person environment that fosters meaningful student-faculty interaction.
- o Creating a course syllabus (with assistance, if desired) and ensuring it is provided to students and posted on the course's Canvas site.
- o Selecting and ordering textbooks and/or procuring other required course materials before classes begin.
- o Grading assignments in a timely manner and posting grades in Canvas.
- o Holding regular office hours and being responsive to student needs. Wheaton's Biology Department is committed to creating an innovative, inclusive learning environment. Our work has been supported by an HHMI grant for inclusive excellence in STEM. As a department focused on equity and supporting diversity within academia, we encourage applications from individuals who have been historically excluded from Biology and from those who are strongly committed to diversifying the field through mentoring students.

Applicants should submit a cover letter, CV, statement of teaching philosophy, and contact information for three references.

Review of applications will begin immediately and will continue until the position is filled.

Minimum Qualifications: Minimum qualifications are An M.S. with strong teaching experience or a Ph.D. at the time of appointment

Salary: The anticipated hiring or recruitment range for this position is \$50 - \$55K. The actual salary offered will be commensurate with the qualifications, education and experience of the candidate hired.

To apply, click here: <https://jobs.wheatoncollege.edu/postings/4899> For information about the position you can contact the Chair of the Search Committee (Prof. Jessie Knowlton) directly: knowlton_jessie@wheatoncollege.edu

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National Museum Cardiff Head of Zoology

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

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

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

We seek a PhD (or equivalent) qualified zoologist with proven experience in museum collections management,

team leadership, and successful grant applications.

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

Applications must be received by 02 November 2026 for consideration.

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

<https://nmw.ciphr-irecruit.com/applicants/vacancy/2726/Head-of-Zoology-National-Museum-Cardiff> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Natural History Museum Los Angeles US Marine Invertebrates Curator

The Natural History Museum of Los Angeles County is currently seeking a Marine Invertebrates Curator (either Assistant or Associate). We'd greatly appreciate your assistance in spreading the word in hopes to reach an audience of integrative biologists. Below is the plain text job description to be posted:

The Natural History Museum of Los Angeles County (NHMLAC) seeks a full-time Assistant OR Associate Curator, commensurate with experience, of Marine Invertebrates. The successful candidate will conduct collection-based research in integrative invertebrate biology, specifically overseeing the growth and stewardship of the Museum's echinoderm collection. We are particularly interested in candidates who can tackle big-picture questions in marine biodiversity science and are able to apply research findings to issues of global importance. This role offers a unique opportunity to conduct integrative, specimen-based research at a globally recognized natural history museum. NHMLAC's marine invertebrate collections are the largest in the western United States, with strengths in benthic macroscopic specimens from the Eastern Pacific as well as globally. These collections house approximately 12 million specimens of extant phyla, with strong emphasis on crustaceans, mollusks, annelids, and echinoderms.

The Curator is expected to have and expand an ac-

tive, public facing, and externally funded research program that includes field work. While research interests should span the globe, the position should emphasize California and Southern California-based studies that address questions in biodiversity science, complementing existing strengths of NHMLAC. Additionally, the Curator will supervise staff and volunteers, mentor students, and develop working relationships with local colleges and universities. Active participation in museum activities—including exhibits, education, community science, public outreach and media interactions, and fundraising—is required.

Applicants must hold a Ph.D. and have a strong track record of peer-reviewed publications and competitive external funding. Experience with the care and management of marine invertebrate wet collections is highly desirable. Candidates must demonstrate excellent communication skills and the ability to engage with culturally diverse audiences. NHMLAC deeply values diversity, equity, inclusion, and access, and enthusiastically encourages applications from all people, including those who identify as a minority in science, person of color, neurodivergent, a woman, a person with a disability, a veteran, and/or part of the LGBTQAI+ community. Salary (\$83,000-112,000) and title (Assistant/Associate) will be commensurate with experience, with a proposed start date of July 1, 2027.

The application deadline is October 15, 2026. Interested candidates should submit all materials as a single PDF to Ciel Ramon-Canas at cramoncanas@nhm.org, including "Marine Invertebrate Curator Search" in the subject line. The application must include the following: - Cover letter - 2-3 page statement of proposed research and collection development (including the application of modern methods and informatics to Museum collections) - 1-3 page statement of interest and experience in public engagement - 1-page statement of experience with and commitment to diversity, equity, inclusion, and access in the natural sciences - Curriculum vitae - Full contact information for at least three references.

NHMLAC's values—adventurous, inclusive, authentic, and intentional—guide our work and visitor experience, committing us to foster a welcoming, safe and respectful workplace environment where innovation and collaboration thrive and every team member can contribute their unique perspectives to advance our mission. NHMLAC seeks candidates who are aligned with our values and priorities, and are passionate about connecting science with the vibrant and diverse communities we serve throughout Los Angeles.

NHMLAC is a nonprofit organization committed to fos-

tering a workplace and public environment that uplifts Kindness, Fairness, Openness and Dignity. These values extend not only to our employees, but to our guests, local community, and organizational partners. If you are interested in this position, we encourage you to apply!

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NortheasternU Marine Science Center MA US Bioinformatician

Job Summary We are seeking a skilled Bioinformatician to join our consortium in Marine Macrogenomics, which seeks to create a database of interoperable population genomic data for 5,000 genomes from 100 species. The successful candidate will play a central role in developing and maintaining scalable computational pipelines for the analysis of large-scale genomic datasets, with a focus on short-read alignment and population-level inference. This is an exciting opportunity to contribute to cutting-edge research in ecological and conservation genomics. **Minimum Qualifications Required** - Master's degree in Biology, Ecology and Evolution, Bioinformatics, Computational Biology, Genetics, or a related field - 2-5 years of hands-on experience in bioinformatics, with demonstrated work in genomics - Proficiency in short-read alignment tools such as BWA, Bowtie2, and STAR - Familiarity with downstream processing tools such as SAMtools, Genome Analysis Toolkit (GATK), and Picard - Experience writing pipelines using workflow management systems such as Snakemake or Nextflow - Solid scripting skills in Python, R, and Bash - Comfort working on the command line, including in a Unix/Linux environment - Familiarity with high-performance computing (HPC) and high-throughput computing (HTC) environments and job schedulers such as SLURM and HTCondor - Experience using application programming interfaces (APIs) to send and receive data and/or experience using tools to transfer large amounts of data between remote servers

Preferred - PhD or 3 years of post-Master's experience preferred - Experience with population genomic analyses and tools such as ANGSD, PLINK, ADMIXTURE, TreeMix, or similar platforms - Familiarity with handling non-model organism genomes or low-coverage sequencing data - Experience with version control systems such as Git and containerization technologies

including Docker and Singularity/Apptainer - Track record of contributing to published research

Key Responsibilities & Accountabilities - Collaborate and coordinate with members of the network, including wet lab and computational team members, to define data standards, ensure analytical reproducibility, and assist with project goals - Design, build, and maintain reproducible bioinformatics pipelines capable of scaling across many population genomic datasets - Align short-read sequencing data, including whole-genome and Restriction Site Associated DNA Sequencing (RADseq) datasets, to reference genomes using standard and emerging tools, and evaluate mapping quality across diverse datasets - Perform downstream population genomic analyses, including variant calling, filtering, and quality control - Document pipelines and analyses clearly for internal use and publication - Develop educational tutorials and assist with website development - Collate publicly available data and metadata, corresponding with authors as necessary to ensure data standards

Apply here: https://northeastern.wd1.myworkdayjobs.com/careers/job/Nahant-MA/Bioinformatician---Lotterhos-Lab_R142449 Review of applications starts on October 1, with a start date as soon as possible.

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PrincetonU AssistantProfessor Ecology Evolution Behavior

Position Title: Assistant Professor - Ecology, Evolution, and/or Behavior Salary Range: \$150,000 - \$180,000 Review Date: November 10, 2026 Candidates should apply through: <https://apply.interfolio.com/193474> Description Princeton University's Department of Ecology and Evolutionary Biology is seeking candidates for an Assistant Professor position in Ecology, Evolution and/or Behavior. We seek a scholar who is eager to interact with a vibrant and interdisciplinary group of colleagues both inside and outside the department. The successful candidate will address bold questions through a rigorous, creative, and integrative research program. The range of potential research areas should be understood broadly. We are excited to consider applicants focused on any timescale or level of biological hierarchy and employing any methodological

approach. Princeton University is an interactive community that fosters cross-disciplinary thought and collaboration. The successful candidate will have opportunities to interact with colleagues across different departments, programs, and institutes including the Lewis-Sigler Institute for Integrative Genomics, the Princeton Neuroscience Institute, the Program in Applied and Computational Mathematics, the Data and Intelligent Systems Hub, the High Meadows Environmental Institute, and the Omenn-Darling Bioengineering Institute. For those applying ecological and evolutionary principles outside its traditional domain, a joint appointment with another academic unit is possible. Qualifications Applicants must hold a Ph.D. in a relevant field. This position is subject to the University's background check policy. Application Instructions Applicants should submit a vision statement, no longer than two pages, that outlines the bold question(s) they would pursue within their first 5 years and that places those questions broadly in the context of major unsolved problems in their field(s). In this respect, the vision statement should draw on, yet go beyond, a summary of the applicant's prior and current research. In addition to the vision statement, applications need to include a cover letter, curriculum vitae, three papers or preprints, and three letters of recommendation. Application review will begin on November 10, 2026.

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SouthernNevada USA Organism Biology Professor at College

Please share this post with interested parties:

The College of Southern Nevada has multiple open positions in the Department of Biological Sciences for instructors of organismal biology, particularly those with a background in mammalogy and ornithology.

See details below and use this link to apply: https://nshe.wd1.myworkdayjobs.com/en-US/CSN-External/job/CSN---Charleston-Campus/Instructor---Biological-Sciences---Tenure-Track---Fall-1-2027_R0153382?clientRequestID=8fca099c05274abe82e95c9663eea79b CORE RESPONSIBILITIES:

Under direct supervision, responsibilities may include, but are not limited to, the following: - Under the direction of the Department Chair, successful applicants will

support the mission of the Nevada System of Higher Education, the College of Southern Nevada, the School of Science and Mathematics, and the Department of Biological Sciences by: - Teaching transferable, entry-level lectures and laboratories for BIOL 189 Fundamentals of Life Science, BIOL 190 Introduction to Cell and Molecular Biology, and one or more of the following: NRES 310 Wildlife Ecology and Management, BIOL 432 Herpetology, BIOL 433 Ornithology, and BIOL 434 Mammalogy (primary teaching assignment). - Applying a variety of instructional strategies appropriate to the needs of the student population and the standards of the discipline. - Developing clear syllabi and effective course materials. - Evaluating student mastery of skills and competencies required by course learning outcomes. - Participating in course and program assessment and curricular development. - Participating in discipline, department, and school meetings and activities. - Serving on department, school, and college-wide committees that focus on unit planning and institutional decision-making. - Establishing and maintaining positive working relationships with students, faculty, and staff of diverse ethnic, cultural, and socioeconomic backgrounds. - Teaching on multiple campuses during the day or evening hours.

KNOWLEDGE, SKILLS, AND ABILITIES (KSAs): - Knowledge of and ability to work effectively with State and Federal resource management agencies.

REQUIRED QUALIFICATIONS: - Master of Science degree in a biological science from an accredited College or University. - One year of experience teaching organismal biology at the college level.

PREFERRED QUALIFICATIONS: - Ph.D. in a biological science from an accredited College or University. - At least one year of experience teaching organismal biology at a community college. - At least one year of experience teaching herpetology, ornithology, or mammalogy at the college level. - Demonstrated experience with the use of technology in the classroom. - Demonstrated experience with assessment of course and program student learning outcomes. - Demonstrated experience working with a diverse/multicultural student body and/or workforce. - Demonstrated experience working with State and Federal resource management agencies.

SALARY: - Initial salary placement is based on educational level and total years of full-time equivalent teaching experience. For example, for an instructor with a Master's degree the salary range would be \$58,046 to \$74,304 annually. The entire salary range is up to \$89,166 annually with a Doctorate and 10 years' experience. A maximum of 10 years of experience will be considered for the initial salary placement purposes. *

About the College of Southern Nevada Founded in 1971 and situated in the greater Las Vegas metropolitan area, the College of Southern Nevada is the most ethnically diverse college in Nevada and the first to receive the HSI designation. We've prioritized providing an affordable, collaborative, and welcoming environment that allows all students to shine. CSN is a fully accredited institution offering hundreds of degrees and certificates in 70 academic programs. CSN proudly hosts students from all 50 states and over 60 countries with a student population that mirrors Clark County Nevada, one of the most diverse counties in the US. More than one-third of our students are first-generation, half are Pell Grant eligible, and nearly three-fourths are part-time. The College of Southern Nevada, a Minority Serving Institution designated as a Hispanic Serving Institution (HSI) and Asian American and Native American Pacific Islander Serving Institution (AANAPISI) provides associates and select bachelor's degrees. Consistent with CSN's mission, vision, and values we are passionate about fostering an environment where our highly diverse students achieve, succeed, and prosper.

Institutional Commitment to Diversity

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

StonyBrookUniversity Postdoc MicrobiomeTraitGenomicsModeling

Postdoctoral Associate: Metagenomic Trait Prediction and/or Modeling Microbial Systems Stony Brook University

The Microbial Genomes And Metagenomes to Unravel Traits Lab (mGAMUT Lab; PI: JL Weissman) at Stony Brook University (<https://microbialgamut.com/>) has openings for two postdoctoral researchers to begin in January 2026 (start date negotiable). We seek researchers interested in (1) building trait prediction models capable of resolving complex microbial traits from genomes and metagenomes, and/or (2) building mathematical models of microbial community dynamics (eco-evo) using a trait-based framework.

More info here: https://www.microbialgamut.com/mGAMUT_postdoc_ad_F26.pdf (to sub-

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SUNY Geneseo Teaching Quantitative Biology

The Department of Biology at SUNY Geneseo invites applications for a tenure track position at the rank of Assistant Professor to begin in August 2027. The department seeks a scientist with training in Quantitative Biology with a passion for teaching who will contribute to the broad education in biology we provide to our majors and to the college community. Expertise may include, but is not limited to, computational biology, mathematical biology, theoretical biology, modeling, biostatistics, and epidemiology. A strong applicant will demonstrate an ability to contribute to Geneseo's growing expertise in the areas of data analytics and bioinformatics. For full details of the position and how to apply, please visit: <https://jobs.geneseo.edu/postings/5643> The mission of the Department of Biology at SUNY Geneseo is to provide students from across New York State and beyond with a well-rounded background in biology, which can be used as a solid foundation for various careers in the biological sciences, health professions, and beyond. As a primarily undergraduate institution (PUI), we aspire to promote belonging among all our students, faculty and staff. This is achieved in part by having smaller class sizes ranging from 12 to 100 students per course, even in required and introductory courses in our popular and vibrant biology programs. Outside the classroom, undergraduate students work closely and directly with faculty to produce research and in other meaningful high-impact experiences, contributing to a high rate of students heading to graduate or professional school.

Our campus has a growing cohort of faculty teaching and working in data science, analytics, and applied AI across multiple departments in the Arts and Sciences and the School of Business. Recent hires, including in bioinformatics and data analytics, offer the opportunity for collaborations within and across disciplines. Geneseo also has two shared, Lambda workstations accessible to faculty and students suitable for research computing tasks, a GIS lab, and multiple computer labs.

The duties of the position include: -Teaching required courses in residence in the Biology programs and/or non-majors biology, and elective courses in quantita-

tive biology. -Developing and maintaining a research program in Quantitative Biology that engages undergraduate students from all backgrounds and generates scholarly products appropriate to the field. Faculty are strongly encouraged to apply for external funding for continuing appointment and promotion. -Academic advising and service to the department, the college, the community, and profession, including contributing to curriculum development in quantitative biology or bioinformatics

Required Qualifications: - PhD in relevant discipline (Biology, Chemistry, Biochemistry, Biostatistics, Bioinformatics, Computer science, etc.). Applicants for this position must have the conferred degree by the appointment date (September 1 2027) -Evidence of interest and ability to teach coursework in the subject of Quantitative Biology (e.g., biostatistics, etc.) and other courses in Biology (e.g., general biology, ecology, genetics, biochemistry, human biology, contemporary biology, advanced electives, etc.) to both introductory and advanced undergraduate students. -Potential to create and maintain a research program in Quantitative Biology that engages undergraduate students at a primarily undergraduate institution (PUI) -A commitment to fostering a welcoming, inclusive, and equitable working and teaching environment for all. -Ability and willingness to work in person on the SUNY Geneseo campus -Candidates for this position must be eligible to work in the United States. VISA sponsorship is not offered.

Preferred Qualifications: -Teaching experience and/or contributions to curricula in Quantitative Biology, or related courses -Research publications in peer-reviewed formats as appropriate to the field -Experience mentoring undergraduate students in research -Demonstrated engagement with building a culture of belonging in the workplace and/or teaching environments -Some post-doctoral and/or professional experience in Quantitative Biology

To apply, submit an online faculty application at <https://jobs.geneseo.edu/postings/5406> Please limit all documents except the CV to five pages total and address the required and preferred qualifications throughout. The application should include: - A Curriculum Vitae (CV) - A cover letter that addresses the required and any preferred qualifications - A statement of teaching interests and pedagogy - A research statement that addresses plans to include undergraduate students - In addition, applicants should be prepared to provide the contact information for three individuals who have agreed to supply a letter of reference.

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TechnicianPosition U Arizona MarineMicrobialEcologyAndBiogeo- chemistry

The Duhamel Lab at the University of Arizona (marine microbial ecology and biogeochemistry) is hiring a part-time Research Laboratory Technician to support a newly funded, three-year National Science Foundation (NSF Biological Oceanography) project carried out in collaboration with the Charvet Lab at Susquehanna University. The project investigates mixoplankton, which are single-celled marine organisms that can both photosynthesize like plants and eat prey like animals, and tests whether prasinophyte green algae switch from photosynthesis to feeding when phosphorus becomes scarce. The work combines continuous algal cultures, radioisotope tracer experiments (^{14}C and ^{33}P), flow cytometry, and transcriptomics to understand how these globally abundant organisms will respond to expanding nutrient-poor regions of the ocean. The technician will be a core member of the experimental team, working closely with the PI (Dr. Solange Duhamel) and a post-doctoral researcher at the University of Arizona, while also helping to coordinate experiments with collaborators at Susquehanna University. Please apply here: <https://arizona.csod.com/ux/ats/careersite/4/home/requisition/26957?c=arizona> Requests for information or inquiries about the position can be sent to: Valerie McClure Human Resources Generalist vmcclure@arizona.edu

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UGoettingenGermany ResearchAssociate GeneticAbundanceEstimation

We have a fulltime position for a research associate available in the Department of Wildlife Sciences at

the Faculty of Forestry Sciences and Forest Ecology, Georg-August-University Göttingen, Germany. The position will focus on the development of methods for genetic estimation of wildlife population sizes. Please see <https://www.uni-goettingen.de/en/644546.html?details=3373> for details and note the application deadline of Sept. 30th. Starting date is negotiable. For questions on the position, please email Niko Balkenhol (nbalken@gwdg.de)

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UHouston EvolutionaryBiology

The Department of Biology and Biochemistry at the University of Houston seeks to hire an evolutionary biologist at the rank of Assistant or Associate Professor. We are particularly interested in applicants with research interests and a record of accomplishments using quantitative approaches to study evolutionary biology. We encourage applications from individuals who will complement existing departmental strengths in evolutionary genetics, genomics, ecology, integrative biology, developmental biology, cancer biology, structural biology, and neurobiology and behavior. The successful candidate would be expected to establish and maintain a nationally competitive and externally funded research program and teach courses in Evolution and/or Genetics.

Applicants must hold a Ph.D. or equivalent doctoral degree in a relevant field. Candidates for appointment at the Assistant Professor level must demonstrate a strong publication record and the potential to establish an independent, externally funded research program. Candidates applying at the Associate level must have a well-established, externally funded research program and a strong record of independent scholarship and scientific leadership.

Salary and rank commensurate with experience.

Apply here: <https://careers.uh.edu/jobs/assistant-or-associate-professor-evolutionary-biology-houston-texas-united-states> The Department of Biology and Biochemistry has over 40 tenured and tenure-track faculty across three research divisions. The University of Houston is a public R1 institution with well-equipped shared resources, including high-performance computing in the Hewlett Packard

Enterprise Data Science Institute, a 925-acre Coastal Center as part of the Institute for Ecological Resilience, advanced microscopy instrumentation at the Biology and Biochemistry Imaging Core, and a Sequencing Core with modern equipment. The University of Houston is also a member institution of the Texas Medical Center and Gulf Coast Consortia, offering access to additional world-class resources, facilities, and collaborators.

Founded in 1927, the University of Houston serves more than 49,000 students across 15 colleges and is recognized for academic excellence, innovation, student success, and public service. Located in the heart of Houston (home to the Texas Medical Center, NASA's Johnson Space Center, a thriving energy industry, and a vibrant cultural scene) UH offers extensive industry partnerships and exceptional opportunities for experiential learning.

Application materials must include: 1) Cover letter, 2) Curriculum vitae, 3) Research statement (maximum 4 pages), 4) Teaching and mentoring statement (maximum 2 pages), 5) Three representative publications; and 6) Contact information for at least three references.

All application materials must be submitted electronically through the UH Job Portal. Review of applications will begin October 21 and will continue until the position is filled.

Please reach out to Rich Meisel (rpmeisel@uh.edu) with any questions.

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U Idaho Asst Prof Genetics Genomics

Assistant Professor in Genetics or Genomics University of Idaho Moscow, ID, USA

The Department of Biological Sciences invites applications for a full-time, academic year, tenure-track Assistant Professor position. We seek a highly collaborative scientist to establish a productive, extramurally funded research program in genetics or genomics. The successful candidate will build upon existing departmental strengths and align with our strategic priorities.

Duties include teaching an average of 1.5 classes per academic year in the medical sciences curriculum or other programs to meet the teaching needs of the department;

maintaining an active research program that includes securing external funding to support research activities in area of expertise; developing research collaborations across the college and university; mentoring undergraduate and graduate students; attending faculty meetings and departmental seminars; serving on department, college, and/or university committees.

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The Department of Biological Sciences offers undergraduate (Biochemistry; Bioinformatics; Biology; Medical Sciences; Microbiology) and graduate (Biology; Microbiology, Molecular Biology and Biochemistry (MMBB); Neuroscience) degrees. Faculty also participate in the Bioinformatics and Computational Biology interdisciplinary graduate program. The department hosts a supportive and collaborative community of researchers with internationally recognized strengths in evolutionary biology, microbiology, host-microbe interactions, genetics and genomics, cellular and molecular biology, ecology, and computational biology. Faculty benefit from numerous opportunities for interdisciplinary collaboration within the department and across the university.

We welcome applicants from all areas of genetics/genomics, including ecology, evolution, or conservation. Priority deadline approaching soon!

Apply here: <https://uidaho.peopleadmin.com/postings/52415> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

U Lausanne Switzerland **BehavioralEcology** **CulturalEvolution**

The Department of Ecology and Evolution (<https://www.unil.ch/fbm/en/home/menuinst/recherche/ssf/dee.html>) at University of Lausanne (Switzerland) is looking to hire a professor in the field of behavioral ecology and cultural evolution. A successful candidate will have expertise in behavioral ecology, cultural evolution, or evolutionary psychology, a strong research track record, and motivation to teach behavioral ecology and related topics. We are open to diverse profiles, with a preference for a person who can contribute to interdisciplinary research in the behavioral or cognitive sciences. You will bring expertise in principles of animal behavior and its evolution, learning and cultural transmission, and causal inference. Priority will be given to candidates who contribute to balance the diversity of organisms studied and to minimize the environmental impact of research programs. Preference will be given to a personality open to communication and cooperation, able to stimulate young colleagues. Managerial skills will be evaluated as part of the recruitment process. The position will be at Associate Professor level, tenured. This position entails the following responsibilities and expectations: an outstanding, internationally recognized, research program; a track record of securing competitive grants; and the ability to teach several courses while contributing to the administration and smooth operation of the department. Candidates at diverse levels of seniority are encouraged to apply. The position comes with a generous startup package and an annual research budget. Prior knowledge of French is not required, but we expect the candidate to be able to teach in French within two years. The research program is expected to contribute to the aims of both the Department and of the Sense (<https://www.the-sense.ch/?lang=en>) (interdisciplinary center for research, innovation, and training in sensory sciences). The Department of Ecology and Evolution covers the breadth of ecology and evolution and aims to cultivate an atmosphere of scientific excellence which is respectful of people. We are composed of 16 independent research groups working on a wide range of different ecological, evolutionary, and conservation biology topics that span fundamental and theoretical research through to more applied research, with nearly 100 postdocs and PhD students from over 30 nationalities. We share the campus and multiple collaborations with other departments, including both theoretical and experimental studies of behavior and of neurosciences, in the Faculty of Biology and Medicine (<https://www.unil.ch/fbm/en/home.html>) as well as in the Faculty of Business and Economics (<https://www.unil.ch/hec/en/home.html>), and there are many inter-departmental interactions and activities. Lausanne is a medium-sized city on the shores of Lake Geneva, surrounded by a wine growing region recognized as a UNESCO World Heritage Site, and within one hour of the Alps. It offers a great variety of cultural, recreational, and outdoor opportunities. For more information, contact Professor Marc Robinson-Rechavi (direction_dee.1@unil.ch). The official description of the position and information about the content of applications can be found here (<https://www.fbm.unil.ch/releve/application/announces/155>) (if a French version of the page opens, you can change to English by clicking in upper-right corner). While the contract is written "6 years, renewable", it is in practice a fully tenured position. Only applications submitted through that website can be considered. Deadline: 30 September 2026.

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UNC-CH Biology MCDB

The Department of Biology at UNC Chapel Hill (<https://bio.unc.edu/>) is searching to hire two tenure track Assistant Professors to study critical questions in Molecular, Cell, and Developmental Biology, broadly defined.

We seek candidates doing basic science driving at new fundamental discoveries using a variety of established, emerging, and new model systems. All candidates must have earned a Ph.D. or equivalent degree, have post-doctoral research experience, and be committed to teaching at the undergraduate and graduate levels. Successful candidates are expected to build an active re-

search group, secure competitive external funding, and participate in the scientific community at UNC-CH.

Therefore, a strong publication record and a track record of obtaining funding appropriate to career stage and eligibility will be considered favorably. Candidates are requested to specify in their cover letter what animal care facilities will be required to support their research program.

Find more information and apply here: <https://unc.peopleadmin.com/postings/325923> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

UniversityCambridge Prof Pathogen Genetics

Assistant/Associate Professor in Pathogen Genetics

<https://www.cam.ac.uk/jobs/assistantassociate-professor-in-pathogen-genetics-pc51175>
Applications are invited for an Assistant or Associate Professorship in Pathogen Genetics to be held in the Department of Genetics. We are searching for a talented individual with a track record of fundamental or applied research on the genetics of pathogens or host-pathogen interactions and a strong commitment to teaching. The post is available from 1st October 2027 or as soon as possible thereafter.

We welcome applications from researchers in the broad field of pathogen biology, whose research addresses fundamental questions at any level of biological organisation, including molecular and cellular mechanisms of infection, immunity and resistance, dynamics within hosts and populations, and evolution and population genetics. Research can focus on any pathogen or host, including humans, other animals and plants. We are particularly interested in candidates who use genetic and genomic approaches, whether experimental, computational or theoretical.

The successful applicant will have a PhD in a relevant subject area and show evidence of research excellence that is reflected in their published work (including pre-prints), as well as the vision and ability to attract grant funding to support an internationally leading research programme (including a track record commensurate with experience). Applicants will also have an aptitude and enthusiasm for teaching at undergraduate and postgraduate levels and will be expected to contribute

to the teaching and other academic activities in the Department. The successful applicant will be motivated to develop innovative teaching in the School of Biological Sciences, across areas such as genetics, pathogen biology, mathematical biology or evolution.

The Department offers an outstanding research and teaching environment with considerable strengths in pathogen biology, genome biology, evolution and population genetics, and computational and mathematical biology. The Department houses the Pathogen Dynamics Unit (PDU) <https://www.pdu.gen.cam.ac.uk>, a research grouping applying epidemiology, disease ecology, and traditional microbiology to real-world problems in human infectious disease through genomics, laboratory experimentation and mathematical modelling. We particularly welcome applications from individuals with impactful research programmes focused on computational and/or experimental approaches to pathogen biology that synergise with ongoing research in the PDU and the wider infection biology community across the School of Biological Sciences.

Across the Department and School of Biological Sciences we will provide laboratory and office space, and access to containment facilities, imaging, genomics and high-performance computing. The starting salary is dependent on the level of appointment being made, as determined by the Selection Committee. Assistant Professorships are in the range of GBP47,389 - GBP59,966 per annum; Associate Professorships are in the range of GBP63,606 - GBP67,468 per annum.

The Department is committed to the Athena SWAN Charter to provide equal opportunities and to advance the representation of women and other under-represented groups in science. The University actively supports equality, diversity and inclusion and encourages applications from all sections of society. Appointment will be based on merit alone. As a signatory of DORA (<https://sfdora.org>) the Department is committed to assessing research on its own merits not on the basis of the journal in which it is published.

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University Southern California Computational Biology Teaching Statistics

The Department of Quantitative and Computational Biology (QCB) in the Dana and David Dornsife College of Letters, Arts and Sciences of the University of Southern California invites applications for a teaching-track faculty position, instructor or lecturer, of Quantitative and Computational Biology. The ideal candidate will have expertise in quantitative, computational, and statistical approaches to solve fundamental questions in biology and biomedicine. The teaching activities of the successful candidate will primarily entail the teaching of statistics courses, including multiple sections of QBIO 305 Statistics for Biological Sciences, as well as the teaching and development of other computational biology courses. It is expected for the successful candidate to have a track record as researcher and educator in quantitative approaches to biology and to have rigorous training in statistics or biostatistics. The successful candidate will join the QCB Department, a group of 12 tenured/tenure-track, teaching, and research core faculty members. The QCB Department has a 45-year history of computational biology research and education, including a rigorous Ph.D. program in Computational Biology and Bioinformatics with 60 students, a Master's program in Quantitative and Computational Biology with 25 students, and an undergraduate major in Quantitative Biology with 130 students that represents modern biology education at the interface of biology, mathematics, and computer science. Members of the QCB Department work closely with other faculty in the Dornsife College of Letters, Arts and Sciences, the Viterbi School of Engineering, the Keck School of Medicine, and other USC schools. The QCB Department is located on the University Park Campus in Los Angeles, California. More information on the QCB Department can be found at: <http://dornsife.usc.edu/qcb/>. The anticipated start date is August 16, 2027. Applicants must have received a Ph.D. (or equivalent) degree by time of appointment and ideally have at least one semester experience as instructor of record of a computational biology course at a higher education institution. Review of applications will begin December 1, 2026. In order to be considered for this position, all candidates must apply via the "Apply" link at the top or bottom of

the page linked below. Please submit a cover letter, a curriculum vitae, a teaching statement, 3 current external letters of recommendation, and any other evidence of teaching effectiveness, including available teaching evaluations. Please direct inquiries to Rokas Oginskis (oginskis@usc.edu) The annual base salary range for this position is \$80,000 - \$90,250. When extending an offer of employment, the University of Southern California considers factors such as (but not limited to) the scope and responsibilities of the position, the candidate's work experience, education/training, key skills, federal, state and local laws, contractual stipulations, grant funding, as well as external market and organizational considerations.

<https://usccareers.usc.edu/job/los-angeles/full-time-teaching-track-faculty-position-in-quantitative-and-computational-biology/1209/94300113920> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net)

U North Texas Assistant-Associate Professor in microbiome research

The Department of Biological Sciences at the University of North Texas (UNT), a Hispanic-Serving Institution and Carnegie R1 Research University, invites applications for a tenure-track Assistant Professor position in Microbiology, with an emphasis on microbiome research as it pertains to organism health and interactions with the environment. The faculty member will contribute to and collaborate with ongoing basic and applied research programs within the Department, as well as the College of Science's Health Sciences cluster-hire initiative. We are interested in a broad range of research areas, and model or non-model systems.

Exceptional candidates with significant experience at the Assistant Professor level, or equivalent, may be considered for hire at the Associate Professor level.

The successful candidate will contribute to a strong tradition of interdisciplinary and collaborative research at UNT by interacting with diverse faculty, staff, and students within and between departments and institutes at the university, including members from the Advanced Environmental Research Institute (AERI) and the BioDiscovery Institute (BDI). This position will complement recent hires in microbiology, biochemistry, environmental science, and health-related fields in the

Department of Biological Sciences at UNT.

More information is available at: <https://careers.untsystem.edu/jobs/assistant-associate-professor-of-microbiology-denton-texas-united-states> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UOklahoma Associate Full ProfessorMicrobiomeResearch

Associate / Full Professor of Biological Sciences - Microbiome Research - George Lynn Cross Endowed Chair University of Oklahoma Norman Campus: Dodge Family College of Arts and Sciences: Biological Sciences Location University of Oklahoma-Norman Campus

Description Description: The School of Biological Sciences (<https://www.ou.edu/cas/biological-sciences>) (SBS) at the University of Oklahoma (OU) invites application for a full-time 9-month tenured or tenure-track position Associate or Full Professor with a start date of August 2027, and will maintain a 1:0 teaching load as a condition of being appointed to the endowed chair position. We seek an innovative, creative, and collaborative colleague with a record of leading scholarship in microbiomes who will bring a highly productive, cross-disciplinary, and externally funded program of scholarship to OU. The ideal candidate will have demonstrated success in using a combination of empirical and computational approaches to problems in metabolic processes. Areas of interest include regulation of inflammation, bacterial pathogenesis, and microbiome-immune system interactions. Further, the successful candidate will have: (1) a record of forming and leading productive interdisciplinary or transdisciplinary teams that work on advancing fundamental knowledge of the role of microbiomes in disease; (2) successfully built collaborations within and outside their institution; and (3) mentored research trainees and taught courses related to the microbiome. The SBS has integrated research strengths in One Health, Behavior, Ecology, and Evolution and is growing in alignment with the Lead On Strategic Plan (<https://www.ou.edu/leadon>); particularly in areas that complement strengths of the OU Health Campus. OU invests in its faculty by providing support and resources through the Center for Faculty Excellence (<https://www.ou.edu/cfe>) and Vice President for Research and Partnerships Office (<https://www.ou.edu/research-norman>). The Dodge

Family College of Arts and Sciences supports faculty development through mentoring, new faculty orientation series, and access to research and educational support. We encourage candidates to apply who are seeking to work in a rapidly growing college with collegial interdisciplinary groups and strong academic units.

University of Oklahoma The University of Oklahoma (OU) is a Carnegie-R1 comprehensive public research university known for excellence in teaching, research, and community engagement, serving the educational, cultural, economic, and healthcare needs of the state, region, and nation from three campuses: Norman, Health Campus in Oklahoma City and the Schusterman Center in Tulsa. OU enrolls over 32,000 students and has more than 2,700 full-time faculty members in 21 colleges.

The Norman Community Norman is a vibrant university town of more than 130,000 inhabitants with a growing entertainment and art scene. With outstanding schools, amenities, and a low cost of living, Norman is a perennial contender in "best place to live" rankings. Visit <https://www.ou.edu/facultyrecruitment> for more information. Within an easy commute, Oklahoma City features a dynamic economy and outstanding cultural venues adding to the region's growing appeal.

Qualifications Required Qualifications: -Ph.D. in Microbiology or a related discipline. -Established record of forming and leading research teams. -Sustained record of high-quality research and publications on microbiomes. -Demonstrated record of sustained nationally competitive extramural funding for research on microbiomes. -Record of scholarship sufficient for appointment as an Associate or Full Professor.

Preferred Qualifications: -Demonstrated record of excellence in teaching. -Familiarity with effective teaching practices and mentoring approaches that support students from a wide range of backgrounds. -Evidence of ability to build partnerships within and across institutions. -Demonstrated experience in convergent and interdisciplinary or transdisciplinary approaches to scholarship.

Application Instructions

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UWyoming Assistant Professor Plant Fungal Genomics

Assistant Professorship in Plant or Fungal Genomics at the University of Wyoming The Department of Botany and the School of Computing at the University of Wyoming are searching for an Assistant Professor (tenure-track) in Plant or Fungal Genomics who addresses fundamental questions in evolutionary biology using computational approaches and genomic data. Scientists with expertise in population genomics, phylogenomics, or any area of evolutionary biology incorporating the generation and analysis of genomic data are especially encouraged to apply. We welcome research that advances understanding of the evolutionary and genomic processes shaping plant or fungal diversity, resilience, symbiosis, ecosystem function, or agricultural systems. This faculty member will also contribute to the university's genomics infrastructure through active involvement and collaboration with the Genome Technologies Lab (GTL). Strong potential for engagement and collaboration with resources such as the Rocky Mountain Herbarium and high-performance computing resources will be looked upon favorably. The appointment will be 75% About the Department of Botany The Department of Botany is an interdisciplinary, collaborative department focused on conducting innovative research, teaching and outreach on the patterns and processes of life. Our research spans broad areas of the ecology and evolution of plants, animals, ecological and evolutionary theory, and statistical developments for the life sciences. We are part of UW's College of Agriculture, Life Sciences, and Natural Resources, and contribute strongly to the University's land-grant mission. The Botany Department is unique at UW in our focus on fundamental research and teaching in biology and biodiversity at population, community, and ecosystem scales. Our faculty conduct basic and applied research relevant to the state, nation and globe. Topics include ecological disturbance, invasive species, symbiosis, global climate change, ecohydrology, forestry, and conservation genetics. Within the department, we offer a B.S. and M.S. in Botany, a B.S. in Biology, and our faculty participate in several interdisciplinary degree programs, including the PhD Program in Ecology and Evolution.

About the School of Computing The School of Com-

puting is dedicated to advancing the use of computing across disciplines while equipping students with essential digital and computational skills. The school emphasizes interdisciplinary, translational research that applies state-of-the-art computing to society's grand challenges. Most faculty in the School of Computing have joint appointments with other academic units or programs, so that research areas span varied applications including animal behavior, astrophysics, atmospheric science, archaeology, computer science, ecology, hydrology and mathematics. The University of Wyoming has access to various computing resources including the Advanced Research Computing Center (ARCC) and Wyoming INBRE Data Science Core. In addition to on-campus resources, the University has a longstanding partnership with the National Center for Atmospheric Research (NCAR) and the NCAR-Wyoming Supercomputing Center, providing dedicated resources for UW researchers.

About The University of Wyoming The University of Wyoming is located in Laramie, a town of 30,000 in southeast Wyoming in the heart of the Rocky Mountain West. Laramie is located in a high mountain valley 20 minutes from the Colorado border and less than 2.5 hours from Denver's international airport. This beautiful mountain landscape offers outdoor recreational opportunities in all seasons in its nearby mountain ranges to the east and the west. How to Apply Candidates must have a Ph.D. in ecology and evolutionary biology or a related field at the time of hiring, excellent written and oral communication skills, high potential for an extramurally funded research program, and demonstrated capacity for effective teamwork and collaboration. Potential candidates should visit the job description at:

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WashingtonU in St. Louis Cluster Hire AI for Modeling The Physical World And Living Systems

Cluster hire in AI for Modeling the Physical World and Living Systems Washington University in St. Louis - Danforth Campus: School of Arts & Sciences

Description: Washington University in St. Louis invites applications for multiple tenure-track faculty positions at the rank of Assistant, Associate, or Full Professor for a +AI cluster search spanning the departments of Biology, Chemistry, Philosophy, Physics, Psychological & Brain Sciences, and Statistics & Data Science. Faculty recruited through this process will join a vibrant cohort of faculty recruited in an earlier Rules of Life search undertaken to promote transdisciplinary collaboration and dialogue to explore fundamental questions regarding living systems and the physical world.

Life operates across a diversity of scales, from molecular-scale processes shaping cellular function to the delicate dynamic balance of our biosphere as a whole. System-level properties and processes are affected by interactions operating at all scales and between scales. Understanding these interconnected systems requires an interconnected and multidisciplinary research community. From AI-driven advances in protein structure and dynamics, to advanced imaging methods enabled by quantum sensing, to imaging and modeling the human brain and behavior, to developing entirely new mathematical and computational frameworks to achieve insight from complex data, transformative advances in life sciences will require the integrated efforts of scientists and scholars working across disciplinary boundaries. Moreover, these advances will be accelerated through the combination of artificial intelligence and machine learning with other experimental and computational approaches. Finally, advances in science and technology raise foundational questions about the nature of artificial and natural intelligence, and how they relate to conscious experience and human values.

We anticipate multiple hires to expand upon a successful Rules of Life cluster search and to create a robust hub of science researchers and philosophers using diverse yet interconnected methods to advance life sciences from molecular to ecological scales while also considering the relationship between AI and humanity. Preference will be given to applicants whose research combines AI-driven inquiry with experimental, computational, or data-science methods, and who demonstrate synergy with current areas of strength at Washington University. Joint applications exhibiting a high degree of potential for research collaboration will also be considered. For more information about this search, specific AI-related themes and contacts for search-related questions, visit <https://insidearts.ci.washu.edu/rules-of-life>. Duties will include conducting research, teaching, advising students, and participating in departmental governance and university service. WashU aims to create an environment that encourages and supports wide-ranging exploration

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

Application Instructions For fullest consideration, applications should be submitted by October 1, though review will continue until available positions are filled.

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WildCommResearchStations ZA

Internship opportunity for evolutionary biologists

Field Research Experience & Independent Projects - South Africa - About Planning your own research project, testing an idea in the field, or building experience for future studies? WildComm Research Stations offers a supportive field-based research setting within a protected private reserve in South Africa, where you can develop projects, test methods and gain hands-on conservation research experience. What We Offer WildComm is situated on a private reserve, with di-

verse wildlife, vegetation and complex savanna ecosystems where you can work with access to on-site research equipment and support from experienced conservation professionals. Research Your Own Project - Behavioural & movement ecology - Population monitoring - Vegetation - Interdisciplinary conservation projects Build Field Research Experience - Test research methods - Conduct pilot or exploratory studies - Build field and data-collection skills - Prepare for future Bachelor's or Master's research Location: Limpopo, South Africa Position: Research placement Start Date: Year-round, with flexible stays from short-term exploratory work to long-term research projects. Monthly Rate: GBP700 per person, including accommodation, research supervision and research equipment. Travel, insurance and meals are not included.

Candidate Requirements - Comfortable working independently and as part of a team - Able to work on foot over uneven terrain and in variable weather - Moderate fitness level (endurance improves with experience) - Careful and reliable approach to data collection and management - No prior field experience required Suitable both for participants bringing their own research project and for those wanting to develop field research skills or prepare for future academic research. How to Apply Please send your CV and a cover letter to applications@wildcomm.org

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YaleU Wu Tsai Institute

The Wu Tsai Institute (WTI) at Yale University seeks candidates for an endowed tenure-track faculty position with a focus on researchers with an integrative

approach, driving experimental or conceptual innovations to advance our understanding of cognition within its broader ecological, biological, or societal contexts, including interactions with technology.

Applicants from a broad range of disciplines, models, and approaches are encouraged to apply. Successful candidates will receive a tenure-track appointment in one or more departments in the Yale Faculty of Arts and Sciences, School of Engineering and Applied Science, and/or School of Medicine. Faculty identified through this search will receive an attractive start-up package, join a growing community of ~220 faculty across Yale, and have access to state-of-the-art lab space and core facilities in our new research building, as well as special funding mechanisms, fellowships for postdocs and students, and other events and programs.

Founded by a historic gift, WTI is dedicated to advancing our understanding of human cognition and human potential by sparking interdisciplinary inquiry. We are building a vibrant community where experimentalists and theorists work together to integrate approaches across disciplines through common mathematical, statistical, and computational frameworks. We foster a welcoming environment that provides equal opportunity to people of a broad range of backgrounds and perspectives.

For more information and to apply, please visit <https://apply.interfolio.com/189343>. The deadline is October 15, 2026.

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Books on Experimental Evolution

Rees Kassen. 2024. Experimental Evolution and the Nature of Biodiversity 2nd ed. Oxford University Press. Sketches a general, empirically grounded theory of biodiversity and is the first synthetic treatment of experimental evolution.

Tony Dean and Dan Dykhuizen. 2026. Experimental Evolution: The Making of A Modern Science. CRC Press. Explores the causes of natural selection from the molecular level through to meta-populations while providing a critical assessment of the literature.

Michael R. Rose , Richard E. Lenski, Margarida Matos, Joseph L. Graves Jr. 2026. A Primer For Experimental Evolution. Dimensions. Provides an introduction to long term evolution experiments and quantifying evolutionary changes using genomic methods.

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New version of Myriads software v1

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Dear Evoldir members, A new version of the Myriads software (v1.4) for multiple hypothesis testing, together with the updated program manual, is now available at: <https://myriads.webs.uvigo.es/> This version includes several corrections and performance improvements: 1. Fixed a minor bug in Binomial SGoF p-value computation. 2. Corrected an edge case in the G-test involving zero observed counts. 3. Reimplemented the exact Binomial SGoF adjusted p-value algorithm to improve performance. 4. Improved the numerical evaluation of binomial tail probabilities. 5. Optimized the computation of G-SGoF adjusted p-values and added protection against floating-point rounding errors. 6. FWER and FDR .txt output files are now overwritten at each run instead of accumulating results from previous runs. Myriads is written in C++11 and is

available as a binary executable for Windows, macOS, and Ubuntu. Source files are also provided, together with a makefile for compilation on Linux and macOS. For questions about the software, please contact me at myriads@uvigo.es or acraaj@uvigo.es. Best wishes, Antonio

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Open Access to new book The Selective Organism-an Expanded Theory of Adaptive Evolution OUP

Hello everyone, My book "The Selective Organism - An Expanded Theory of Adaptive Evolution" is now published (Oxford University Press). Here is a link to its website (<https://global.oup.com/academic/product/the-selective-organism-9780198876007?cc=es&lang=en&%23>), which provides further information. Thanks to funding from the Spanish Ministry of Science, the book is not only available in print but also available under Open Access (i.e., can be downloaded as pdf for free): link to downloadable version (<https://academic.oup.com/book/63165?login=false>). In this book I take a hard look at the classical requirements for adaptive evolution - variation, selection, and inheritance. I find that our biological interpretations of each can, and probably should, be expanded. I then combine these three expanded interpretations into a single causal model, and analyse the consequences of these expansions for the process of evolution. And I find that these expansions result in some interesting known phenomena, but that they also generate a novel second driver of adaptive evolution (besides the well-known driver of natural selection on genetic variation). This second driver nicely unifies a variety of seemingly unrelated biological phenomena, such as evolution via epigenetic inheritance or via habitat choice, and cultural evolution. If you want to know more what this expanded and more general framework is all about, then a good place to start is the Preface (<https://academic.oup.com/book/63165/chapter/568747047>).

This will give you a quick overview of the contents of the book, and whether it is interesting for you, for your students, for your literature discussion group, for other people you know (including non-biologists), etcetera. I made the book freely available because I would like people to read it and to find it useful. So please feel free to share my email with others or some mailing lists, talk about it in person or on social media, approach a journal to write review, recommend it to your institutional library, or let people know about its existence by any other way you can think of. Best wishes, Pim (edelaar@upo.es) Full professor, University Pablo de Olavide, Spain Guest professor, Lund University, Sweden

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Quantifying Analytical Variation in Species Delimitation

QUANTIFYING ANALYTICAL VARIATION IN SPECIES DELIMITATION A multi-investigator assessment of species delimitation practices

Why are we doing this?

Species delimitation lies at the heart of evolutionary biology, systematics, and conservation. Yet speciation is a continuous process, meaning that species boundaries are often subjective. We invite the evolutionary biology community to participate in a collaborative experiment examining how analytical choices and interpretation influence species delimitation. Our goal is not to identify a single correct answer, but to quantify variation among researchers and explore its implications.

This project is NOT

- A competition among methods
- An attempt to identify the 'best' workflow
- An evaluation of individual researchers

Instead, this project aims to

- Quantify variation in analytical decisions
- Explore how interpretation influences biological inference
- Discuss implications for evolution, taxonomy, and conservation

Project workflow

Phase I - Blind species delimitation

- Receive a blinded genomic dataset in several formats.
- Analyze the data using your preferred methods.
- Determine the number of species and assign individuals.
- Submit results within approximately three months.

Phase II - Revisiting your conclusions

- Receive additional taxonomic, phenotypic, and geographic information.
- Keep or revise your conclusions based on the new evidence.
- Submit your final interpretation within approximately two months.

Ground rules

- Work independently (labs should submit one joint analysis).
- Do not discuss analyses with other participating groups.
- Contact us with questions rather than other participants.

Optional call for datasets

We are also seeking empirical datasets for this project. Ideal datasets:

- Contain genomic data suitable for species delimitation.
- Include independent ecological, morphological, or geographic information.
- Represent challenging evolutionary scenarios (e.g., introgression, hybridization, recent divergence).
- Are unpublished or only partially analyzed.

Why participate?

- Contribute to a unique community-wide experiment.
- Help improve understanding of species delimitation practices.
- Be invited to join the resulting manuscript as a co-author.

The concept has received encouraging feedback from the editors of Systematic Biology, who considered it a timely and worthwhile research direction. Interested in participating?

Participation form: <https://forms.gle/Cz7jf4N5BZw2N2LG9> Call for datasets: <https://forms.gle/vPN75k4yyH84cbdW8> Contacts

Bhuwan Singh Bist PhD Candidate, Jezkova Lab [bist](#)

bs@miamioh.edu

Dr. Tereza Jezkova Associate Professor of Biology Miami University jezkovt@miamioh.edu

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RecMapDB-open database of eukaryote recombination rates contributions welcome

Dear colleagues, I have released RecMapDB, an open, community-extensible database of genome-wide recombination rates estimated from published linkage maps across eukaryotes: <https://github.com/jessstapley/RecMapDB> doi:10.5281/zenodo.22769468 The database is seeded from our paper Stapley et al. (2017, Phil. Trans. R. Soc. B, doi:10.1098/rstb.2016.0455) and has been extended and re-curated. It currently holds 494 linkage map records across 459 species (animals, plants, fungi and protists), every record linked to its source publication, with recombination rate derived for 483 of them. Every value carries its provenance - the reference DOI for each map, and the assembly accession or C-value source for each genome size - and all data are plain CSV under a CC0 licence, readable directly into R or Python from the repository (see the README for one-line examples). I would like to continue to build this database and this is where I would welcome your help. If you have built a linkage map for any eukaryote please consider uploading the information to the database. Contributors are credited as authors on the citable dataset releases. Adding it takes a few minutes. Either open an issue on the repository, choose "Add a linkage map record", and fill in the form (DOI, species, map length, marker and linkage-group counts). Larger contributions can come as pull requests. Or if you don't have a GitHub account you can download the template spreadsheet fill it in and send it to me. I also appreciate any corrections - a wrong genome size, a better reference, a map we have mischaracterised. Records that fail quality criteria are flagged rather than deleted, so the full history of every value is visible.

Best wishes, Jessica Stapley jessstapley@me.com <https://github.com/jessstapley/RecMapDB> <https://doi.org/10.5281/zenodo.22769468> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

ScientificIllustrator AvailableForCommissionedWorld

Scientific illustrator available for commissioned work: I am a scientific illustrator trained in biology looking for new opportunities to collaborate with researchers, journals or other science communication outlets. If you are interested in getting your science illustrated for research, teaching or outreach, you can access my portfolio, including examples of published work - graphical abstracts, figures, cover art, and other illustrations in classical naturalist and digital styles - here www.lalealpar.com or contact me at illustrator@lalealpar.com (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Systematics Association Founders Lecture

WHAT: Systematics Association Founders' Lecture 2026

WHERE: The Linnean Society, Burlington House, London, UK

WHEN: 6PM Thursday October 8th 2026

We are delighted to announce that this year's Founders' Lecture will be delivered by Dr Mark Wilkinson, The Natural History Museum, London, who served as Association President between 2016 and 2019.

TITLE: Caecilians and the growth of knowledge

ABSTRACT: When I was growing up what was best known about caecilian amphibians was how poorly known they were. I became fascinated by them and by this lack of knowledge. In this talk I will give a quasi-autobiographical review of caecilian biology that highlights some amazing biological discoveries and advances in caecilian systematics while reflecting on scientific progress and its problems as exemplified by caecilian biology.

REGISTER: <https://forms.gle/UyyPzcfdwseJRdmy7> The event is free but we ask that you register, so

we can plan appropriately for the post-lecture off-site reception.

– Ana Serra Silva Communications Officer for the Sys-

tematics Association

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BallStateU ConservationGenomics

A full-time postdoctoral researcher position in conservation genomics is available in the Department of Biology at Ball State University (Muncie, IN), with field

research conducted at the Southwestern Research Station (SWRS) in Portal, AZ, and partner sites. Position Overview: The successful candidate will direct Chiricahua Leopard Frog breeding experiments at field sites during the summer breeding seasons and lead genomics projects, sample processing, and bioinformatic analyses during the academic year. The postdoc will integrate research efforts across academic and conservation partners, mentor undergraduate researchers, present find-

ings at conferences, and lead peer-reviewed publications. Start Date & Compensation: - Start Date: May 2027 - Salary: \$62,374 (full-time, grant-funded) - Benefits: Comprehensive benefits package Qualifications: - Minimum: Ph.D. in biology, conservation genomics, applied wildlife biology, evolution and ecology, or a closely related field by date of appointment; at least one year of research experience in a university setting. - Preferred: A blended background in conservation genomics and applied wildlife biology with an interest in bioinformatics; experience with amphibian husbandry; experience coordinating remote fieldwork logistics; strong collaborative skills across conservation agencies, non-profits, and academic partners; and experience mentoring undergraduate researchers.

To Apply: Applications must be submitted through the Ball State University job portal: https://bsu.wd12.myworkdayjobs.com/en-US/External/job/Postdoctoral-Researcher-in-Conservation-Genomics_R-02991 Required materials include a Cover Letter and CV/Resume (please do not use the portal's autofill feature when uploading). Application Deadline: September 29, 2026 (12:01 AM) For informal inquiries or questions about the position, please contact Dr. Robert Denton at robert.denton@bsu.edu. Ball State University is an Equal Opportunity/Affirmative Action employer.

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BielefeldU CollectiveBehaviour Dispersal

Postdoctoral Research Position in Evolutionary Biology - Bielefeld University, Germany The Department of Evolutionary Biology at Bielefeld University invites applications for a full-time postdoctoral researcher (E13 TV-L, 2 years) to join a DFG-funded project investigating how individuals balance cooperation and competition when making collective decisions that affect dispersal success and survival. The project uses the nematode *Caenorhabditis elegans* as an experimentally tractable model system and combines behavioural experiments, quantitative analyses of natural populations, and evolutionary approaches. We will investigate how social interactions, genetic relatedness and phenotypic plasticity influence individual dispersal strategies under changing ecological conditions. We are looking for

candidates with a PhD in evolutionary biology, ecology, zoology, animal behaviour, behavioural ecology, or a related field, experience in hypothesis-driven experimental research, and quantitative data-analysis skills (R, Python and/or MATLAB). Experience with nematodes/invertebrate model systems, fluorescence microscopy, image analysis, automated behavioural tracking, or genetic approaches would be advantageous. The position offers substantial scope for developing independent research questions within the broader project, as well as opportunities for scientific publications, conference presentations and further academic development. Start: as soon as possible and no later than February 2027 Duration: 2 years Position: Full-time, E13 TV-L Location: Bielefeld, Germany Application deadline: 25 September 2026 Full details and application portal link: https://jobs.uni-bielefeld.de/job/view/5138/research-position-m-f-d-postdoc?page_lang=en&utm_source=chatgpt.com For informal enquiries: daniela.malgarini@uni-bielefeld.de

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CornellU Evolution Populationgenetics Speciation

A postdoctoral position is available in the Shaw lab at Cornell University, Ithaca, NY, USA. The Shaw lab engages in interdisciplinary studies centered on the origins of species, asking questions about behavior, evolution, genetics, ecology and phylogeny. The postdoc will contribute to our NSF funded studies of the genetics of natural populations and artificial selection of mating songs and preferences in the Hawaiian cricket *Laupala*. The primary role of the post doc is to engage in innovative research designs to analyze the role of linkage disequilibrium/genetic correlations of mate recognition behaviors in natural and artificially selected cricket populations, and their relationship to speciation. Techniques to be employed include selection line analyses, genomic sequencing and associated bioinformatic and statistical analyses to answer questions about the population genetics of natural populations. It is expected that the postdoc will write up the results for publication in quality peer-reviewed scientific journals and will present the work at national and/or international research conferences. The successful candidate will enjoy a high degree of intellectual and day-to-day independence, enabling valuable interactions within the

larger community of evolutionary biologists at Cornell. The successful candidate will hold a PhD degree in a relevant life sciences field, have experience in genomics and DNA sequencing and associated statistical and bioinformatic expertise. Strong candidates will show independence, effective oral and written communication skills, and past mentorship experiences. Continued professional training and postdoctoral mentoring will be supported. To apply: Applications received before Oct . 1, 2026 will receive priority. Please submit (to KLS4@cornell.edu) a CV and cover letter describing your research experience, interest in the position, employment history and/or timeline for completion of the PhD. Please include the names and contact information for two referees. A full list of Shaw Lab publications is available on Google Scholar under Kerry Shaw. See also: <https://shawlab.weebly.com/>. (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

DEE ULausanne Switzerland Quantitative evolutionary genetics of experimental evolution in plants

Postdoctoral position: Quantitative evolutionary genetics of experimental evolution in plants Department of Ecology and Evolution, University of Lausanne, Switzerland A postdoctoral position in plant evolutionary biology is available in the research group of John Pannell in the Department of Ecology and Evolution at the University of Lausanne. The position is initially for one year, with the possibility of extension for up to five years.

The successful applicant will investigate the quantitative genetics and genomics of rapid evolutionary change in sex allocation, mating systems and sexual systems in the annual plant *Mercurialis annua*. The project builds on a unique long-term experimental-evolution study that has been running for approximately 15 years. The experiment exploits the remarkable diversity of sexual systems found within *Mercurialis*, in which closely related species and natural populations vary in the expression of combined versus separate sexes. In our experimental populations, removal of males from initially dioecious populations led to the rapid evolution of male function in females and the breakdown of dioecy. Continued experimental evolution has subsequently produced striking further changes in sex allo-

cation, including the emergence and spread of a novel, strongly male-specialised phenotype. The advertised position offers an unusual opportunity to study evolutionary transitions in real time. We have extensive phenotypic and genomic data documenting evolutionary change through the experiment, together with stored material from successive generations that permits direct comparisons between ancestral and evolved populations. Resources are available for further experimental work with evolved populations and for genomic, transcriptomic and quantitative-genetic analyses. The project is running in parallel to a more recently begun experimental study of responses to selection under different regimes of admixture at and beyond species range margins; there will be opportunities to contribute to this research too, depending on the interests, expertise and creativity of the successful candidate.

For details of current research in the laboratory and a list of publications, see <https://www.unil.ch/dee/pannell-group>. Research scope and skills sought We are looking for an evolutionary biologist with a strong interest in using genomic, transcriptomic, quantitative-genetic and phenotypic data to address fundamental questions in evolution. Candidates should have a strong conceptual foundation in evolutionary biology, population genetics and/or quantitative genetics, together with skills in bioinformatics and statistical analysis. Particularly relevant expertise would include the analysis of whole-genome sequence data, population-genomic data, transcriptomic or gene-expression data, quantitative phenotypic data, or some combination of these. Experience in experimental design and the analysis of complex evolutionary experiments would be valuable. We are particularly interested in candidates who combine technical strength with conceptual curiosity: the experimental system provides considerable freedom to formulate and test new evolutionary hypotheses, and we would expect the postdoc to play an important role in shaping the direction of the research.

The successful candidate should also have excellent communication and interpersonal skills, an ability to work collaboratively, and an enthusiasm for contributing to the intellectual life of a diverse research group

Host department and university The Department of Ecology and Evolution at the University of Lausanne hosts a broad range of research groups, and its members enjoy a lively intellectual and social life. Although the University of Lausanne is francophone, the department is highly international, and all its research activity and seminars are conducted in English. The University has seven faculties and approximately 14,300 students and 3,900 researchers from over 120 countries. It is situated on a beautiful campus on the shore of Lake Geneva, and

is close to the Swiss and French Alps.

Applications Informal enquiries should be sent to John Pannell (john.pannell@unil.ch). Formal applications should be sent to John Pannell as a single pdf that should include: a cover letter detailing your research interests, experience and motivation for applying; your CV; and the names of two or three referees. In addition, you will also need to upload your application to the University of Lausanne recruitment platform following this link: <https://tinyurl.com/56ny3nsf> All applications received by 30 September 2026 will receive full consideration.

University equality policy

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

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

Duhamel Lab UArizona USA Marine Microbial Ecology

Postdoctoral position in Marine Microbial Ecology The Duhamel Lab at the University of Arizona (Marine Microbial Ecology and Biogeochemistry) is hiring a Postdoctoral Research Associate in Marine Microbial Ecology. In this role, you will lead NSF-funded laboratory research (the P-MixSwitch project, in collaboration with Susquehanna University) investigating whether prasinophyte mixoplankton switch from photosynthesis to prey ingestion when phosphorus becomes scarce. Please apply here: <https://arizona.csod.com/ux/ats/careersite/4/home/requisition/27025?c=arizona> Requests for information or inquiries about the position can be sent to: Valerie McClure Human Resources Generalist vmcclure@arizona.edu

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Edinburgh GermlineChromosomeEvolution

Dear all,

I am recruiting a postdoctoral researcher to investigate one of the most striking departures from conventional genetics: why fungus gnats carry chromosomes that are retained in the germline but systematically eliminated from somatic cells. Working with Bradysia coprophila, the project will explore how these germline-restricted chromosomes are maintained, how they are regulated epigenetically, and whether they provide essential functions for germline development or represent selfish genomic elements tolerated by the host. We are particularly interested in candidates who enjoy combining lab-based chromosome and molecular biology with bioinformatic analysis of genomic and epigenomic data. The project will establish Bradysia as a powerful model for understanding genome regulation, chromosome inheritance, and programmed DNA elimination.

The position is fixed-term until July 2028 (starting asap) and will be based at the School of Biology at the University of Edinburgh. Closing date is the 7th of September

Further details about the position and how to apply are available here https://elxw.fa.em3.oraclecloud.com/hcmUI/CandidateExperience/en/sites/CX_1001/job/14867 Please email me directly if you have any questions,

best wishes, Laura Ross Chair of non-Mendelian genetics

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Goodheart Lab AmericanMuseumNaturalHistory Postdoc

Dear Colleagues, The Goodheart Lab in the Division of Invertebrate Zoology at the American Museum of Natural History is seeking a full-time Postdoctoral

Fellow (three-year term) to perform comparative genomic, transcriptomic, and functional analyses and experiments with mollusks on a Human Frontiers Science Program grant in collaboration with Dr. Victoria Sleight at the University of Aberdeen and Dr. Manabu Bessho-Uehara at Tohoku University. The overall aim of the grant is to understand the role of gene family expansions in the evolution of novel complex traits in mollusks, and the role of the Postdoctoral Fellow will be to investigate the molecular evolution and diversification of molluscan pattern recognition receptors and perform functional experiments with the nudibranch species *Berghia stephanieae*. Applicants may apply at <https://careers.amnh.org/postings/4920/>. First review will be Nov 10th, 2026. We are looking for someone to start before April 2027.

Best, Jessica

– Dr. Jessica Goodheart (she/her) Assistant Curator, Invertebrate Zoology Assistant Professor, Richard Gilder Graduate School American Museum of Natural History

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GreifswaldU Germany Postdoc position in Evolutionary Biology

Job announcement

University of Greifswald, Department of General and Systematic Zoology

Research Associate (post-doctoral researcher) in Evolutionary Biology

Application deadline: 31.10.2026

The Uhl-Group of the Zoological Institute and Museum at the University of Greifswald is seeking to fill a position of a Research Associate (m/f/d) in Evolutionary Biology (40h/week) Starting date: preferably from 01. February 2027 The position is suited for qualification on the post-doc/habilitation level. The contract will be issued for an initial period of three years. After positive evaluation and the fulfilment of the legal requirements, the position can be extended for a maximum of another three years.

Within an evolutionary framework, the Uhl-Group

investigates i) reproductive strategies, including behaviour and functional morphology, ii) chemosensing, including ultrastructural, molecular and electrophysiological aspects, iii) adaptations to changing environments using behavioural, morphological and genetic methods. We mainly work on spiders, millipedes and beetles. [https://zoologie.uni-greifswald.de/en/organization/departments/general-and-systematic-zoology/Your Profile - University degree \(PhD\) in biological sciences - research is based on evolutionary biology. Focus can be on reproductive biology, behavioural ecology, functional morphology, population genetics, gene expression analysis - ideally, several of these aspects are covered - research topics with arthropods as model organisms due to existing infrastructure is favourable - development of a coherent concept for the integration of your own research topics in the department - strong publication record and interest in acquiring external funding - teaching experience either in zoology, evolutionary ecology, and behavioural ecology - or in combination - very good oral and written communication skills in English - Basic knowledge of the German language to support teaching in the Bachelor's degree programs - ability to work both independently and as part of a team Main Responsibilities: - Participation in the fulfilment of the teaching obligations of the department with 4 CPs \(Practical courses in Systematics/Anatomy of animals in the bachelor programme; Evolutionary Ecology in the Master programme "Biodiversity, Ecology and Evolution", Excursions\). - Active participation in the research projects of the department with your own focus that complements the expertise of the group We offer - salary according to remuneration level 13 TV-L - internal and external training opportunities - flexible working hours - collegial working environment University of Greifswald: The University of Greifswald is one of the oldest universities in Germany and the Baltic Sea Region, founded in 1456. Its research strength mainly originates in the intensive interdisciplinary collaboration of the five faculties, and offers excellent research infrastructure. The University invites people of all origins and convictions to take part in academic education and to work together to enhance knowledge. <https://www.uni-greifswald.de/en/university/information/profile/short-profile/>The city of Greifswald is situated at the Baltic sea in the north-east of Mecklenburg-Western Pomerania, about 200 km north of Berlin. The area offers diverse outdoor activities such as hiking and water sports. Application Procedure: We are looking forward to receiving your application including a motivation letter, a research statement and a concept of how your research can complement the research fields of the group, CV, links to](https://zoologie.uni-greifswald.de/en/organization/departments/general-and-systematic-zoology/Your%20Profile%20-%20University%20degree%20(PhD)%20in%20biological%20sciences%20-%20research%20is%20based%20on%20evolutionary%20biology.%20Focus%20can%20be%20on%20reproductive%20biology,%20behavioural%20ecology,%20functional%20morphology,%20population%20genetics,%20gene%20expression%20analysis%20-%20ideally,%20several%20of%20these%20aspects%20are%20covered%20-%20research%20topics%20with%20arthropods%20as%20model%20organisms%20due%20to%20existing%20infrastructure%20is%20favourable%20-%20development%20of%20a%20coherent%20concept%20for%20the%20integration%20of%20your%20own%20research%20topics%20in%20the%20department%20-%20strong%20publication%20record%20and%20interest%20in%20acquiring%20external%20funding%20-%20teaching%20experience%20either%20in%20zoology,%20evolutionary%20ecology,%20and%20behavioural%20ecology%20-%20or%20in%20combination%20-%20very%20good%20oral%20and%20written%20communication%20skills%20in%20English%20-%20Basic%20knowledge%20of%20the%20German%20language%20to%20support%20teaching%20in%20the%20Bachelor's%20degree%20programs%20-%20ability%20to%20work%20both%20independently%20and%20as%20part%20of%20a%20team%20Main%20Responsibilities:%20-%20Participation%20in%20the%20fulfilment%20of%20the%20teaching%20obligations%20of%20the%20department%20with%204%20CPs%20(Practical%20courses%20in%20Systematics/Anatomy%20of%20animals%20in%20the%20bachelor%20programme;%20Evolutionary%20Ecology%20in%20the%20Master%20programme%20)

relevant publications, account of teaching experience, and certificates. Your application should be sent via email to Prof. Gabriele Uhl in a single PDF document (Name_26/Wi17.pdf). University of Greifswald Zoological Institute and Museum Prof. Dr. Gabriele Uhl (she/her) Loitzer Strasse 26 17489 Greifswald, Germany Email: gabriele.uhl@uni-greifswald.de Official announcement on Greifswald university website (in German): 26/Wi17: <https://www.uni-greifswald.de/universitaet/information/stellenausschreibungen/wissenschaftliches-personal/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

**iDiv Leipzig U JenaGermany
Macroevolution and
macroecology-3yrs**

Dear colleagues,

I have an open position in my lab for a 3-year postdoc position at iDiv in Leipzig / University of Jena in Germany. The focus is on macroevolutionary and macroecological analyses of vertebrates, ideally birds or mammals. The job includes some university teaching commitment in ecology & evolution, as well as opportunities for postdoctoral career development.

Find more details here: <https://jobs.uni-jena.de/jobposting/c3cc4240273f9296a2fdefef3d8e24c3d2c79e120> Application closes 30 September 2026.

Please spread this in your networks!

Thanks and best wishes Susanne Fritz

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**INRAE France Phylodynamics of
avian influenza viruses**

Hi everyone,

we offer a fully funded 2-year postdoctoral position starting early January 2027 as part of ERC Starting Grant TrackFLU project (<https://trackflu.inrae>

[-envt.com/](https://envt.com/)). The position aims at identifying the drivers of avian influenza viruses evolution and transmission in live bird market networks in Cambodia using longitudinal epi and genetic data collected as part of the project. The postdoctoral candidate will be based in our epidesa (<https://epidesa.weebly.com/>) research group (Toulouse, France). We are seeking a highly motivated candidate with a PhD degree in disease evolution, epidemiology or related disciplines. Prior experience in phylodynamics and strong interest in animal health is required. The deadline for applications is October 25th 2026, so please encourage potential candidates as soon as possible! For more information about the position and application process, please visit <https://jobs.inrae.fr/en/ot-30570> If you have any questions, please do not hesitate to contact me at claire.guinat@envt.fr

Best wishes, Claire

Claire GUINAT DVM, MSc, PhD epidesa group, UMR INRAE-ENVT IHAP

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**JohnInnesCentre Symbiosis
Development**

An opportunity has arisen for a Postdoctoral Researcher to join the group of Dr Hassan Salem at the John Innes Centre in the Department of Molecular Microbiology. This post is funded by a European Research Council (ERC) grant. Closes: 16th September 2026 Salary: GBP39,000 - GBP46,500 per annum depending on qualifications and experience <https://www.jic.ac.uk/vacancies/postdoctoral-researcher-salem-group-2/> About the Salem Group The Salem Group studies the evolution, function, and adaptive consequences of herbivore-microbe symbioses. Our research focuses on how extracellular bacterial symbionts upgrade host digestive physiology, enable dietary specialization, thereby facilitating herbivory. The Role The candidate will investigate the developmental basis of symbiosis in beetles, focusing on how symbiotic organs form, mature, and are maintained across host life stages. This role will include: -Characterizing the developmental origin and morphogenesis of symbiotic organs that house bacterial symbionts, from embryo through to adult. -Applying tissue- and cell-type-specific transcriptomic

and genomic approaches to symbiotic organs across developmental stages. -Using functional genetic tools, including RNAi, CRISPR/Cas9, and microinjection, to manipulate host developmental pathways and test their role in symbiont acquisition and organ formation. -Applying confocal microscopy, whole-mount and cross-sectional fluorescence in situ hybridization (FISH), and immunostaining to visualize symbiont colonization and host tissue differentiation. -Integrating developmental, molecular, and evolutionary data to understand how host development has been shaped by symbiosis. -Disseminating results through preprints, publications, conference presentations, and mentoring of students. The ideal Candidate You will have a PhD (or equivalent) in developmental biology, entomology, molecular biology, evolutionary developmental biology (evo-devo), or microbiology, or a related discipline. A starting salary of GBP40,100 is guaranteed for candidates who can evidence their PhD certificate on appointment. The successful candidate will have: -Experience with insect developmental biology techniques, such as microinjection, in situ hybridization, and live imaging. -Experience with functional genetic manipulation (e.g., RNAi, CRISPR/Cas9) in insects, ideally non-model species. -Proficiency in confocal microscopy and image analysis software (e.g., Fiji/ImageJ, Imaris). -Experience with RNA-seq or spatial/tissue-specific transcriptomics analysis, ideally in non-model organisms. -Strong computational skills for biological data analysis (preferably R and/or Python). -Demonstrated ability to develop independent, hypothesis-driven research at the interface of development and symbiosis. You will also have excellent communication skills, experience mentoring students or visitors, and the ability to work both independently and collaboratively in an interdisciplinary research environment. Additional information For further information and details of how to apply can be found here (<https://www.jic.ac.uk/vacancies/postdoctoral-researcher-salem-group-2/>) or contact the Human Resources team on 01603 450814 or nbi.recruitment@nbi.ac.uk quoting reference 1006173. This role meets the criteria for a visa application, and we encourage all qualified candidates to apply. Where the successful applicant requires a visa, we will fund the costs for their visa and the Immigration Health Surcharge. Please contact the Human Resources Team if you have any questions regarding your application or visa options. We are an equal opportunities employer, actively supporting inclusivity and diversity. As a Disability Confident organisation, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy. We are proud to hold a prestigious Gold Athena SWAN award in recognition of our inclusive culture, commitment and good practices

towards advancing of gender equality. We offer an exciting, stimulating, diverse research environment and actively promote a family friendly workplace. The Institute is also a member of Stonewall's Diversity Champions programme.

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JohnInnes CentreUK MolecularMicrobiology

An opportunity has arisen for a Postdoctoral Researcher to join the group of Dr Hassan Salem at the John Innes Centre in the Department of Molecular Microbiology. This post is funded by a European Research Council (ERC) grant. Closes: 16th September 2026 Salary: GBP39,000 - GBP46,500 per annum depending on qualifications and experience. <https://www.jic.ac.uk/vacancies/postdoctoral-researcher-33/>About the Salem Group The Salem Group studies the evolution, function, and adaptive consequences of herbivore-microbe symbioses. Our research focuses on how extracellular bacterial symbionts upgrade host digestive physiology, enable dietary specialisation, thereby facilitating herbivory. The Role The candidate will use comparative and population genomic approaches to reconstruct the origin, maintenance, and evolutionary consequences of symbiosis in beetles. This role will include: -Generating and analysing comparative and population genomic datasets across symbiotic and non-symbiotic beetle lineages. -Performing phylogenomic reconstruction and divergence-time estimation to trace the origins of symbiotic associations. -Applying macroevolutionary methods to test how symbiosis relates to diversification rates and ecological niche breadth. -Analysing long-read host genome assemblies and symbiont genomes to characterise genomic signatures of symbiotic transitions. -Applying molecular evolution approaches, such as selection analyses and ortholog identification, to identify genes and pathways shaped by symbiosis. -Integrating genomic, ecological, and phylogenetic data to test hypotheses about symbiosis-driven diversification. -Disseminating results through preprints, publications, conference presentations, and mentoring of students. The Ideal Candidate You will have a PhD (or equivalent) in evolutionary genomics, population genetics, bioinformatics, or entomology, or a related discipline. A starting salary of GBP40,100 is guaranteed for candidates who can ev-

idence their PhD certificate on appointment The successful candidate will have:

- Experience with comparative and/or population genomic analyses, including variant calling and phylogenomics.
- Proficiency in phylogenetic and phylogenomic software (e.g., IQ-TREE, RAxML, MrBayes, ASTRAL) and divergence-time estimation.
- Experience with macroevolutionary and diversification-rate analyses (e.g., BAMM, MEDUSA) is desirable.
- Strong programming skills (R and/or Python, Unix/Bash) for large-scale genomic data analysis.
- Experience handling long-read and short-read sequencing data, including genome assembly and annotation, is desirable.
- Demonstrated ability to develop independent, hypothesis-driven research in evolutionary genomics.

You will also have excellent communication skills, experience mentoring students or visitors, and the ability to work both independently and collaboratively in an interdisciplinary research environment. Additional information For further information and details of how to apply can be found here: <https://jobs.jic.ac.uk/Details.asp?vacancyID=21480> or contact the Human Resources team on 01603 450814 or nbi.recruitment@nbi.ac.uk quoting reference 1006175. This role meets the criteria for a visa application, and we encourage all qualified candidates to apply. Where the successful applicant requires a visa, we will fund the costs for their visa and the Immigration Health Surcharge. Please contact the Human Resources Team if you have any questions regarding your application or visa options. We are an equal opportunities employer, actively supporting inclusivity and diversity. As a Disability Confident organisation, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy. We are proud to hold a prestigious Gold Athena SWAN award in recognition of our inclusive culture, commitment and good practices towards advancing of gender equality. We offer an exciting, stimulating, diverse research environment and actively promote a family friendly workplace. The Institute is also a member of Stonewall's Diversity Champions programme. The John Innes Centre is a registered charity (No. 223852) grant-aided by the Biotechnology and Biological Sciences Research Council.

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JohnInnesCentreUK Symbiosis EvolutionaryBiochemistry

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- Cloning, heterologously expressing (in E. coli and insect cell lines), and purifying proteins underlying obligate symbiosis.
- Performing biochemical and kinetic assays, including DNS assays, thin layer chromatography, and substrate-binding assays, to characterize enzyme activity and specificity.
- Solving protein structures by X-ray crystallography or Cryo-EM and applying computational structure prediction tools (e.g., AlphaFold) to compare host- and symbiont-encoded proteins.
- Applying site-directed mutagenesis to identify residues underlying functional divergence.
- Applying mass spectrometry-based proteomic approaches to profile symbiont-secreted and host secreted proteins.
- Integrating structural, biochemical, and evolutionary data to relate enzyme architecture to symbiotic function.
- Disseminating results through preprints, publications, conference presentations, and mentoring of students.

The ideal Candidate You will have a PhD (or equivalent) in biochemistry, structural biology, protein chemistry, or molecular biology, or a related discipline. A starting salary of GBP40,100 is guaranteed for candidates who can evidence their PhD certificate on appointment. The successful candidate will have:

- Experience with recombinant protein expression and purification, in bacterial and/or insect cell systems.
- Experience with enzymology and enzyme kinetics assays.
- Experience with X-ray crystallography or other structural biology techniques (e.g., cryo-EM, NMR); fa-

miliarity with structure determination software (e.g., Phenix, Coot) is desirable. -Experience with mass spectrometry-based proteomics. -Familiarity with computational structural biology tools (e.g., AlphaFold, PyMOL, Rosetta). -Strong computational skills for biochemical and structural data analysis (preferably R and/or Python). -Demonstrated ability to develop independent, hypothesis-driven research at the interface of biochemistry and evolution. You will also have excellent communication skills, experience mentoring students or visitors, and the ability to work both independently and collaboratively in an interdisciplinary research environment. Additional information For further information and details of how to apply, please visit our website <http://jobs.jic.ac.uk> or contact the Human Resources team on 01603 450814 or nbi.recruitment@nbi.ac.uk quoting reference 1006174. This role meets the criteria for a visa application, and we encourage all qualified candidates to apply. Where the successful applicant requires a visa, we will fund the costs for their visa and the Immigration Health Surcharge. Please contact the Human Resources Team if you have any questions regarding your application or visa options. We are an equal opportunities employer, actively supporting inclusivity and diversity. As a Disability Confident organisation, we guarantee to offer an interview to all disabled applicants who meet the essential criteria for this vacancy. We are proud to hold a prestigious Gold Athena SWAN award in recognition of our inclusive culture, commitment and good practices towards advancing of gender equality. We offer an exciting, stimulating, diverse research environment and actively promote a family friendly workplace. The Institute is also a member of Stonewall's Diversity Champions programme. The John Innes Centre is a registered charity (No. 223852) grant-aided by the Biotechnology and Biological Sciences Research Council.

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MichiganStateU EvolutionaryBiology

The Ecology, Evolution, and Behavior (EEB) program at Michigan State University invites applications for a Postdoctoral Fellowship in Ecology, Evolution, and Behavior. The MSU EEB Presidential Postdoctoral Fellowship is a two-year position that includes a generous salary and research stipend. Fellows are fully partici-

pating members of EEB. They are expected to develop cutting-edge research programs and innovative community engagement initiatives, and will be mentored by two or more EEB core faculty members. A list of possible faculty mentors can be found here: <https://eeb.msu.edu/people/core-faculty.aspx>. Candidates should contact potential faculty mentors before applying.

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

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

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MississippiStateU Starkville MS USA Postdoctoral Position in the Smith Lab

Postdoctoral Associate Location: Mississippi State University, Starkville, MS

Department of Biological Sciences

An NSF-funded postdoc position is available in the Smith in the Department of Biological Sciences at Mississippi State University. The project aims to develop robust, user-friendly machine learning tools for population genetic inference and to apply these tools to uncover the drivers of diversification in several empirical systems. The lab has developed a Python package for demographic inference using machine learning, and the successful candidate will extend these methods along several axes.

In addition to the current project, the lab is pursuing a

wide range of empirical and computational research in phylogenetics and population genetics. To learn more about our work visit smithlabbio.github.io.

If you're interested, please reach out to ms4438@msstate.edu.

Full job ad: <https://explore.msujobs.msstate.edu/jobs/postdoctoral-associate-main-campus-s-tarkville-ms-mississippi-united-states-5910a504-5ad7-462e-ac4c-0389e7741a96?l=ApplicationSubSourceID> Best, Megan Megan L. Smith Assistant Professor Department of Biological Sciences Mississippi State University

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Montpellier France Postdoc position on drug resistance evolution

Postdoc position on drug resistance evolution in Montpellier, France

I am looking for a postdoc to work on drug resistance evolution in malaria (*P. faciparum*) and *E. coli* bacteria.

What is the project?

The goal of the project is to uncover the rules that determine the dynamics of drug resistance in different pathogens. I use modeling techniques from ecology, evolution and epidemiology and publicly available data from surveillance programs and genomic databases. I work on various pathogens (HIV, *E. coli* and *P. falciparum*) to be able to compare and contrast. The postdoc will work on two of the three sub projects.

Sub project 1: Resistance to antimalarials in *P. falciparum*

This subproject focuses on resistance to mefloquine which is caused by a gene amplification of the *Pfmdr-1* gene which is known to occur recurrently. However, despite the high rate of de novo evolution of resistance, resistance had not reached fixation in the population. The goal of this subproject is to determine the fitness cost of the amplification and determine whether this cost explains why it is not fixed. We will use publicly available sequencing data, determine amplification breakpoints to identify independently evolved resistance alleles and infer the fitness cost of carrying the resistance alleles using phylogenetic approaches.

Sub project 2. Diversity of resistance in *E. coli* populations

It is known that for many drug-bacteria pairs, consumption levels of drugs correlate with resistance levels. We hypothesize that higher levels of resistance in countries with higher treatment levels are caused by more origins of resistant strains. We plan to test this hypothesis by determining diversity of resistant bacterial strains in different countries and at different time points using subsets of the Enterobase database which contains several hundred thousand *E. coli* genomes.

Sub project 3: Reusable machine learning models to predict drug resistance

Machine learning models to predict antibiotic resistance phenotypes are usually specific to one particular dataset. This limits their practical usefulness. We propose here to align genomes to a standardized reference pan-genome to capture information on SNPs and gene presence-absence in a standardized way. This means that a model that was trained on one dataset can be tested on new genomic data which will allow us to determine how generalizable the models are.

Why this is a great opportunity

* Because drug resistance evolution is a cool & important topic. * Because Montpellier is a great city (if you don't mind the heat in the summer). It has good & free public transport (though today the tram didn't go because of a demonstration / it's France!), reasonable bikability, more affordable than Amsterdam, Paris, San Francisco, with the beach nearby and fast trains to Paris and from there to London and Amsterdam. * Because you'll be part of a friendly, international team (<https://eec.edu.umontpellier.fr/people/>) with PhD students, postdocs and researchers from many different countries. The EEC team consists of around 20 people with 8 different nationalities. * I have lots of experience in bridging evolutionary biology and public health, I have published many times with students and postdocs, and I fully expect that the postdoc I hire will get a really nice publication (or 2) out of this. Because I have a research-only position I will have sufficient time to dedicate to supporting you / collaborating with you.

Practical info

The official ad is here: <https://euraxess.ec.europa.eu/jobs/468402> The postdoc position can start on the first of Nov 2026 (though I have never hired someone in France, so I honestly cannot guarantee that this timeline will actually work as planned). The contract has to end on Sept 30 2028. So best case this would be a job for 23 months. The ad says that "The net monthly salary is between EUR2,200 and EUR2,380"

per month.

How to apply?

Send a 1-2 page cover letter that describes your motivation for the project and your experience in bioinformatics, your CV, a paper (or draft) written by you, and names and email addresses for three references to pleuni.pennings@umontpellier.fr. Only pdf's please! The deadline is Oct 25th but I will start reading applications on the 10th. Feel free to let me know ahead if you are planning to apply.

Skills/Qualifications

I am looking for a curious and motivated candidate with a PhD in biology or bioinformatics with skills in bioinformatics and sequence analysis and experience coding in Python or R or related languages. Other useful (not required) skills and interests would be modeling, simulations, evolutionary / population genetics, statistics, writing, reading primary literature, and public health.

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

NationalMuseumNaturalHistory Insect pollinator comparative genomics

The National Museum of Natural History (NMNH) invites applicants for the position of Postdoctoral Researcher, as part of a project focused on mass digitization of insect pollinating species in the NMNH collections. As part of this project, the position will focus on insect pollinator comparative genomics.

This is a full-time, 2-year temporary appointment with full Smithsonian benefits to be filled at the IS-11 level, equivalent to Federal GS-11. The full position title is: Entomologist (Postdoctoral Research Fellow) IS-0414-11. Application deadline is October 8, 2026 with no exceptions allowed.

For details and application information, please see the job announcement below:

<https://trustcareers.si.edu/en/postings/4c622f59-51d7-49a9-92e3-151f67c74da4> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net)

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

NaturalisBiodiversityCenter Netherlands Postdoc

An exciting opportunity to join us at the Naturalis Biodiversity Center.

We are looking for a Postdoctoral Researcher to join our Tropical Botanic Group and work closely with Angelica Cibrian-Jaramillo and Paola de Lima Ferreira.

This is a unique opportunity to work and develop innovative approaches that combine genomic data and AI to improve species identification and accelerate the discovery of plant diversity. The project offers the opportunity to push the boundaries of how we discover, delimit, and understand plant species in the genomic era.

More information is available at <https://www.naturalis.nl/en/about-us/job-opportunities/postdoctoral-fellow-in-integrative-taxonomy-genomics-ai> (to subscribe/unsubscribe the EvoDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

NewYork US American Museum of Natural History

Dear Colleagues,

The Goodheart Lab in the Division of Invertebrate Zoology at the American Museum of Natural History is seeking a full-time Postdoctoral Fellow (two-year term) to perform comparative genomic and transcriptomic analyses on nudibranchs related to an NSF-funded project in collaboration with Dr. Rebecca Tarvin at UC Berkeley to study the process of kleptocnidy, the theft and storage of microscopic stinging structures (nematocysts), in nudibranch mollusks. We are interested in whether this unique process evolved through specialization of phagocytosis, an ancient cellular process used across animals for immune defense and intracellular digestion (project link: https://www.nsf.gov/awards/search/show-award?AWD_ID=2611236).

The Postdoctoral Fellow will design and execute orig-

inal research projects related to the grant under the supervision of Dr. Jessica Goodheart. The position will involve field work, the care of invertebrates, and genomics. Scholarly impact, including through publication in refereed literature and presentation at conferences, workshops, and seminars, is a major goal of this position. This position is intended to be a period of mentored advanced training, scientific research, and/or pedagogical contributions designed to enhance the incumbent's professional, research, and scholarly proficiency.

Applicants may apply at <https://careers.amnh.org/postings/4908>. Please share widely! Best, Jessica

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PostdocsX2 UCL UK BacterialEvolution AntimicrobialResistance

Two, three-year postdoctoral Research Fellow positions are available in Dr Gemma Murray's group in the Department of Genetics, Evolution and Environment at UCL, as part of a Wellcome-funded programme investigating the evolution, spread and persistence of antimicrobial resistance (AMR). The research programme is using *Streptococcus suis*, a common commensal and opportunistic pathogen of pigs, as a model system to understand AMR across scales, from transmission within host populations to long-term evolutionary dynamics.

Post 1: AMR dynamics within and between hosts This project will generate and analyse longitudinal genomic data from commercial pig farms in Spain, combining repeated sampling of individual pigs with deep sequencing to reconstruct within-host *S. suis* strain diversity and dynamics, and to investigate the transmission of strains and AMR genes within a farm. <https://www.jobs.ac.uk/job/DSU266/research-fellow-in-within-host-microbial-genomics> Post 2: Evolutionary genomics of global AMR dynamics This project will integrate genomic datasets generated across multiple countries and years to investigate how resistance is gained, lost and spread over longer evolutionary timescales. The work will combine population genomics, phylogenetics and comparative approaches to understand the processes shaping global patterns of AMR. <https://www.jobs.ac.uk/job/DSU268/research-fellow-in-microbial-evolutionary-genomics>

Both posts offer scope to develop independent ideas within the broader programme. Candidates with strong quantitative skills and backgrounds in microbial evolution, population genetics, comparative genomics, phylogenetics or related areas are particularly encouraged to apply.

For further information, please see the job adverts above and email Dr. Gemma Murray for more information (gemma.gr.murray@ucl.ac.uk).

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SenckenbergSocietyforNatureResearch Frankfurt Germany Evolutionary Genomics of Mammals

Senckenberg Society for Nature Research (SGN), headquartered in Frankfurt am Main, is seeking to fill the following position at the Senckenberg Biodiversity and Climate Research Centre (SBIK-F), starting as of 01 November 2026: Postdoc Researcher (m/f/d) in Evolutionary Genomics of Mammals (m/f/d) (Full time / part time options available) Location: Frankfurt am Main Employment scope: Full-time; part time options are available Type of contract: Temporary, limited to 2 years Remuneration: Collective agreement of the state Hesse (TV-H) / E13

The Senckenberg Society for Nature Research is a member of the Leibniz Association and has been investigating the "Earth System" worldwide for more than 200 years, examining the past, analysing the present, and developing projections for the future. We conduct integrative geobiodiversity research with the aim of understanding nature in all its complexity and diversity in order to preserve it as the foundation of life for future generations and to ensure its sustainable use. Across eight institutes and five research stations throughout Germany, scientists from more than 40 countries conduct research at the highest international level. The mission of the Senckenberg Biodiversity and Climate Research Centre is to study the complex interactions between biodiversity and climate change. There is an exciting opportunity for a talented and motivated applicant to join the working group of Prof. Dr. Axel Janke. The applicant will be closely involved in gene flow, evolutionary, population or phylo-genetics to study speciation in mammals (bears, giraffe, kangaroos or allies) at the genomic level and in MSc and BSc teach-

ing. Strong own and proven research interests including other vertebrate groups will be considered. Your tasks - Conduct genomic research on mammalian evolution and speciation, including evolutionary, population and phylogenomic analyses - Investigate phylogenetic relationships, gene flow and genomic signatures of evolutionary and environmental processes using genomic and bioinformatic approaches - Apply and further develop bioinformatic methods for the analysis of genomic data, including population genomics, genome assembly and species distribution modelling - Organise and teach university courses and supervise BSc and MSc theses - Independently prepare and publish research results in peer-reviewed journals and contribute to the acquisition of third-party funding Your profile - PhD degree in Biology, Genetics, Bioinformatics or a related field - Strong interest and proven skills in evolutionary, population or phylogenomics. - Knowledge of gene-flow analyses and/or drift processes is an advantage - Experience in population genomics, genome assembly and script programming, including R - Very good written and oral communication skills in English - Interest in species distribution modelling, paternal inference, conservation genetics and epigenetics We offer - access to an international network of scientists, policymakers and research organizations - an attractive job within the inspired and dynamic working environment of an internationally recognized research institution - flexible working hours - mobile working options - employee ID card with free admission to Senckenberg museums - annual special payment - collectively agreed vacation entitlement - company pension plan Senckenberg is committed to diversity. We benefit from the different expertise, perspectives and personalities of our staff and welcome every application from qualified candidates, irrespective of ethnic or cultural origin, gender, religion or belief, age, sexual identity or disability. Women are particularly encouraged to apply, as they are underrepresented in the field of this position; in the case of equal qualifications and suitability they will be given preference. Applicants with a severe disability will be given special consideration in case of equal suitability. Senckenberg actively supports the compatibility of work and family and places great emphasis on an equal and inclusive work culture. How to apply? Please upload your application as a single PDF by 5 October 2026, including: - CV - Letter of motivation - Academic transcripts and certificates/credentials - Two relevant publications - Contact details of two potential references Please compress the files where possible. If the two publications cause the file to exceed the upload limit, they may be uploaded separately. Contact Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main For specific

questions about this role, please contact Prof. Dr. Axel Janke at axel.janke@senckenberg.de For data protection information on the processing of personal data as part of the application and selection process, please refer to the privacy policy on our homepage at <https://www.senckenberg.de/en/imprint/>

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

StockholmU Sweden Epidemiology meets sexual selection

A postdoc position is available with me, Jess Stephenson (<https://stephensonlab.com/>), in the Department of Zoology, Stockholm University, Stockholm, Sweden.

We are looking for a highly motivated postdoc to join an international research project that investigates the role of sexual selection in epidemics. The project uses the guppy *Poecilia reticulata* and its gyrodactylid parasites as model organisms. This project is funded through a European Research Council Starting Grant "EpiSex: The effects of sexual selection on epidemic outcomes" (<https://cordis.europa.eu/project/id/101218205>).

Sexual selection has two important but often overlooked consequences for epidemics. First, infectious diseases spread when individuals come into contact with each other. Reproduction is an important driver of such contacts: mate choice affects who meets whom and thus the opportunities for parasite transmission. Second, individuals who choose a mate with high parasite resistance may indirectly benefit because their offspring can inherit this resistance. If such choices consistently lead to offspring being produced with genetically most resistant partners, the parasite resistance of the population may increase over generations.

The project will use experimental epidemics, existing artificially selected lines of guppy, AI-based behavioral tracking, mathematical modeling, and laboratory experiments to investigate how female mate choice affects epidemic dynamics. The postdoc will have a leading role in the experimental work, data collection and quantitative analyses, and contribute to international collaborations. You can read more about our work here:

<https://stephensonlab.com/> I am particularly looking for someone with experience with one or more aspects of the project, and an excellent publication record. Start date is flexible, but ideally early 2027. If this sounds like you, please get in touch with any questions: jess.stephenson@jess.stephenson@zoologi.su.se

***Apply here: <https://su.varbi.com/what:job/jobID:967077/> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

SusquehannaU USA Marine microbial ecology transcriptomics

Good morning!

The Charvet Lab at Susquehanna University seeks a highly motivated Postdoctoral Scientist for a two-year position supported by a collaborative National Science Foundation grant. The successful candidate will join the P-MixSwitch project, a collaboration between Susquehanna University and the University of Arizona, investigating the physiological and genetic mechanisms that enable small marine mixoplankton to switch between photosynthetic and predatory lifestyles.

About the P-MixSwitch Project Mixoplankton are ecologically important eukaryotic microorganisms that acquire energy and nutrients through both photosynthesis (phototrophy) and prey consumption (phagotrophy). This dual nutritional strategy allows mixoplankton to play a critical role in global carbon and nutrient cycling. However, the environmental and cellular factors that regulate transitions between phototrophic and phagotrophic modes remain poorly understood.

The P-MixSwitch project seeks to uncover the mechanisms underlying this metabolic flexibility by tracking carbon and phosphorus fluxes through nutrient uptake, photosynthetic carbon fixation, and phagotrophic ingestion of prey. Using physiological, molecular, and transcriptomic approaches, the project will characterize the cellular and subcellular changes associated with trophic switching in ecologically important prasinophyte mixoplankton. This work will advance understanding of the role of marine mixoplankton in carbon cycling within oligotrophic ocean ecosystems.

Research Environment The Charvet Lab at Susquehanna University uses molecular biology and bioinformatics approaches to investigate genes and pathways

involved in mixoplankton phagotrophy under varying environmental conditions. As part of the P-MixSwitch project, the Postdoctoral Scientist will participate in collaborative experimental work with the University of Arizona, followed by RNA extraction, transcriptome sequencing, and gene expression analyses of key prasinophyte strains.

This is a full-time, two-year postdoctoral appointment funded by the National Science Foundation, with an anticipated start date of January 2027.

Apply here! <https://www.schooljobs.com/careers/susqu/jobs/5479265/postdoctoral-scientist?pagetype=jobOpportunitiesJobs> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

UArizona US Disease Ecology and Evolution

The McNew Lab is hiring a postdoc to study the genomic basis of adaptation to emerging disease in Galapagos birds. Competitive candidates will have experience with genomics, and birds and/or parasites. Position based in Tucson, a livable city with exceptional culture and biodiversity. Position is fully funded for 2+ years and will be paid on NIH scale. Details and apply here: <https://tinyurl.com/59ha2u68> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

U Calgary RepeatedAdaptationGenomics

Postdoctoral position: Genomics of Repeated Adaptation Yeaman Lab Department of Biological Sciences, University of Calgary

The Yeaman lab is looking to hire a postdoctoral researcher to work on a large project focusing on the genomics of repeated adaptation. This position will be contributing to the MacroMar and RepAdapt projects, which are jointly building a large interoperable dataset with genome sequence data from thousands of individuals and hundreds of species of plants, animals, and fungi.

We currently have ~130 datasets re-processed through a common pipeline, and are working on dramatically expanding this. Duties will include some combination of: a) finding new publicly-available sequence datasets, processing them through our bioinformatic pipeline, and helping curate submissions, b) developing new methods for evolutionary inference and statistical analysis of the datasets and/or test performance of existing methods, c) using this multi-species population genomic dataset to test evolutionary hypotheses of interest. We are particularly interested in studying repeated adaptation, but these datasets enable the exploration of many other questions at a broad scale. There is lots of potential for creative science and extensive collaboration with ~150 other scientists who are participating in these initiatives. The position will be in-person at University of Calgary.

Funding is in place to cover an 18-month position, with several grant applications underway that should hopefully extend this further (CAD \$60k salary + benefits).

TO APPLY: Please send a CV and a short description of your interest in the position and any relevant research experience to samuel.yeaman@ucalgary.ca, along with the names and emails of three people I could contact for reference letters. I will begin reviewing applications on October 1st, 2026, but please contact me to check in if you need to make a quick decision.

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UC Davis Population Genomics

POSTDOCTORAL RESEARCHER Population Genomics & Adaptive Introgression Among African Malaria Vector Species Join an interdisciplinary research program investigating the evolutionary genomics of Africa's most important malaria vectors. We are seeking an outstanding Postdoctoral Researcher to investigate interspecific hybridization, gene flow, and adaptive introgression among members of the *Anopheles gambiae* species complex. Research will involve the application of cutting-edge long-read sequencing and population genomic approaches. **THE RESEARCH** Closely related *Anopheles* species frequently occur in sympatry and, despite strong reproductive isolation, do exchange genetic material in nature. This project will use PacBio HiFi and other long-read genomic technologies to resolve the genomic architecture of species

boundaries and determine how adaptive genetic variation moves across them. Research will focus on: - Interspecific hybridization and gene flow within the *Anopheles gambiae* complex - Adaptive introgression and the movement of advantageous alleles across species boundaries - Long-read genome assembly and haplotype resolution - Discovery and characterization of structural variation, including inversions and other complex genomic variants - Population genomic and phylogenomic analysis of species differentiation and genomic barriers to gene flow - The evolutionary history of loci associated with insecticide resistance, environmental adaptation, and vector biology - Integration of genomic, geographic, ecological, and phenotypic data to understand adaptation in malaria vectors **RESPONSIBILITIES** The successful candidate will contribute to the development and analysis of high-quality genomic resources and population datasets and will have substantial latitude to develop independent research questions. Methods may include: PacBio HiFi sequencing o haplotype-resolved assembly o structural variant discovery o pangenomics o population genomics o phylogenomics o demographic inference o introgression analysis o selection scans o computational genomics **QUALIFICATIONS** Required - Ph.D. in population genetics, evolutionary biology, genomics, computational biology, entomology, genetics, bioinformatics, or a related field - Demonstrated research experience in genomics, population genetics, or evolutionary biology - Strong quantitative and analytical skills Preferred - Experience with long-read sequencing, particularly PacBio HiFi - Genome assembly or structural-variant analysis - Experience detecting gene flow, admixture, or introgression - Proficiency in R, Python, Linux/HPC, or comparable computational tools Experience with mosquitoes in the genus *Anopheles* is valuable but not required. We welcome candidates bringing expertise from evolutionary genomics, computational biology, or population genetics who are excited to apply their skills to vector-borne disease biology. **SIGNIFICANCE** Malaria remains a major global health challenge, particularly in underserved communities in sub-Saharan Africa. Understanding how malaria-vector species evolve, exchange genetic variation, and adapt to their environments is essential for anticipating changes that may influence malaria transmission and vector control. This research sits at the intersection of evolutionary biology, genomics, vector biology, and global health, providing an opportunity to address fundamental questions about species evolution while contributing to the scientific foundation for sustainable malaria control and elimination. **JOIN US** Location: University of California, Davis Position: Postdoctoral Researcher Start Date: ASAP Duration: Two years minimum Application Deadline: Open un-

til filled To apply: Submit a CV, brief statement of research interests, and contact information for three references to vectorgeneticslab@gmail.com Questions? Contact: Christine Coleman, Executive Assistant— cmhandy@ucdavis.edu — <https://vectorgeneticslab.ucdavis.edu> We are committed to fostering an inclusive research environment and encourage applications from candidates with diverse backgrounds and perspectives.

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within the broader research programme. Candidates with strong quantitative skills and backgrounds in microbial genomics, population genetics, evolutionary genomics, phylogenetics or related areas are particularly encouraged to apply.

For further information, please see the job adverts above and email Dr. Gemma Murray for more information (gemma.gr.murray@ucl.ac.uk).

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UCL UK Two postdocs in bacterial evolutionary genomics and antimicrobial resistance

Two three-year postdoctoral Research Fellow positions are available in Dr Gemma Murray's group in the Department of Genetics, Evolution and Environment at UCL, as part of a Wellcome-funded programme investigating the evolution, spread and persistence of antimicrobial resistance (AMR).

The research programme is using *Streptococcus suis*, a common commensal and opportunistic pathogen of pigs, as a model system to understand AMR evolution across different scales, from transmission within host populations to long-term evolutionary dynamics.

Post 1: AMR dynamics within and between hosts

This project will generate and analyse longitudinal genomic data from commercial pig farms in Spain, combining repeated sampling of individual pigs with deep sequencing to reconstruct within-host *S. suis* strain diversity and dynamics, and to investigate the transmission of strains and AMR genes within a farm.

<https://www.jobs.ac.uk/job/DSU266/research-fellow-in-within-host-microbial-genomics> Post 2: Evolutionary genomics of global AMR dynamics

This project will use genomic datasets generated across multiple countries and years to investigate how AMR genes are gained, lost and transferred. The work will combine comparative genomics and phylogenetics to understand the processes shaping the horizontal transfer of AMR genes through microbial communities.

<https://www.jobs.ac.uk/job/DSU268/research-fellow-in-microbial-evolutionary-genomics> Both posts offer scope to develop independent ideas

UC Riverside Insect conservation genomics

We are seeking a postdoctoral researcher for a two-year appointment to work in the lab of Dr. Zachary MacDonald at the University of California, Riverside in close collaboration with Dr. Brad Shaffer at the University of California, Los Angeles on a range of landscape and conservation genomics projects focused on butterflies and other insects. Several of these projects are associated with the broader California Conservation Genomics Project (ccgproject.org). The position will be based in person at UC Riverside, with frequent visits to UCLA. Remote appointments are not possible. The MacDonald and Shaffer labs have multiple whole-genome insect datasets already generated and ready for analysis and publication. Additional conservation genomics projects are also getting underway in collaboration with the U.S. Fish and Wildlife Service and the Washington Department of Fish and Wildlife. For applicants interested in contributing to new and emerging projects, opportunities for fieldwork are available. Required qualifications include a PhD in bioinformatics, evolutionary ecology/biology, or a related field. We are looking for candidates with strong bioinformatics experience and a demonstrated publication record, including experience assembling reference genomes using HiFi or other long-read sequencing data, generating VCF files with GATK or related pipelines, and conducting whole-genome analyses. The anticipated start date is Nov 1, 2026, or as soon as possible thereafter. The initial appointment will be for two years, with the possibility of extension subject to funding and satisfactory performance. Salary will be commensurate with experience and follow the University of California Postdoctoral Scholar salary scale (\$71,491-\$85,736 annually as of October 1, 2026). The position includes the compre-

hensive UC Postdoctoral Scholar Benefits Plan, including medical, dental, and vision coverage. Applicants should submit a CV, a brief cover letter describing research experience and interests, and contact information for three references to zmacdona@ucr.edu with the subject line "Postdoc inquiry: [Last Name]." Review of applications will begin immediately and continue until the position is filled.

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U GothenbergSweden ComputationalGenomics

Dear all,

We would like to inform you about two postdoc positions in Computational Genomics available in our lab in Gothenburg, Sweden. Apply here: <https://CGRlab.github.io/join/> Research project 1. Only 2

Research project 2. This project focuses on studying genetic variation and determining how different variants co-occur on the same paternal or maternal haplotype. We previously developed methods for haplotype phasing in humans and polyploids. In this project, we aim to develop machine learning models to advance the characterization of genetic variations.

Research project 3. De novo genes are genes that arise from previously non-coding DNA rather than being inherited from an existing gene during the course of evolution. They are important because they can introduce new functions and contribute to the evolution and adaptation of organisms. We will develop methods to study how de novo genes evolve in eukaryotes.

Best regards, Sina Majidian

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UMadrid Spain Forest Genomics and Global Change

POSTDOC We are seeking a postdoctoral researcher to apply for a three-year Juan de la Cierva fellowship at the Agro-Food and Environmental Genomics Research Group, Complutense University of Madrid, Spain (<https://www.ucm.es/genomicaagroalimentariayambiental/inenglish>). The research will focus on forest genomics and global change.

Applicants should submit a CV and a brief cover letter describing their research experience and interests to jhorreo@ucm.es, with the subject line "Juan de la Cierva candidate". Review of applications will begin immediately and continue until the position is filled.

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UOklahoma ConservationEvolutionaryGenomics

Postdoctoral Research Associate of Anthropology Evolutionary, Conservation, and Anthropological Genomics University of Oklahoma, Norman, Oklahoma, USA The Department of Anthropology and the Laboratories of Molecular Anthropology and Microbiome Research (LMAMR) at the University of Oklahoma invite applications for a Postdoctoral Research Associate in evolutionary, conservation, and ancient/anthropological genomics. The initial research will focus primarily on cuscuses, addressing questions involving diversification, systematics, biogeography, conservation, and the evolutionary consequences of human-mediated translocations. The researcher will also have opportunities to contribute to projects involving shrews and other mammalian systems and to develop related research questions that align with their interests. This is a combined wet-laboratory and computational position in a collaborative, interdisciplinary research environment. The successful candidate will generate and analyze genomic data from modern, museum, historical, archaeological, and other degraded biological

materials, including work in LMAMR's ancient-DNA laboratory. Candidates should have some experience with laboratory protocols and be willing to conduct wet-lab work. Prior ancient-DNA experience is welcome but not required; training in laboratory and computational methods will be provided as needed. The postdoc will have opportunities to lead publications, mentor students, collaborate with museum researchers and conservation partners, and develop grant proposals and new research directions with Dr. Lilly Parker. We welcome candidates with complementary backgrounds and do not expect applicants to have experience in every method listed in the full advertisement. Applicants must have a Ph.D. in a relevant life science, computer science, or anthropology field. The position is full-time, with salary commensurate with experience and University of Oklahoma benefits. The initial appointment is for one year, with the possibility of renewal. The start date is flexible. Review of applications begins October 15, 2026, and will continue until the position is filled. Full details and application instructions: <https://apply.interfolio.com/193521> Questions may be directed to Dr. Lilly Parker at lilly.parker@ou.edu.

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URochester Population Quantitative Genetics postdoc

The Carlson Lab in the Department of Biology at the University of Rochester (<https://marync.github.io/carlsonlab/index.html>) is launching in January 2027 and is seeking a postdoctoral researcher. The lab works at the interface of population and quantitative genetics, statistics, and evolutionary biology. An immediate focus of the group is the development of methods and theory to interpret empirical fitness landscapes in the context of population genetic and evolutionary data. Work in the lab will typically involve some combination of theory, statistical methods development, simulation, and data analysis. Independent research that complements the group's research themes is most welcome.

Preferred qualifications include: - Strong quantitative background - Broad intellectual interests within and outside of (evolutionary) genetics - Self-motivation and independence

The position offers a competitive salary and benefits. The start date must be January 1, 2027 or later, but is

otherwise flexible. Interested candidates should contact Maryn Carlson at maryn.carlson@rochester.edu. Please include a CV and a brief statement of your research experience and interests.

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UT Austin US Stengl-Wyer Postdoctoral Scholars in Biodiversity Sciences

Stengl-Wyer Postdoctoral Scholars in Biodiversity Sciences - UT Austin

Learn more and apply here: <https://biodiversity.utexas.edu/about-center/endowments-biodiversity/stengl-wyer-endowment/stengl-wyer-scholars-program> Scholars are expected to be independent and propose their own research project. The project start date at UT should be between August 1, 2027 and September 30, 2027. Applicants should identify one or more faculty members from UT's College of Natural Sciences (CNS; <https://cns.utexas.edu/>) who will serve as a mentor as well as provide laboratory space to the Scholar. Applicants should also discuss their proposed educational and/or community engagement activities with their proposed mentor. Scholars will be encouraged to interact broadly and collaborate with other faculty, postdocs, and graduate students at UT. 2027 Scholar awardees will receive the following: - \$70,000 annual salary plus UT benefits - \$10,000 annual allowance for research and travel expenses - Up to \$3,000 relocation expenses Applications close December 7, 2026.

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UVirginia Schield Lab Bioinformatics Evolutionary Genomics Population Genetics

The Department of Biology at the University of Virginia (UVA) invites applications for a postdoctoral Re-

search Associate with expertise in bioinformatics, evolutionary genomics, and population genetics to work in the lab of Dr. Drew Schield (www.schildlab.org). The Research Associate will join a collaborative team investigating speciation, adaptation, and sex chromosome evolution using genome-scale datasets. In particular, the researcher will lead in our efforts to generate and analyze long-read genome assemblies for populations of rattlesnakes (*Crotalus*) that exchange gene flow in secondary contact. These data will be used in pangenome graph analysis to address questions related to nucleotide and structural variation underlying adaptive trait evolution (e.g., venom and cryptic coloration), sex chromosome structural diversity, and the roles of structural variants in complex speciation with gene flow. They will also have the opportunity to lead projects leveraging substantial whole genome sequencing and RNAseq data available in the lab, and to participate in annual collecting trips in the field. Specific project directions are flexible so as to enhance the researcher's interests and career goals while building on existing expertise in the lab. Strong candidates for the position will have excellent bioinformatics skills for processing and analysis of large genomic datasets as well as knowledge of population genetics analyses, especially those related to demographic inference, identifying signatures of selection, and detecting hybridization and introgression. Experience with genome assembly and annotation is also preferred. The successful candidate will also ideally have molecular laboratory skills associated with DNA and RNA extraction, library preparation, and the ability to troubleshoot and refine protocols. Applicants should be self-driven, have excellent data management skills, demonstrate verbal and written communication skills, and be able to work with a collaborative team. Strong candidates will also have a record of scientific productivity. The Research Associate will work closely with the PI and members of the Schield lab at UVA while collaborating with the labs of Drs. Blair Perry (Michigan State University), Matthew Holding (University of Michigan), Marjorie Matocq (University of Nevada Reno), Todd Castoe (University of Texas at Arlington), Jesse Meik (Tarleton State University), and Mark Margres (University of South Florida) for access to additional training opportunities. They will also have access to groups within the Evolution, Ecology, and Behavior community at UVA (www.EEBvirginia.org). In the Schield lab, the Research Associate will have the opportunity to mentor graduate and undergraduate students, design and lead research integrating field, molecular, and computational components, prepare conference presentations and publications, and gain teaching experience to the extent that it matches their career

goals. The completion of a PhD degree in Biology or a related field by the start date of the appointment is required. The ideal start date of the appointment will be between October 2026 and March 2027, but other start dates will be considered for highly qualified applicants. This is a one-year appointment that may be renewed for an additional two years (in one-year increments), contingent upon available funding and satisfactory performance. Salary The anticipated hiring salary is \$60,000 - \$65,000 commensurate with experience. Application Procedure Apply online at Apply online at <https://jobs.virginia.edu/us> and search for position number R0087489. Applicants should upload: - A cover letter summarizing your research interests, accomplishments, and professional goals - Curriculum vitae with a list of publications and scientific presentations - Contact information for three professional references Please note that multiple documents may be uploaded in the application portal. Application Deadline Review of applications will begin on October 1, 2026 will be given full consideration; however, the position will remain open until filled. The University will perform background checks on all new hires prior to employment. Applicants with questions about the position, research goals, and training opportunities are encouraged to contact Drew Schield at drew.schild@virginia.edu. For questions about the application process, please contact Richard Haverstrom, Academic Recruiter, at rkh6j@virginia.edu. For more information on the benefits available to a Research Associate at UVA, visit hr.virginia.edu/benefits.

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UWarsaw ParasiticProtistEvolution

Postdoctoral Position in parasitic protist diversity, ecology, evolution and interactions

We are looking for a postdoctoral researcher for a 3-year position in the Diversity, ecology, and interactions of Perkinsea parasitic protists in freshwater ecosystems PERKFresh project, funded by the Polish National Science Centre and the Czech Science Foundation and led by Dr Anna Karnkowska (University of Warsaw) and Dr Elisabeth Hehenberger (Biology Centre, Czech Academy of Sciences).

The PERKFresh project investigates the diversity, ecology, and host-parasite interactions of Perkinsea, a diverse and widespread group of unicellular eukaryotic parasites that are particularly abundant in freshwater ecosystems but remain poorly understood. We will study Perkinsea communities across lakes of the Masurian Lakeland in northeastern Poland, spanning environmental gradients from relatively pristine to strongly human-impacted habitats. The project will combine field sampling, long-read metabarcoding, CARD-FISH, network analyses, single-cell transcriptomics, phylogenomics, and laboratory infection experiments to determine which Perkinsea lineages occur in freshwater, what hosts they infect, how they interact with their hosts, and what ecological roles they play. By linking parasite diversity and abundance with environmental conditions and host populations, the project will provide new insights into the role of parasitism in freshwater ecosystems and how anthropogenic pressures may influence these interactions.

We are looking for a candidate with expertise in one or more of the following: - Protistology, parasitology or microbial eukaryotes - Environmental biology, freshwater ecology - Metabarcoding, environmental sequencing - Bioinformatics, statistical analysis of biological data

We are especially interested in candidates who enjoy working across field biology, molecular methods, bioinformatics and evolutionary ecology. You will join the Genomics and Evolution of Microbial Eukaryotes team led by Anna Karnkowska at the Institute of Evolutionary Biology, University of Warsaw.

Start: 1 January 2027 or later

Application deadline: 6 November 2026

Full job advertisement: <https://euraxess.ec.europa.eu/jobs/466845> Project website: <https://ibe.biol.uw.edu.pl/en/projects/perkfresh/> Please feel free to reach out with any questions at the email address listed below.

Anna Karnkowska Institute of Evolutionary Biology Biological and Chemical Research Centre University of Warsaw, Warsaw, Poland

Web Lab.: <https://ibe.biol.uw.edu.pl/en/835-2/research-groups/eukaryotic-microorganisms/genomics-and-evolution-of-eukaryotic-microorganisms/> Anna Karnkowska a.karnkowska@uw.edu.pl

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UWarsaw Poland Postdoc Co-phylogeny and extinction modelling

Hi,

We have the following advertisement for a 2-year postdoc position at the University of Warsaw (Deadline: 10/11/2026): <https://euraxess.ec.europa.eu/jobs/469223> Happy to provide more information.

All the best, Kenneth

– Dr. Hab. Kenneth De Baets Institute of Evolutionary Biology Faculty of Biology, University of Warsaw
Zwirki i Wigury 101 Warsaw 02-089 Poland

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WarsawU Poland Postdoc position

The Institute of Evolutionary Biology, Faculty of Biology, University of Warsaw, invites applications for a full-time Postdoctoral Researcher / Assistant Professor position in the NCN-funded SONATA project "How changes in meristem patterning drive evolutionary innovations: insights from syncephalia in the sunflower family (Asteraceae)" PI: Dr Jakub Baczynski Location: University of Warsaw, Warsaw, Poland Expected start: March 2027 Duration: 12 months, with the possibility of extension for an additional 12 months Salary: approximately 8,700 PLN gross/month + 13th-month salary and seniority allowance Application deadline: 13 November 2026 The project investigates the evolutionary-developmental mechanisms underlying the formation of syncephalia ("heads of heads") in Asteraceae. We combine comparative genomics and developmental transcriptomics with morphological analyses, and in situ analyses of gene expression to understand how changes in meristem patterning generate evolutionary innovations and increased structural complexity in plants. We are looking for a researcher with a PhD in biological sciences or a related discipline and experience in one or both of the following areas: - plant evolutionary-developmental biology,

including experience with techniques such as in situ hybridization, tissue culture optimization, plant regeneration and/or transformation; and/or - evolutionary research using comparative genomics and comparative transcriptomics of eukaryotes. Candidates should have a good publication record, international research experience, very good command of English, and the ability to work independently. Experience supervising students and research mobility are additional assets. The PhD must have been awarded in the year of employment or within the seven years preceding 1 January of the year of employment. If hired, the University of Warsaw must be the candidate's primary place of employment. Applications should be submitted by 13 Novem-

ber 2026 to both: j.baczynski@uw.edu.pl dzienka.nat.biol@uw.edu.pl Full English version of the call: <https://drive.google.com/file/d/1Jr1HpVDtGiga-tbhCQ2CFd7QaQ2KtMXc/view?usp=sharing> Official announcement (in Polish): <https://bazaogloszen.nauka.gov.pl/oferta/adiunkt-26965/> Interviews will be conducted in the second half of November 2026, and the results will be communicated by 4 December 2026. For questions about the position, project, eligibility, or application procedure, please contact Jakub Baczynski at j.baczynski@uw.edu.pl

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Course GeneticDataAnalysis ConGen2026 Online SeptToNov

Genomics Data Analysis Course: 'ConGen' 2026 Online

Course Objectives: To provide training in conceptual and practical approaches for using genomic data to address key questions in ecology, evolution, and conservation. Learn next-generation sequencing data analysis and interpretation from raw sequence reads through filtering and genotyping. Participants will learn to conduct genome assembly, estimate effective population size (N_e), assess inbreeding and gene flow, detect selection, conduct metabarcoding (for biodiversity assessment and diet analyses), apply genomic approaches to forensics, and conduct landscape genomics, and more. See lecture topics below & www.umn.edu/congen/ Who should apply: Advanced undergraduates, M.S. and Ph.D. students, post-docs, faculty, with a basic understanding of population genetics. We teach R and Linux skills the first week to help maximize your learning. Where: Online (Zoom). Lectures are video-recorded to facilitate asynchronous participation by international participants. When: Monday, Wednesday & Friday, 8-10:00 AM-ish, Sept. 24th - Nov. 13th (20 + lectures by 15 + experts) Instructors: Eric Anderson, Ellie Armstrong, Matt DeSaix, Chris Funk, Marty Kardos, Brenna Forester, Will Hemstrom, Paul Hohenlone, Bruce Ranala, Rena Schweizer, Arun Sethuraman, Steven Spear, Robin Waples, Schuyler Liphardt, Steve Spear, and more... To apply, email leif.howard@flbsad.umn.edu or go to www.umn.edu/congen/Course credit: A course certificate and academic credit are available through the University of Montana (BIOB 591 Pop Gen Data Analysis). Selected lecture topics: see www.umn.edu/congen/ for the full list & instructors The role of genomics in population genetics, ecology, and conservation. Pop genomics: Concepts and tools to answer eco-evo questions R & Linux basics, FastQ file format for next-generation sequencing data Scripting, data handling, & organizing bioinformatics projects Probability, Bayesian statistics, MCMC, and genotype likelihood calculations The Coalescent: Theory and applications Raw sequence read filtering and

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genotype calling (with and without a reference genome) Filtering (QC) best practices and effects on downstream analyses (HWE, selection tests...) Inbreeding and runs of homozygosity (RoH) Forensics applications and non-invasive genetics (PID, assignment tests) Genome sequencing and assembly: Conceptual and practical aspects PacBio representatives will present recent technologies and services Inferring population structure and conservation units Effective population size estimation Assignment tests for quantifying gene flow, dispersal, and forensics assignments (WGSassign, GeneClass) Gene flow estimation (BayesAss) Detecting local adaptation and selection signatures (Landscape Genomics) Phylogeny and phylogenomics eDNA Metabarcoding applications (biodiversity monitoring, diet analysis, microbiomes, etc.) Uses of AI in genomics data analysis. Detection of selective sweeps.

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Course Online AnalysingSpeciesData Biodiversity systematics

As you prepare to launch research projects this fall, do you or your grad students need refreshers on how to make your biodiversity data reproducible? How to handle species data is a topic that is mostly ignored by universities even though species are the basic units of biodiversity studies – so most of us never learned. However, these concepts are imperative to understanding your species data, whether you can trust species IDs in GenBank or GBIF, and understanding how the missing data from undiscovered "dark taxa" species can impact your research. This crash course will cover all of these ideas as well as where systematics is heading in the era of genomics and AI. The crash course will be Oct 5-9 and limited spots remain; you can register here: <https://www.transmittingscience.com/courses/evolution/decoding-species-the-foundation-of-biodiversity-data/> If you have any questions

about the course, please contact me: bernardj@hawaii.edu. For questions about registration, please contact courses@transmittingscience.com.

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Course Online Population Genomic Inference Low-coverage WGS 26-29 Oct

Join our online course "Population genomic inference from low-coverage whole-genome sequencing data", taking place 26-29 October.

Over four days, you'll learn practical, best-practice approaches for population genomic inference using genotype likelihoods, ANGSD and related tools – from processing sequencing data to analysing population structure, demographic history and signatures of natural selection.

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

The course combines interactive lectures with hands-on practical exercises using provided datasets, making it ideal for researchers looking to confidently incorporate low-coverage WGS into their own studies.

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

Frankfurt CCLENS Spring School Apr5-9 2027

Applications are open for the CCLENS Spring School 2027:

Critical Computational Literacy for Earth-Nature-Society Futures

5-9 April 2027 Frankfurt am Main, Germany

CCLENS is a five-day interdisciplinary spring school for early-career researchers interested in how compu-

tational models are built, connected, interpreted, and critically examined across ecology, biodiversity science, climate science, Earth-system science, economics, data science, computational social science, Science and Technology Studies, philosophy of science, and related fields.

We particularly welcome PhD candidates, early post-docs, and advanced Master's students interested in modelling at the interface of climate, biodiversity, and society.

Participants will work across four interconnected tracks:

Natural Sciences Models

Human-Earth System Models

Socio-Economic Models

Modelling Reflection and Science and Technology Studies

The school combines hands-on work with computational models with critical reflection on uncertainty, assumptions, model integration, and the movement of knowledge across disciplines.

There is no application or participation fee. Accommodation is fully covered, and travel support and childcare support can be requested.

Application deadline: 15 October 2026

Further information and application details: <https://www.c3s-frankfurt.de/what-we-do/cclens-spring-school> Please feel free to circulate this announcement to students, colleagues, and relevant networks.

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FUBerlin Programming For Evolutionary Biology- March 2027

Course on Programming for Evolutionary Biology

When: March 5th - 22nd 2027

Location: Berlin, Germany

Detailed information about the course content and how to apply: <https://www.evop-bioinf.de/> Founded in 2012, our well established course is back with established and novel content! In this intensive 16 days course, students will learn how to survive in a Linux en-

environment, get hands-on experience in two widely used programming languages (Python and R), and statistical data analysis. The classes will be given by experts in the field and consist of lectures and exercises with the computer. The aim of the course is to provide the students with the necessary background and skills to perform computational analyses with a focus on solving research questions related to genomics and evolution. The philosophy of the course will be "learning by doing", which means that the computational skills will be taught using examples and real data from evolutionary biology for the exercises. During the course, students will also propose projects of their own interest and perform them as final projects in small groups under the supervision of a teaching assistant. This course is open for students from all countries and targeted toward PhD students and postdocs of evolutionary biology or related research fields with no or little programming experience who want to become proficient in computational evolutionary biology in a couple of weeks.

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

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MachineLearningForGenomics Online

Machine Learning for Evolutionary Genomics (MLEG01) - Applications for Evolutionary Biology Only 4 places left! https://prstats.org/course/machine-learning-for-evolutionary-genomics-mleg01/?utm_source=chatgpt.com Delivered by Dr. Nikolay Oskolkov, a bioinformatician, computational biologist, and data scientist with extensive experience in machine learning, deep learning, population genomics, metagenomics, ancient DNA, dimensionality reduction, and computational biology. Learn how to apply machine learning and AI methods to evolutionary and genomic datasets using R and Python. Machine learning is increasingly important in evolutionary biology, providing powerful approaches for extracting patterns from large, complex, and high-dimensional genomic datasets. Applications range from population genomics and detecting introgression to ancient DNA, metagenomics, dimensionality reduction, sequence classification, and evolutionary inference. This course

provides practical training in classical and modern machine-learning approaches, with hands-on examples drawn from evolutionary biology and genomics. What you'll gain A strong understanding of supervised and unsupervised machine learning Practical experience implementing machine-learning methods in R and Python Skills using PCA, t-SNE, and UMAP to investigate high-dimensional genomic data Experience applying machine learning to population and evolutionary genomics Understanding of machine-learning approaches for identifying introgressed genomic regions Applications to ancient DNA and ancient-status inference Experience with Random Forests and artificial neural networks Introduction to deep learning and convolutional neural networks Understanding of machine-learning applications in metagenomics and microbial evolution Experience treating DNA sequences as data for natural language processing (NLP) approaches Confidence selecting and evaluating machine-learning methods for evolutionary research

Course format 5-day live, instructor-led online course 25 hours of training Hands-on practical exercises in R and Python Real-world biological and genomic datasets Strong focus on practical applications in evolutionary biology and genomics All sessions recorded

Who is this course for? Evolutionary biologists Population and evolutionary geneticists Evolutionary genomic researchers Bioinformaticians and computational biologists Researchers working with ancient or environmental DNA Researchers analysing population-genomic and other high-dimensional biological datasets PhD students and early-career researchers interested in applying machine learning to evolutionary questions Participants should have a basic background in R or Python and some familiarity with biological datasets. Prior experience with machine learning or deep learning is not required.

Why take this course? Evolutionary genomics increasingly involves datasets containing thousands or millions of genetic variables across individuals, populations, and species. Machine learning provides powerful methods for discovering structure within these high-dimensional datasets and tackling questions that can be difficult to address using conventional statistical approaches alone. The course has particularly strong applications to evolutionary biology through its coverage of population genomics, introgression, ancient DNA, genomic sequence analysis, dimensionality reduction, metagenomics, and evolutionary inference. Participants will explore how machine-learning methods can identify genomic patterns, classify biological sequences, investigate population history, and extract meaningful information from complex evolutionary datasets. Whether you're in-

investigating population structure, introgression, adaptation, genomic variation, ancient DNA, microbial evolution, or other evolutionary genomic questions, this course provides a practical foundation for incorporating modern machine-learning approaches into your research. Course dates 14-18 September 2026 25 hours — Live online — GBP400 Learn more & enrol https://prstats.org/course/machine-learning-for-evolutionary-genomics-mleg01/?utm_source=chatgpt.com Questions? Email: oliver@prstats.org

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Online Accessible Bioinformatics for Windows Users Oct2-6

Hello EVOLDIR members

Evolutionary studies increasingly depend on practical access to sequencing analysis workflows. Accessible Bioinformatics for Windows Users is a 2-day seminar livestreaming October 2 and 6, led by Andres Zhou Tsang (Adelaide University). Configure a Windows-based bioinformatics environment with WSL and use Linux tools alongside native applications. Process sequencing data through basecalling, genome assembly, alignment, annotation, and RNA-seq differential expression workflows. Apply these methods to evolutionary and genetic questions using data generated on a Windows computer.

Details and registration: Please circulate this information if it is relevant to colleagues or students.

Best wishes Michael Zyphur Professor and Director Instats

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Online Advanced R Programming 27-30October

Dear all, Ready to take your R skills to the next level?

Join our online workshop "Beyond Beginner R: Advancing Your Coding Skills", taking place 27-30 October.

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

Across four days, you'll move beyond the basics and learn how to build clean, reproducible, collaborative, and publication-ready R workflows – from advanced tidyverse programming and purrr to ggplot2, Quarto, GitHub, and AI-assisted coding.

The workshop is designed for researchers with working knowledge of R who want to write better code, structure projects effectively, and learn how to use AI coding tools critically and responsibly.

A practical workshop to sharpen your R skills and bring your research workflows to the next level.

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

Carlo —————

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

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Online Advanced Statistical Methods for Genetic Association Studies Sep8-10

Hello EVOLDIR members A reminder - Explore statistical approaches for connecting genetic variation with evolutionary research questions. Advanced Statistical Methods for Genetic Association Studies is a 2-day seminar livestreaming September 8 and 10 with Jingjing Yang (School of Medicine, Emory University). Use genotype quality control, mixed-model association tests, and population-structure correction in analyses of genetic variation. Compare molecular QTL mapping, co-localization, Mendelian Randomization, and TWAS approaches while assessing their assumptions. Develop reproducible R, Python, and Bash workflows for documenting evolutionary genetic analyses and interpreting polygenic signals. Details and registration: Further information is available on the seminar page Michael Zyphur, Professor and Director, Instats

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Online AgenticAIforLifeSciences 3-4Dec

Dear all,

We are pleased to announce the 3rd edition of Agentic AI for Life Sciences, a practical online course taking place on 3-4 December.

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

This course will give life scientists the practical skills to work with AI agents, build reusable research workflows, and critically evaluate their outputs.

Participants will learn to: -Use coding agents for data analysis, visualisation, and presentations -Build interactive data portals from omics data -Create reusable AI skills and agent configurations -Connect agents to PubMed, GitHub, and other knowledge sources using RAG and MCP -Integrate AI into reproducible research workflows -Understand where AI helps, where it fails, and how to use it responsibly The course is designed for biologists, bioinformaticians, data scientists, and other life sciences researchers.

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

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

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Online Ancient DNA Analysis 26-30Oct

Ancient DNA Analysis (ADNA01) - Applications for Evolutionary Biology <https://prstats.org/course/ancient-dna-analysis-adna01/> Delivered by Dr Nikolay Oskolkov, a bioinformatician, computational biologist and data scientist with extensive experience in genomics, metagenomics, population genomics and ancient DNA analysis. Learn how to analyse ancient DNA

(aDNA) and ancient metagenomic datasets, from raw sequencing reads through quality control, authentication and contamination assessment to population structure, ancestry and evolutionary interpretation. Ancient DNA provides evolutionary biologists with a unique opportunity to investigate biological change directly through time. Ancient genomic data can reveal changes in population structure, ancestry, migration, admixture and gene flow, allowing evolutionary hypotheses to be investigated using genetic information recovered from historical and ancient material.

What you'll gain Understand the principles of ancient genomics and ancient metagenomics Understand DNA degradation, low sequencing coverage and post-mortem damage Perform quality control, adapter trimming and read merging using fastp Align ancient DNA reads using BWA and Bowtie2 Perform taxonomic profiling of ancient metagenomic datasets using Kraken and sourmash Identify, evaluate and mitigate modern contamination Authenticate ancient DNA using characteristic damage patterns Use mapDamage and PMDtools Work effectively with low-coverage ancient sequencing data Use genotype likelihoods and probabilistic variant calling with ANGSD Analyse population structure using PCA, t-SNE and UMAP Infer ancestry using ADMIXTURE and STRUCTURE Use population-genetic approaches to investigate evolutionary history Understand and apply F2, F3 and F4 statistics Use D-statistics / ABBA-BABA to investigate gene flow and introgression Investigate ancestry, migration, admixture and population relationships Develop complete workflows from raw ancient sequencing data to evolutionary interpretation

Course format Dates: 26-30 October 2026 Duration: 5 days, 25 hours total Format: Live online Combination of theoretical instruction and hands-on computational analysis Practical analysis of ancient genomic datasets R/RStudio and Python/Jupyter used alongside specialist bioinformatics tools All sessions recorded 30 days' access to recordings 30 days of post-course email support Course fee: GBP400

Who is this course for? The course is particularly relevant to students and researchers working in: Evolutionary biology Evolutionary genomics Population genetics and population genomics Ancient DNA and palaeogenomics Molecular evolution Human evolution Archaeogenetics Phylogeography Admixture and introgression Population history and demographic change Conservation and evolutionary genetics Ancient metagenomics It is particularly useful for researchers interested in using genomic information to reconstruct population relationships, ancestry, migration, admixture, gene flow and evolutionary change through time. Participants should

have a basic understanding of genetics and molecular biology and some familiarity with command-line computing and bioinformatics. Previous experience with next-generation sequencing is useful but not essential.

Why take this course? Most evolutionary genomic studies infer historical processes from genetic variation observed in living populations. Ancient DNA adds a temporal dimension, allowing researchers to analyse individuals and populations that existed at different points in evolutionary history. This can substantially improve our understanding of processes such as population turnover, migration, admixture, introgression and changing population structure. Rather than relying exclusively on present-day genetic patterns, ancient genomes can provide direct evidence of populations and genetic relationships that may no longer exist in modern samples. The course combines the specialist challenges of working with ancient DNA – including degradation, contamination, post-mortem damage and low sequencing coverage – with population-genomic methods for evolutionary inference. Approaches including ANGSD, PCA, ADMIXTURE, STRUCTURE, F-statistics and D-statistics allow participants to move from authenticated ancient sequence data to questions concerning ancestry, population history, gene flow and evolutionary relationships. For evolutionary researchers, this provides a practical workflow connecting ancient genomic data processing with population genetics and evolutionary inference. Please feel free to share this course with colleagues, friends, research groups, labs, and others within your institute, organisation, or wider research network.

Learn more & enrol Ancient DNA Analysis (ADNA01) <https://prstats.org/course/ancient-dna-analysis-adna01/Questions?>

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Online BayesianModellingUsingR-INLA 21to25Sept

Bayesian Modelling Using R-INLA (BMIN04) - Applications for Evolutionary Biology <https://prstats.org/course/bayesian-modelling-using-r-inla-bmin04/>

<https://prstats.org/course/bayesian-modelling-using-r-inla-bmin04/> Only 3 places left! Delivered by Dr. Virgilio Gomez-Rubio, a statistician with extensive expertise in Bayesian inference, spatial statistics, statistical computing, and the application of Integrated Nested Laplace Approximation (INLA) to complex data. He is the author of Bayesian Inference with INLA and has extensive experience developing and applying Bayesian and spatial modelling methods in R. Learn how to use Bayesian modelling and R-INLA to analyse hierarchical, spatial, temporal, and other complex datasets, with methods highly applicable to evolutionary biology, evolutionary ecology, and comparative research. Evolutionary datasets frequently contain hierarchical structure, phylogenetic or population-level grouping, spatial and temporal dependence, repeated observations, missing data, and multiple sources of uncertainty. Bayesian modelling provides a powerful framework for handling these complexities, while INLA provides an efficient alternative to conventional MCMC for fitting a broad class of sophisticated Bayesian models.

What you'll gain A strong understanding of Bayesian inference and prior specification Practical experience fitting Bayesian models using R-INLA Skills fitting GLMMs and multilevel models Experience modelling hierarchical biological datasets Practical training in spatial Bayesian modelling Skills for analysing time-series and spatiotemporal data Understanding of latent effects and advanced INLA model structures Experience comparing models using DIC and WAIC Skills interpreting posterior distributions and quantifying uncertainty Approaches for handling missing values and imputation Confidence applying Bayesian modelling workflows to complex evolutionary datasets

Course format 5-day live, instructor-led online course Combination of lectures and hands-on practical exercises Dedicated practical sessions throughout Opportunity to discuss participants' own datasets and research questions All code, datasets, and presentation materials provided All sessions recorded 30 days of recording access and post-course email support

Who is this course for? Evolutionary biologists Evolutionary ecologists Population and quantitative biologists Evolutionary geneticists Researchers working with spatial or temporal evolutionary data Researchers analysing hierarchical and repeated-measures datasets Researchers studying variation among individuals, populations, or species PhD students and researchers wanting to develop Bayesian modelling skills in R

Why take this course? Evolutionary datasets often have structures that are difficult to accommodate with simple statistical models. Researchers may need to ac-

count simultaneously for variation among individuals and populations, repeated measurements, geographic structure, temporal dependence, environmental effects, and uncertainty. Bayesian hierarchical modelling provides a flexible framework for these problems, and R-INLA makes many complex Bayesian models computationally efficient to fit. This makes the approach particularly useful for large or structured biological datasets where conventional MCMC methods can become computationally demanding. The methods taught have potential applications to evolutionary ecology, population dynamics, geographic variation, spatial evolutionary processes, longitudinal studies, comparative biological datasets, and analyses incorporating multiple levels of biological variation. Whether you're investigating variation among populations, evolutionary responses across environments, spatial or temporal patterns in traits, population dynamics, or other complex evolutionary questions, this course provides a practical framework for incorporating Bayesian inference into your research. Course dates 21-25 September 2026 14:00-21:30 UK time 5 days — Live online — GBP500 Learn more & enrol <https://prstats.org/course/bayesian-modelling-using-r-inla-bmin04/Questions?> Email: oliver@prstats.org

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Online Bayesian Statistics for Biomedical Data Science Nov30-Dec4

Dear all,

We are pleased to announce our upcoming online course Bayesian Methods for Biomedical Data Science, taking place November 30-December 4.

Online sessions: 14:00-18:00 Berlin time (CET)

Course website: <https://www.physalia-courses.org/courses-workshops/bayesian-in-compgen/>

This five-day course provides a practical introduction to Bayesian methods for researchers working with computational and biomedical data. Participants will develop a solid understanding of Bayesian estimation and inference, while gaining hands-on experience implementing and evaluating Bayesian models using biological datasets and freely available computational tools.

The course will cover Bayesian modelling and compu-

tation, including prior specification, posterior inference, MCMC and convergence diagnostics, hierarchical and generalized linear models, regularization, variational inference, and Bayesian approaches to multimodal data integration and uncertainty quantification. The programme combines lectures, practical exercises, and discussion, with an emphasis on developing the skills needed to apply these methods independently.

The course is aimed at advanced MSc, PhD, and post-doctoral researchers in statistics, biostatistics, and computational biology.

For the full list of our courses and workshops, please visit: <https://www.physalia-courses.org/courses-workshops/> Best regards, Carlo —————
– Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR
info@physalia-courses.org

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Online Bioacoustics Data Analysis19-23Oct

Hi everyone, Bioacoustics Data Analysis (BIAC06) - Applications for Evolutionary Biology 19-23 October 2026 — 20 hours — GBP400 — Live Online <https://prstats.org/course/bioacoustics-data-analysis-biac06/> Delivered by Dr Marcelo Araya-Salas, a behavioural ecologist and scientific programmer specialising in animal communication and bioacoustics. Marcelo is the developer of several R packages for bioacoustic research, including warbleR, Raven and baRulho. His research combines behavioural ecology, evolutionary biology and quantitative acoustic analysis to investigate the diversity and evolution of animal communication. Learn how to analyse animal acoustic signals using R, from the fundamental principles of digital sound and spectrograms through to quantitative measurements, signal comparison, acoustic spaces and the analysis of vocal sequences. Acoustic signals are complex phenotypic traits that can vary among individuals, populations and species. Quantitative bioacoustic methods therefore provide powerful tools for investigating signal evolution, geographic and population-level variation, behavioural divergence, communication systems and the diversification of acoustic traits.

What you'll gain Understand the fundamentals of digital sound and bioacoustic data Import, manipulate and

manage audio data in R Work with different audio formats and wave objects Understand Fourier transforms and spectrograms Produce and customise spectrograms Filter, resample and process acoustic recordings Measure the frequency, duration and amplitude of acoustic signals Import and work with Raven Pro annotations Automate acoustic measurements using warbleR Perform quality control on acoustic measurements Analyse harmonic structure and timbre Work with Mel-frequency cepstral coefficients (MFCCs) Compare acoustic signals using cross-correlation Apply dynamic time warping to signal comparison Understand and quantify signal-to-noise ratio Analyse songs, calls and other vocal sequences Explore acoustic spaces and vocal diversity Quantify variation in acoustic traits among individuals, populations and species Develop reproducible bioacoustic workflows in R

Course format Dates: 19-23 October 2026 Time: 13:30-17:30 UK time each day Duration: 5 days, 4 hours per day (20 hours total) Format: Live online Combination of lectures and hands-on practical exercises Practical analysis conducted in R Course materials and example datasets provided All sessions recorded 30 days' access to recordings 30 days of post-course email support Course fee: GBP400

Who is this course for? The course is particularly suitable for students and researchers working in: Evolutionary biology Evolutionary ecology Animal communication Behavioural ecology Bioacoustics and ecoacoustics Acoustic trait evolution Population and geographic variation Comparative biology Ornithology Marine mammal research Wildlife biology Biodiversity and conservation research It will be particularly useful for evolutionary researchers interested in variation and divergence in acoustic traits, including studies comparing vocalisations among individuals, populations, species, geographic regions or evolutionary lineages. Participants should have a basic understanding of statistics and some previous experience using R. Why take this course? Animal vocalisations provide rich quantitative phenotypic data for investigating evolutionary questions. Differences in signal frequency, duration, structure and complexity can reflect variation among individuals and populations, environmental conditions, behavioural processes and evolutionary divergence. This course provides the practical tools needed to convert recordings into quantitative acoustic measurements, allowing researchers to characterise and compare vocal variation systematically. Methods such as cross-correlation, dynamic time warping, MFCCs and acoustic-space analysis provide different approaches for quantifying similarities and differences among signals. For evolutionary biologists,

these approaches can contribute to research on signal diversification, geographic variation, population differentiation, behavioural evolution and the evolution of animal communication, while providing reproducible workflows for analysing acoustic data in R. Please feel free to share this course with colleagues, friends, research groups, labs, and others within your institute, organisation, or wider research network. Learn more & enrol Bioacoustics Data Analysis (BIAC06) <https://prstats.org/course/bioacoustics-data-analysis-biac06/Questions?> Email: oliver@prstats.org

Best wishes, Oliver Hooker

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Online Biodiversity foundations crash course Oct5-9

Dear EvolDir community, Only a handful of seats remain for an online crash course on biodiversity foundations, running Oct 5-9. You are likely gearing up for starting research projects right now, so this is a great time for you and/or your students to get a primer on the basics of handling species data. This course will include - how to make your species identification repeatable (don't fall into the same trap as many other researchers) - how to standardize your species names - things to bear in mind when using species data from public databases like GenBank, BoLD, GBIF, or iNaturalist - the high chance that you will come across an unknown species - And more! This course covers things that are not covered in universities, although they are fundamental to any evolutionary or ecological study that uses species.

You can register here: <https://www.transmittingscience.com/courses/evolution/decoding-species-the-foundation-of-biodiversity-data/> For course-related questions, please contact me: bernardj@hawaii.edu. For registration-related questions, please contact courses@transmittingscience.com. Apologies for cross-posting! Thank you, Jared Bernard

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Online Building AI Research-Teams Sep23-25

Hello EVOLDIR members A reminder - Develop a documented approach to AI-supported evolutionary research. Building AI Research Teams is a 2-day seminar livestreaming September 23 and 25 with Michael Zyphur (Instats). Structure specialist AI roles for literature review, evidence extraction, analysis, verification, and synthesis with explicit human approval. Evolutionary researchers can apply these methods to genetics questions, comparative evidence, and computational research tasks. The seminar considers how traces, shared state, and failure recovery support transparent evaluation of coordinated workflows. Details and registration: Full details are available on the Instats seminar page. Best wishes Michael Zyphur Professor and Director Instats

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Online Building Websites With Quarto

We are pleased to announce a two-day online hands-on course, "Building and Publishing a Website with Quarto," taking place on 29-30 September, 9:00 AM-1:00 PM Berlin time.

Course website: <https://www.physalia-courses.org/courses-workshops/quartowebiste/> The course will introduce participants to creating, customising, and publishing a professional website with Quarto and GitHub Pages. It is aimed at researchers, PhD students, postdocs, educators, and data professionals. No prior Quarto experience is required.

Participants will build their own website throughout the course, covering content creation, customisation, Git/GitHub, and online publishing.

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

Online Causal AI Methods for Computational Biology 2-6 November

Dear all, We are pleased to announce the online course "Causal AI Methods for Computational Biology", taking place 2-6 November.

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

This five-day course introduces causal inference, causal machine learning, and AI methods for computational biology, combining foundational concepts with practical, hands-on exercises using biological datasets and publicly available tools.

The course is aimed at advanced MSc, PhD, and postdoctoral researchers in statistics, biostatistics, and computational biology. Working knowledge of R/Bioconductor is required.

Participants will learn how to formulate causal questions, work with DAGs, apply classical causal estimation methods, and use modern causal AI and machine learning approaches in computational biology and multi-omics workflows.

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 Data Apps in Python with Streamlit

Hello EVOLDIR members Interactive apps can make evolutionary datasets easier to explore and communicate. Data Apps in Python with Streamlit led by Ari Lamstein (American Statistical Association) is now available as an on-demand streaming seminar. Python and Streamlit can turn complex evolutionary and genetic datasets into interactive data apps with filters

and dynamic visualisations. Participants use pandas, Jupyter Notebooks, GitHub, virtual environments, and reproducible project structures to build and deploy an app. Evolutionary researchers can apply these skills to share explorations of genetic variation, trait data, or population patterns with collaborators and audiences. Course details: Further information is available on the Instats course page.

Best wishes Michael Zyphur Professor and Director Instats

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Online DeepLearningForEvoGenomics 5to9Oct

Deep Learning for Evolutionary Genomics (DLEG01) - Applications for Evolutionary Biology <https://prstats.org/course/deep-learning-for-evolutionary-genomics-dleg01/> Only 4 places left! Delivered by Dr. Nikolay Oskolkov, a bioinformatician, computational biologist, and data scientist working at the intersection of biology, statistics, and artificial intelligence. His expertise includes machine learning, deep learning, population genomics, ancient DNA, metagenomics, dimensionality reduction, and computational biology. Learn how to apply deep learning and neural networks to evolutionary and genomic datasets, with methods highly applicable to evolutionary genomics, population genetics, molecular evolution, adaptation, introgression, functional genomics, and ancient DNA research. Modern evolutionary research increasingly involves large, complex, and high-dimensional genomic datasets. Deep learning provides powerful approaches for identifying patterns in genomic sequences, extracting structure from population genomic data, detecting introgressed regions, analysing ancient DNA, identifying functional genomic elements, and modelling biological sequences. This course provides practical training in these methods using examples drawn directly from evolutionary biology and genomics.

What you'll gain An understanding of the theoretical foundations of artificial neural networks and deep learning Practical experience implementing deep learning approaches in R and Python Understanding of feed-forward neural networks, CNNs, RNNs, and LSTM networks Applications of neural networks to popula-

tion and evolutionary genomics Use of feed-forward neural networks to identify introgressed genomic regions Experience using autoencoders for dimensionality reduction and representation learning Comparison of autoencoders with PCA, t-SNE, and UMAP Applications of CNNs to gene annotation, promoter prediction, enhancer detection, and functional genomic analysis Approaches for analysing DNA using natural-language-processing concepts Deep-learning applications to ancient DNA and ancient-status inference Understanding of transformer architectures and their applications to biological sequence modelling Experience extracting biological patterns from complex, high-dimensional genomic datasets

Course format 5-day live, instructor-led online course 25 hours of training Combination of lectures and hands-on practical exercises Practical implementation in R and Python Examples from evolutionary biology, population genomics, functional genomics, metagenomics, and ancient DNA Opportunity to discuss participants' own data All code, datasets, and presentation materials provided All live sessions recorded 30 days of recording access and post-course email support

Who is this course for? Evolutionary biologists Evolutionary and population geneticists Evolutionary genomic researchers Molecular evolution researchers Researchers studying adaptation, introgression, and population history Ancient DNA and palaeogenomic researchers Functional genomic researchers Bioinformaticians and computational biologists Postgraduate students and early-career researchers Participants should have a basic background in R or Python and some familiarity with biological datasets. A foundation in statistics, probability, and machine learning is helpful but not required, and prior experience with neural networks or deep learning is not necessary.

Why take this course? Evolutionary genomics increasingly relies on datasets containing millions of genetic variants, complex sequence information, and high-dimensional representations of individuals and populations. Extracting evolutionary information from these datasets presents computational and statistical challenges that are particularly well suited to modern machine-learning approaches. Deep learning can identify nonlinear patterns and complex relationships that may be difficult to capture using conventional methods. In population genomics, autoencoders can be used for representation learning and dimensionality reduction, while neural networks can be applied to problems such as identifying introgressed genomic regions and reconstructing aspects of population history. The course also explores applications to functional genomics and ancient DNA, including CNN-based identification

of functional genomic elements and deep-learning approaches for ancient-status inference. Transformer architectures extend these ideas to biological sequence modelling, providing an introduction to some of the newest AI approaches being applied to genomic research. Whether you're investigating population history, adaptation, introgression, genomic variation, ancient DNA, functional evolution, or biological sequence evolution, this course provides a practical foundation for incorporating modern deep-learning methods into evolutionary research. Course dates

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Online Deep Learning for Evolutionary Genomics 5-9Oct

Deep Learning for Evolutionary Genomics (DLEG01) - Applications for Evolutionary Biology <https://prstats.org/course/deep-learning-for-evolutionary-genomics-dleg01/> Delivered by Dr. Nikolay Oskolkov, a bioinformatician, computational biologist, and data scientist working at the intersection of biology, statistics, and artificial intelligence. His expertise includes machine learning, deep learning, population genomics, ancient DNA, metagenomics, dimensionality reduction, and computational biology. Learn how to apply deep learning and neural networks to complex evolutionary and genomic datasets, with applications to population genomics, molecular evolution, adaptation, introgression, functional genomics, ancient DNA, and evolutionary inference. Modern evolutionary research increasingly generates large and high-dimensional genomic datasets. Deep learning provides powerful approaches for identifying complex patterns in genomic sequences, extracting structure from population genomic data, detecting introgressed regions, analysing ancient DNA, identifying functional genomic elements, and modelling biological sequences.

What you'll gain An understanding of the foundations of artificial neural networks and deep learning Practical implementation of deep-learning methods in R and Python Understanding of feed-forward neural networks, CNNs, RNNs, and LSTM networks Applications of neural networks to population and evolutionary genomics

Use of neural networks for identifying introgressed genomic regions Autoencoders for dimensionality reduction and representation learning Comparison of autoencoders with PCA, t-SNE, and UMAP Applications of CNNs to gene annotation and functional genomic elements Approaches for analysing DNA as sequence data Deep-learning applications to ancient DNA Introduction to transformer architectures for biological sequence modelling Practical experience extracting biological information from complex, high-dimensional genomic datasets

Course format 5-day live, instructor-led online course 25 hours of training Combination of lectures and hands-on practical exercises Practical implementation using R and Python Examples from evolutionary biology, population genomics, functional genomics, metagenomics, and ancient DNA Opportunity to discuss participants' own data All code, datasets, and presentation materials provided All live sessions recorded 30 days of recording access and post-course email support

Who is this course for? Evolutionary biologists Evolutionary and population geneticists Evolutionary genomic researchers Molecular evolution researchers Researchers studying adaptation and population history Researchers investigating hybridisation, gene flow, and introgression Ancient DNA and palaeogenomic researchers Functional genomic researchers Bioinformaticians and computational biologists Postgraduate students and early-career researchers Participants should have a basic background in R or Python and some familiarity with biological datasets. Foundational knowledge of statistics, probability, and machine learning is useful but not required, and no previous experience with neural networks or deep learning is necessary.

Why take this course? Evolutionary genomics increasingly involves datasets containing millions of genetic variants, complex sequence information, and high-dimensional representations of individuals and populations. Extracting evolutionary information from these datasets presents computational and statistical challenges for which modern deep-learning methods provide an expanding toolkit. For population and evolutionary genomics, neural networks can be used to identify complex genomic patterns associated with processes such as introgression, while autoencoders provide approaches for representation learning and dimensionality reduction. These methods complement established approaches such as PCA, t-SNE, and UMAP and can help reveal structure within high-dimensional genomic datasets. The course also explores applications to functional evolution and ancient DNA. CNNs can be applied to identifying functional genomic elements, while recurrent neural networks and transformer archi-

tectures provide approaches for modelling biological sequences. Deep-learning methods for ancient-status inference introduce further applications to evolutionary and palaeogenomic research. Whether you're investigating population history, adaptation, introgression, genomic variation, ancient DNA, functional evolution, or biological sequence evolution, this course provides a practical foundation for incorporating modern deep-learning approaches into evolutionary research. Course dates 5-9 October 2026 25 hours — Live online — GBP400 Learn more & enrol <https://prstats.org/course/deep-learning-for-evolutionary-genomics-dleg01/>

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Online Environmental Metagenomics 12-16October

Dear all, There are only a few seats left for our upcoming online course Environmental Metagenomics: From Reads to Genomes, taking place 12-16 October.

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

Join us for a hands-on week exploring how to go from raw sequencing reads to taxonomic profiles, metagenome-assembled genomes (MAGs), and functional insights. We'll cover practical workflows for both short- and long-read data, including quality control, assembly, binning, MAG assessment, and functional analysis.

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 ExploringAndVisualizingOmicsData 25-26Nov

We are pleased to announce the online course "Exploring and Visualizing Omics Data", taking place on 25-26 November, from 13:00-17:00 CET each day. Course website: <https://www.physalia-courses.org/courses-workshops/isee/> This two-day course provides a practical introduction to iSEE, a Bioconductor package for interactive exploration and visualization of omics datasets, with a particular focus on single-cell and bulk RNA-seq data. The course combines introductory lectures with hands-on exercises, including interactive data exploration, reproducible workflows, and applications to participants' own projects.

The course is aimed primarily at students and researchers with some familiarity with sequencing and single-cell data.

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

Online GenomeAssembly Sept 22-24

The Computational Biology Core at the University of Connecticut is hosting virtual bioinformatics workshops this Fall! We still have space available in our Genome Assembly Workshop (virtual but live instruction - Sept. 22-24). Whether you're new to genome assembly or looking to refine your expertise, this hands-on training will walk you through sequencing strategies, quality control, and assembly methods. Learn sequencing techniques, short & long-read assembly, hybrid approaches, and QC best practices—all from your own laptop! Learn more & register here: [<https://bioinformatics.uconn.edu/cbc-workshops/>] (<https://bioinformatics.uconn.edu/cbc-workshops/>) WHERE: Virtual (MS Teams) WHEN: 10:00 AM - 2:00 PM EST COST: \$500 (UConn affiliates)/\$600 (Exter-

nal participants) Registration is first come, first served. Questions? E-mail: cbcsupport@helpspotmail.com

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Online Genomics for Ecological and Evolutionary Studies

Hello EVOLDIR members

Genomic evidence can connect sequence variation with questions about evolutionary history and adaptation. Genomics for Ecological and Evolutionary Studies led by Giulio Formenti (Vertebrate Genome Lab, The Rockefeller University) and Guido Gallo (Department of Biosciences, University of Milan) is now available as an on-demand streaming seminar. Compare sequencing technologies and use command-line bioinformatics tools to align reads, call variants, and inspect variant call files. Analyse short and long reads with Bowtie 2, Samtools, Freebayes, and Minimap2, then compare alignments and draft genome assemblies. Evolutionary researchers can apply these workflows to investigate biodiversity, evolutionary history, and adaptation using genomic data.

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

Best wishes

Michael Zyphur Professor and Director Instats

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Online Joint Species Distribution Modelling JSMD using HMSC 26-29Oct

Joint Species Distribution Modelling (JSMD) using HMSC: A Hierarchical Modelling Approach (JSMD01) - Applications for Evolutionary Biology <https://prstats.org/course/joint-species-distribution-modelling-jsdm01/> Delivered by Dr Bastien Parisy, a community ecologist and postdoctoral researcher at the

University of Helsinki. His research focuses on community ecology and species interactions, particularly plant-soil microbe interactions and responses to environmental change. His work combines field and experimental ecology with quantitative approaches including network analysis and Joint Species Distribution Models (JSDMs), particularly HMSC. Learn how to analyse multi-species ecological and evolutionary data using Joint Species Distribution Models in R, integrating environmental responses with species traits, phylogenetic relationships, spatial and temporal structure, and patterns of species co-occurrence. Using the Hierarchical Modelling of Species Communities (HMSC) framework, participants will learn how phylogenetic relationships and species traits can be incorporated directly into hierarchical community models. This makes HMSC particularly useful for research at the interface of evolutionary biology, community ecology, trait evolution and biogeography.

What you'll gain Understand the principles of Joint Species Distribution Modelling (JSDMs) Understand the structure and applications of HMSC Prepare and structure multi-species datasets Integrate environmental, trait and phylogenetic information Relate species occurrences or abundances to environmental covariates Investigate how species traits influence environmental responses Examine whether evolutionary relationships help explain similarities and differences among species Account for spatial and temporal structure Build hierarchical community models in R Translate evolutionary and ecological hypotheses into HMSC models Understand the Bayesian and MCMC methods underlying HMSC Assess model convergence and quality of fit Evaluate predictive performance using cross-validation Interpret results at species and community levels Investigate species co-occurrence and residual associations Explore relationships between environmental responses and species characteristics Relate model outputs to niche theory and community assembly Produce and visualise HMSC outputs Report HMSC analyses appropriately in scientific manuscripts HMSC explicitly allows environmental covariates, traits and phylogeny to be incorporated within the same modelling framework.

Course format Dates: 26-29 October 2026 Time: 12:00-17:30 UK time each day Duration: 4 days, 5.5 hours per day (22 hours total) Format: Live online Combination of lectures and hands-on practical exercises in R Participants are encouraged to bring their own datasets for discussion Code, datasets and presentation materials provided All sessions recorded 30 days' access to recordings 30 days of post-course email support Course fee: GBP450

Who is this course for? The course is particularly rel-

evant to students and researchers working in: Evolutionary biology Evolutionary ecology Community ecology Phylogenetic community ecology Trait-based ecology Comparative ecology Biogeography and macroecology Community assembly Biodiversity research Species-environment relationships Spatial and temporal ecology Quantitative ecology It will be especially useful for evolutionary researchers working with multi-species datasets containing trait or phylogenetic information, and for those interested in connecting evolutionary relationships and species characteristics with ecological responses.

Why take this course? Species are not necessarily evolutionarily independent units. Shared evolutionary history may be associated with similarities in traits and ecological characteristics, while divergence among lineages can contribute to differences in how species respond to their environments. HMSC provides a framework for incorporating species traits and phylogenetic relationships directly alongside environmental, spatial and temporal predictors. This allows researchers to investigate multi-species patterns while considering both ecological variation and evolutionary relationships. For evolutionary biologists, this provides a useful framework for questions concerning trait-environment relationships, niche differentiation, community assembly, phylogenetic structure and variation in environmental responses among species. Participants will learn how to formulate these questions as hierarchical models and then fit, validate, interpret and report them using HMSC in R. Please feel free to share this course with colleagues, friends, research groups, labs, and others within your institute, organisation, or wider research network. Learn more & enrol Joint Species Distribution Modelling (JSDM) using HMSC: A Hierarchical Modelling Approach (JSDM01)

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Online Measuring Latent Variables with Questionnaires Sep30-Oct2

Hello EVOLDIR members A reminder - Comparative research benefits from evidence about how survey measures function. Measuring Latent Variables with Ques-

tionnaires is a 2-day seminar livestreaming September 30 and October 2 with Bert Weijters (Faculty of Psychology and Educational Sciences, Ghent University). Measurement invariance and confirmatory factor analysis can test whether questionnaire constructs support defensible evolutionary and genetics comparisons. Participants will evaluate factor structure, reliability, response biases, and ordinal items in R. These skills can assist research on attitudes toward evolution, genetic literacy, perceived ancestry, and reported biological beliefs. Details and registration: Please circulate this reminder if it is relevant to colleagues or students.

Best wishes Michael Zyphur Director Instats

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Online Path Analysis Structural Equations and Causal Inference 19-30Oct

Path Analysis, Structural Equations and Causal Inference for Biologists (PSCB04) - Applications for Evolutionary Biology <https://prstats.org/course/path-analysis-structural-equations-and-causal-inference-for-biologists-pscb04/> Delivered by Prof. John William (Bill) Shipley, Professor Emeritus at Universite de Sherbrooke and a plant and statistical ecologist internationally recognised for his work on causal modelling, path analysis and structural equation modelling. Prof. Shipley is the author of *Cause and Correlation in Biology* and has published more than 170 peer-reviewed papers. Learn how to use path analysis, structural equation modelling (SEM) and causal inference in R to investigate complex cause-and-effect relationships in evolutionary and biological data. Evolutionary systems frequently involve networks of interacting processes rather than simple relationships between individual predictors and responses. Environmental conditions, phenotypic traits, evolutionary history and other biological processes can exert both direct and indirect effects. This course provides a rigorous framework for translating such relationships into explicit causal hypotheses and evaluating them using observational data typical of ecological and evolutionary research.

What you'll gain Understand causal inference using experimental and observational data Translate biological and evolutionary hypotheses into directed acyclic graphs (DAGs) Understand d-separation and statisti-

cal conditioning Construct and test causal path models Distinguish direct and indirect causal effects Conduct piecewise structural equation modelling Use the piecewiseSEM package in R Incorporate mixed models and phylogenetic corrections Understand equivalent models and compare competing causal hypotheses Use AIC to compare non-equivalent models Conduct covariance-based path analysis Fit structural equation models using lavaan Construct and interpret latent variables and measurement models Incorporate nested and mixed models into SEM Work with non-normal biological data Fit and interpret multigroup models Understand causal heterogeneity Evaluate model fit and statistical power Deal with missing data and small sample sizes Report SEM results appropriately in scientific publications

Course format Dates: 19-30 October 2026 Duration: 35 hours Approximately 20 hours of lectures and 15 hours of practical work Format: Live online Practical analyses conducted in R and RStudio R scripts, datasets and supporting materials provided Opportunities to work with and receive feedback on your own data All sessions recorded 30 days' access to recordings 30 days of post-course support Course fee: GBP450

Who is this course for? The course is particularly suitable for students and researchers working in: Evolutionary biology Evolutionary ecology Comparative biology Trait evolution and functional biology Phenotypic variation Behavioural evolution Life-history research Evolutionary responses to environmental variation Quantitative and statistical evolutionary biology It will be particularly useful for researchers working with observational datasets containing multiple interacting variables, where the aim is to move beyond identifying correlations and instead formulate and evaluate hypotheses about the causal processes connecting biological variables. Participants should have experience using R and RStudio for statistical analysis and a basic understanding of statistical inference and regression. Familiarity with GLMs or mixed models is useful but not required.

Why take this course? Evolutionary questions often involve interconnected causal pathways. Environmental variation may influence a phenotype directly while also affecting other traits or biological processes that subsequently influence the same response. Similarly, apparent associations between traits can arise through indirect pathways, confounding variables or shared biological structure. Path analysis and SEM provide a framework for representing these hypotheses explicitly and evaluating whether observed data are consistent with the proposed causal structure. Participants will learn both piecewise SEM, which can accommodate mixed

models and phylogenetic corrections, and covariance-based SEM, including latent-variable approaches. Importantly, the course goes beyond learning how to fit SEMs in R. It develops the underlying logic of causal inference from observational biological data, including d-separation, equivalent models, direct and indirect effects, and the circumstances under which causal interpretations can be justified. These methods provide evolutionary biologists with a powerful framework for testing complex hypotheses involving multiple interacting processes.

Learn more & enrol Path Analysis, Structural Equations, and Causal Inference for Biologists (PSCB04)

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Online PhylogeneticsProteinStructure Nov2-6

Dear colleagues, Transmitting Science is offering the live online course "Structural Phylogenetics: putting protein structure into phylogenetic inference". Course webpage: <https://www.transmittingscience.com/courses/evolution/structural-phylogenetics> /This course introduces the principles and applications of structural phylogenetics, focusing on how protein structure can inform phylogenetic inference. As protein structure is typically more conserved than sequence, this approach supports phylogenetic problems where amino acid sequence similarity is highly decayed due to long time periods or rapid evolution (e.g. viruses). In such situations, alignment and accurate phylogenetic inference become very difficult. Through live online sessions, you'll explore how structural data complements sequence-based approaches. The programme combines conceptual explanations with guided practical exercises, giving you hands-on experience with structural datasets. For any questions, please write to courses@transmittingscience.com Best regards, Haris – Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net

Online
PopGenomicsAndStructureAnalysis
28SepTo2ndOct

Population Genomics and Structure Analysis (PGSA01) - Applications for Evolutionary Biology Only 6 places left! <https://prstats.org/course/population-genomics-and-structure-analysis-pgsa01/> Delivered by Dr. Nikolay Oskolkov, a bioinformatician, computational biologist, and data scientist with extensive experience in population genomics, evolutionary biology, ancient DNA, statistical modelling, dimensionality reduction, clustering, and computational biology. Learn how to analyse population structure, genetic differentiation, ancestry, gene flow, introgression, and genomic variation, using methods with direct applications across evolutionary biology, population genetics, evolutionary genomics, and studies of adaptation and demographic history. Population genomic data provide powerful opportunities to investigate the evolutionary processes shaping genetic variation within and among populations. Patterns of genomic differentiation can reveal population divergence, migration, admixture, introgression, demographic history, and signatures of selection, helping researchers reconstruct evolutionary histories and understand how populations have responded to natural selection and past environmental change.

What you'll gain Practical skills for processing and analysing population genomic data Understanding of genetic variation, SNP discovery, and variant calling Experience analysing low-coverage sequencing data using ANGSD Skills using PCA, MDS, t-SNE, and UMAP to explore population structure Understanding of the effects of sampling design on population genomic inference Practical experience with ADMIXTURE, STRUCTURE, and NGSadmix Skills investigating ancestry and admixture among populations Experience using ChromoPainter and fineSTRUCTURE to investigate fine-scale population structure Understanding and interpretation of FST, F2, and F3 statistics Approaches for conducting selection scans and identifying population differentiation Experience using F4 and D-statistics to investigate introgression and gene flow Confidence interpreting genomic patterns in an evolutionary context

Course format 5-day live, instructor-led online course

25 hours of training Practical analysis of population genomic datasets Hands-on experience with widely used population-genetic software Training across R, Python, and computational genomic workflows All course materials provided All sessions recorded 30 days of recording access and post-course email support

Who is this course for? Evolutionary biologists Population and evolutionary geneticists Evolutionary genomic researchers Molecular evolution researchers Researchers studying adaptation and population divergence Researchers investigating gene flow, admixture, and introgression Researchers studying demographic and evolutionary history Conservation and molecular geneticists Postgraduate students and early-career researchers A basic background in genetics and molecular biology is expected, together with some familiarity with R, Python, or Bash. Previous experience with population genetics or next-generation sequencing is beneficial but not essential.

Why take this course? Population genomics provides a powerful framework for investigating the evolutionary forces responsible for shaping genetic diversity within and among populations. Processes including natural selection, genetic drift, migration, population isolation, demographic change, hybridisation, and introgression all leave detectable signatures in genomic data. This course introduces practical methods for identifying and interpreting those signatures. PCA and ancestry-based approaches can reveal population structure and evolutionary relationships, while F-statistics provide tools for quantifying differentiation and examining shared ancestry. Selection scans can identify genomic regions potentially affected by natural selection, while D-statistics and related approaches can be used to investigate introgression and historical gene flow. These methods have particularly strong applications in evolutionary genetics, population genomics, adaptation, speciation research, hybridisation, demographic history, and comparative population studies. Whether you're investigating population divergence, evolutionary history, local adaptation, genetic differentiation, ancestry, admixture, selection, or introgression, this course provides practical tools for using genomic data to address fundamental questions in evolutionary biology. Course dates 28 September - 2 October 2026 25 hours — Live online — GBP400 Learn more & enrol <https://prstats.org/course/population-genomics-and-structure-analysis-pgsa01/> Questions? Email: oliver@prstats.org

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Online Population Genomics and Structure Analysis 28Sep-2Oct

Population Genomics and Structure Analysis (PGSA01) - Applications for Evolutionary Biology <https://prstats.org/course/population-genomics-and-structure-analysis-pgsa01/> Delivered by Dr. Nikolay Oskolkov, a bioinformatician, computational biologist, and data scientist with extensive experience in population genomics, evolutionary biology, ancient DNA, dimensionality reduction, clustering, and computational biology. Learn how to analyse population structure, genetic differentiation, ancestry, gene flow, introgression, and genomic variation, with methods directly applicable to evolutionary genetics, evolutionary genomics, adaptation, population divergence, and demographic history. Population genomic data provide powerful insights into the evolutionary processes shaping genetic diversity within and among populations. Genomic patterns can reveal population divergence, migration, admixture, introgression, demographic history, and signatures of selection, allowing researchers to investigate how natural selection, genetic drift, gene flow, and historical processes have shaped populations through time.

What you'll gain Practical skills for processing and analysing population genomic data Analysis of genetic variation and low-coverage sequencing data using ANGSD PCA, MDS, t-SNE, and UMAP for investigating population structure Understanding of sampling effects and potential biases in population genomic inference Ancestry and population structure analysis using ADMIXTURE, STRUCTURE, and NGSadmix ChromoPainter and fineSTRUCTURE for fine-scale population structure Interpretation of FST, F2, and F3 statistics Selection scans for identifying signals of population differentiation F4 and D-statistics for investigating admixture, introgression, and gene flow Practical experience interpreting genomic patterns within an evolutionary framework

Course format 5-day live, instructor-led online course 25 hours of training Lectures combined with practical population genomic analyses Hands-on experience with widely used population-genetics software Practical

work using R, Python, Google Colab, and Posit Cloud Code, datasets, and presentation materials provided All sessions recorded 30 days of recording access and post-course email support

Who is this course for? Evolutionary biologists Population and evolutionary geneticists Evolutionary genomic researchers Molecular evolution researchers Researchers studying adaptation and population divergence Researchers investigating gene flow, admixture, hybridisation, and introgression Researchers reconstructing population and demographic history Conservation and population genomic researchers Postgraduate students and early-career researchers

Why take this course? Many fundamental questions in evolutionary biology concern how and why populations become genetically differentiated. Natural selection, genetic drift, migration, demographic change, geographic isolation, admixture, and hybridisation can all leave characteristic signatures in genomic data. Population genomics provides a powerful toolkit for identifying and interpreting these signatures. Dimensionality-reduction and ancestry methods can reveal population structure and relationships, while F-statistics provide approaches for quantifying differentiation and shared ancestry. Selection scans can identify genomic regions showing unusual patterns of differentiation, and F4 and D-statistics can be used to investigate admixture, introgression, and historical gene flow. These approaches have particularly strong applications in evolutionary genetics, population genomics, adaptation, speciation, hybridisation, demographic history, and the reconstruction of evolutionary relationships among populations. Whether you're investigating population divergence, adaptation, genetic structure, ancestry, selection, gene flow, hybridisation, introgression, or demographic history, this course provides practical tools for incorporating population genomic analyses into evolutionary research. Course dates 28 September - 2 October 2026 25 hours — Live online — GBP400 Learn more & enrol <https://prstats.org/course/population-genomics-and-structure-analysis-pgsa01/> Questions? Email: oliver@prstats.org

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OnLine Population Genomics Data Analysis Course workshop-Sep25-Nov13

Genetic Data Analysis Course Online

Course Objective: To provide training in conceptual and practical approaches using genomic data to address key research questions. We emphasize next-generation sequencing data analysis and interpretation of outputs from key statistical approaches, pipelines, and software, taught by 18 expert instructors. You'll take raw reads through to genotype calling, assemble a genome, estimate pop effective sizes (N_e), inbreeding, gene flow, detect selection (landscape genomics), and more. See lecture titles and instructors here www.umontana.edu/congen/ Who should apply: Advanced undergraduates, M.S. and Ph.D. students, post-docs, faculty, with a basic understanding of population genetics.

Where: Online (Zoom). Lectures are video-recorded for asynchronous participation by overseas participants, and for rewatching later.

When: Monday, Wednesday & Friday, 8-9:50 AM, Sept 24th - Nov. 13th (20 + lectures by 18 experts)

To apply, email 'gordon.luikart@umontana.edu and leif.howard@flbsad.umn.edu or go to www.umn.edu/congen/ Selected lecture topics and instructors: see also www.umn.edu/congen/ . The role of genomics in population genetics, ecology, and conservation. Pop genomics: Concepts and tools to answer eco-evo questions. R & Linux basics, FastQ file format for next-generation sequencing data. Scripting, data handling, & organizing bioinformatics projects. Probability, Bayesian statistics, MCMC, and genotype likelihood calculations. The Coalescent: Theory and applications. Raw sequence read filtering and genotyping (with and without a reference genome). Filtering (QC) best practices & effects on downstream analyses (HWE, N_e tests etc.). Inbreeding and runs of homozygosity (RoH). Genome sequencing and assembly: Conceptual and practical aspects. PacBio representatives will present recent technologies and services. Inferring population structure and conservation units. Effective population size estimation. Assignment tests for quantifying gene flow, dispersal, & forensics (WGSassign, GeneClass), Gene flow estimation (BayesAss). Detecting local adaptation and selection signatures (Landscape Genomics). Phylogeny

and phylogenomics. eDNA Metabarcoding (biodiversity monitoring, diet analysis, microbiomes, etc.)

Past course review publications: Hendricks et al. 2018: <https://onlinelibrary.wiley.com/doi/full/10.1111/eva.12659>; Rena Schweizer et al. 2021: <https://doi.org/10.1093/jhered/esab019> Schiebelhut et al 2023: doi.org/10.1111/1755-0998.13893 ; Hemstrom et al. 2024: Next-generation data filtering. doi: 10.1038/s41576-024-00738-6

Instructors: Eric Anderson, Ellie Armstrong, Matt DeSaix, Chris Funk, Marty Kardos, Brenna Forester, Will Hemstrom, Paul Hohenlone, Bruce Ranala, Rena Schweizer, Arun Sethuraman, Steven Spear, Robin Waples, Schuyler Liphardt, and more...

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Online Python for biologists 19-22October

Dear colleagues, We are pleased to announce our upcoming online course Introduction to Python Programming for Biologists, taking place 19-22 October.

Course website: <https://www.physalia-courses.org/courses-workshops/python24/> This four-day, hands-on course is designed for biologists and life scientists with little or no previous programming experience. Participants will learn how to use Python to process, analyse, and visualise biological data, with practical projects covering DNA sequences, field data, BioPython, statistics, and data visualisation.

Whether you are a student, researcher, or group leader, this course will provide a practical foundation for using Python in your own 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 RADseq 7-11December

Dear colleagues, Working with RAD-seq, ddRAD, 2bRAD or GBS data?

Join our online course: RAD-seq Data Analysis

Dates: 7-11 December 2026

Course website: <https://www.physalia-courses.org/courses-workshops/course16/>

This hands-on course provides a practical introduction to reduced-representation genome sequencing data analysis, with a strong focus on Stacks and applications to non-model organisms.

You will learn how to: - Assess and preprocess high-throughput sequencing data - Perform de novo and reference-based loci assembly - Select informative genetic markers - Analyse RAD-seq data for population genetics, GWAS and phylogenetics - Work with both organisms with and without a draft reference genome - Use UNIX tools for genomic data analysis The course combines short lectures, instructor-led demonstrations and hands-on practical exercises, with opportunities to discuss and interpret results throughout the week.

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 RNaseq 9-18November

Dear colleagues,

We are pleased to announce our upcoming online course Introduction to RNA-seq Data Analysis with R/Bioconductor, taking place on November 9, 11, 13, 16, 17 and 18.

Online sessions: 15:00-18:00 Berlin time (CET)

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

[rg/courses-workshops/course19/](https://www.physalia-courses.org/courses-workshops/course19/)

This practical course is designed for biologists and bioinformaticians who want to develop the statistical skills needed to analyse high-throughput genomic and transcriptomic data. Starting from the fundamentals of statistical analysis in R, participants will progressively work through key steps of genomic data analysis, including hypothesis testing, data visualization, genomic region analysis, RNA-seq data processing, differential expression, and gene set analysis.

The course combines clear introductions to the underlying statistical concepts with hands-on exercises in R and Bioconductor, providing participants with practical experience using widely used tools and packages such as DESeq2 and edgeR.

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 Sex Chromosome Evolution 12-16October

Dear all,

there are still a few seats left for our online course on Sex Chromosome Evolution

Dates: 12-16 October

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

How do sex chromosomes evolve, and what can genomic and transcriptomic data tell us about their differentiation?

This hands-on online course will introduce practical approaches for identifying sex chromosomes and studying their evolution. Across five live sessions, we'll work with genomic and transcriptomic data to explore recombination suppression, evolutionary strata, sex-biased gene expression, dosage compensation, gene gain and loss, and genome divergence.

The course combines short lectures with practical computational exercises using Linux command-line tools and R and Bioconductor. Participants will work with

real datasets and learn how to analyse and interpret genomic patterns in an evolutionary context.

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

Best regards, Carlo

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

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Online Spatial Transcriptomics Oct28-30

Dear colleagues, Registration is open for the Transmitting Science live online course "Introduction to Spatial Transcriptomics". Course webpage:

<http://www.transmittingscience.com/courses/genetics-and-genomics/introduction-to-spatial-transcriptomics/> Course overview:

Standard RNA sequencing captures a cell's transcriptional status but loses its spatial context - the neighbouring cells and tissue organisation around it. This course introduces the fundamentals of spatial transcriptomics, covering both imaging-based and sequencing-based methods, and how gene expression patterns can be tracked across tissue types and diseases. Using publicly available datasets, participants will gain hands-on practice from data loading and quality control through to integration and niche identification. Highlights: Overview of spatial transcriptomics platforms (imaging-based and sequencing-based) Cell segmentation Cell typing Neighbourhood and niche identification For queries, please write to courses@transmittingscience.com. Best regards, Haris – Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.com (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Online Spatial transcriptomics with R Bioconductor 14-18December

Dear all,

Join our 5-day online course, "Spatial transcriptomics with R/Bioconductor," taking place 14-18 December.

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

Through lectures and hands-on labs, participants will learn how to analyse spatial and single-cell omics data using R/Bioconductor—from QC and cell segmentation to spatial mapping, niche analysis, and cell-cell communication. The course is aimed at researchers, graduate students, and professionals with basic R/Bioconductor experience.

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 Species Distribution Modelling with Bayesian Statistics 6-8Oct

Species Distribution Modelling with Bayesian Statistics (SDMB08) - Applications for Evolutionary Biology <https://prstats.org/course/species-distribution-modelling-with-bayesian-statistics-sdmb08/> Delivered by Dr Marcia Barbosa, a biogeographer and macroecologist with extensive experience in species distribution modelling, GIS and ecological modelling, with a particular focus on open, transparent and reproducible analytical workflows. Learn how to build, evaluate and interpret species distribution and ecological niche models using Bayesian Additive Regression Trees (BART) in R, providing a flexible Bayesian approach for investigating relationships between species occurrences and environmental conditions. For evolutionary biolo-

gists, species distribution and ecological niche models provide important tools for investigating environmental niches, geographic distributions, environmental associations and spatial patterns across species and populations. These approaches can complement evolutionary and biogeographic research examining how environmental conditions relate to observed distributions.

What you'll gain An understanding of species distribution and ecological niche modelling An introduction to Bayesian Additive Regression Trees (BART) Practical experience fitting Bayesian distribution models in R Working with species occurrence and climatic/environmental variables Selecting appropriate spatial resolution and geographic extent Computing and fine-tuning BART models to predict geographic distributions Interpreting posterior predictions, credible intervals and uncertainty Evaluating and cross-validating models Quantifying environmental variable importance Selecting relevant environmental predictors Producing partial dependence plots and maps Developing reproducible workflows that can be adapted to participants' own species and research questions

Course format 3-day live, instructor-led online course 12 hours of training Lectures combined with hands-on practical exercises in R Complete worked example from data preparation through to model interpretation Annotated R scripts that participants can adapt to their own species Opportunity to discuss participants' own data Code, datasets and presentation materials provided All sessions recorded 30 days of recording access and post-course email support

Who is this course for? Evolutionary biologists Evolutionary ecologists Biogeographers and macroecologists Researchers studying species niches and geographic distributions Researchers investigating environmental associations across species or populations Conservation and biodiversity researchers Researchers interested in integrating spatial and environmental information into evolutionary studies Postgraduate students and early-career researchers Participants should already be familiar with the concept of species distribution models (SDMs) or ecological niche models (ENMs) and have some basic experience using R. No previous knowledge of Bayesian statistics is required.

Why take this course? Understanding where species occur – and how their distributions relate to environmental conditions – is important across evolutionary ecology, biogeography and biodiversity research. Species distribution and ecological niche models allow researchers to quantify these relationships and explore geographic variation in environmental suitability. Bayesian Additive Regression Trees offer a flexi-

ble approach for modelling potentially complex species-environment relationships. The method can generate predictions while also allowing researchers to map the uncertainty and credible intervals associated with local predictions. The course goes beyond simply fitting a distribution model. Participants learn how to make decisions about spatial extent and resolution, evaluate predictive performance, cross-validate models, assess variable importance and examine partial responses to environmental predictors. These skills are particularly useful when distribution modelling forms part of a broader investigation into species' environmental niches, biogeography or spatial patterns of biodiversity. Whether you're studying species distributions, ecological niches, biogeography, environmental associations, biodiversity patterns or evolutionary ecology, this course provides practical training in applying Bayesian methods to spatial species data. Course dates 6-8 October 2026 14:00-18:00 UK time 12 hours — Live online — GBP385 Learn more & enrol <https://prstats.org/course/species-distribution-modelling-with-bayesian-statistics-sdmb08/> Questions? Email: oliver@prstats.org

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Online Structural Equation Modeling with AI Sep30-Oct2

Hello EVOLDIR members

A reminder - Strengthen inference about linked evolutionary processes from complex observational evidence. Structural Equation Modeling with AI is a 2-day seminar livestreaming September 30 and October 2 with Michael Zyphur (Instats). Evolutionary researchers can use latent variable models to evaluate theoretical pathways across noisy or multi-indicator genetic and phenotypic data. R and Mplus examples develop confirmatory factor analysis, mediation, bootstrapping, latent interactions, and instrumental variable SEM. AI-supported workflows address code drafting, estimation diagnostics, interpretation, and clear documentation for empirical evolutionary studies.

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

Best wishes

Michael Zyphur Director Instats

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Online Tidy Data Visualisation and AI Sep21-22

Hello EVOLDIR members A reminder - Evolutionary inference depends on records whose structure remains clear from import to figure. Tidy Data, Visualisation, and AI is a 2-day seminar livestreaming September 21-22 with Flavio Lombardo (Institute for Statistical and Data Science). Tidy data principles and reproducible graphics can help evolutionary researchers prepare observational and genetic datasets for analysis. Participants diagnose inconsistent codes and missing-value markers, then recode and reshape data with dplyr and tidyr. They also build ggplot2 figures that can communicate variation, comparisons, and patterns in manuscripts or supplementary materials.

Details and registration: Further information is available on the seminar page. Best wishes Michael Zyphur Professor and Director Instats

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RNAseqAnalysis U Edinburgh Online

RNA-Seq Analysis (RNAA02) - Applications for Evolutionary Biology Only 3 places left! https://prstats.org/course/rna-seq-analysis-rnaa02/?utm_source=chatgpt.com Delivered by Dr. Frances Turner, a bioinformatician at the University of Edinburgh with extensive experience supporting life-science researchers in the analysis and interpretation of high-throughput sequencing data. Her expertise includes transcriptomics, genomics, metagenomics, data quality, reproducible bioinformatics workflows, and down-

stream biological interpretation. Learn how to analyse bulk RNA-Seq data, from experimental design and raw sequencing data through quality control, alignment, gene-expression quantification, differential expression, visualisation, and functional analysis. RNA-Seq has become a powerful tool in evolutionary biology, allowing researchers to investigate how changes in gene expression contribute to adaptation, phenotypic variation, evolutionary responses, and divergence among populations and species. Transcriptomic approaches can reveal the molecular mechanisms underlying responses to environmental pressures, identify genes associated with adaptive traits, and help connect genomic variation with phenotype. This course provides comprehensive, hands-on training in RNA-Seq analysis, with methods highly applicable to evolutionary biology, evolutionary ecology, and comparative genomics.

What you'll gain: A strong understanding of RNA-Seq experimental design Practical experience with raw sequencing data and quality control Skills in sequence alignment and post-alignment quality assessment Understanding of gene-expression quantification and its potential pitfalls Practical experience performing differential expression analysis with DESeq2 Skills in PCA for investigating patterns of transcriptomic variation Experience analysing complex experimental designs, covariates, and continuous variables Skills in visualising differential expression using volcano plots, MA plots, and other approaches Understanding of functional analysis of differentially expressed genes using FGSEA

Course format: 4-day live, instructor-led online course Hands-on practical exercises throughout Real RNA-Seq analysis workflows Interactive discussions and opportunities to discuss participants' own datasets All code, datasets, and presentation materials provided Sessions recorded with 30 days of recording access and post-course email support

Who is this course for? Evolutionary biologists and evolutionary ecologists Population and evolutionary geneticists Evolutionary genomic researchers Researchers studying adaptation and phenotypic variation Researchers working with transcriptomic and high-throughput sequencing datasets PhD students and quantitative life scientists Participants should have basic experience with R, RStudio, and Linux, together with a basic understanding of transcriptomics and molecular biology.

Why take this course? Understanding evolutionary change increasingly requires researchers to investigate not only variation in DNA sequence, but also how genes are expressed and regulated. RNA-Seq provides a powerful framework for examining how gene

expression varies between populations, species, environments, treatments, and phenotypes. Transcriptomic approaches can be used to investigate adaptation, phenotypic plasticity, environmental responses, population divergence, evolutionary development, host-pathogen interactions, and the molecular basis of complex traits. Integrating RNA-Seq with genomic and ecological data can therefore provide important insights into the mechanisms connecting genotype, phenotype, and evolutionary processes. This course equips you with the practical skills needed to take RNA-Seq data from initial quality assessment through to differential expression and functional interpretation. Whether you're investigating adaptation, population divergence, environmental responses, comparative transcriptomics, or genotype-phenotype relationships, you'll gain a reproducible analytical workflow that can be applied directly to evolutionary research. Course dates 21-24 September 2026 18:00-21:30 UK time 14 hours — Live online — GBP350 Questions? Email: oliver@prstats.org

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Spain Evolution course Jan2027

Dear colleagues,

We are happy to launch the 4th Edition of "Principles of Evolution Course: biology through time & organizational levels" (POE), on behalf of the Spanish Society for Evolutionary Biology (SESBE), and Donana Biological Station (EBD-CSIC).

The course will take place at Reserva Biologica de Donana, within the National Park (Huelva, Spain) 11-22 January 2027.

This intensive course will cover broad aspects of the evolutionary process, across multiple timescales, organizational levels, and phylogenetic breadth. It will balance teaching of essential concepts with in-depth discussions of the forefront topics in each of the subdisciplines. It will combine theoretical and hands-on sessions, with ample opportunity for discussion, in an exceptional natural environment. The course will address multiple central topics in evolutionary biology:

Origin of life and eukaryogenesis - Evolution of multicellularity - Paleobiology and paleoanthropology - Phylogenomics and macroevolution - Population genetics - Phylogeography, landscape genetics and speciation -

Epigenetics - Sexual selection - Evolutionary developmental biology - Evolutionary ecology

The course is aimed at 15 early career researchers (PhD students and early postdoctoral fellows) with a strong focus in evolutionary biology in their projects.

Patricia Alvarez - Marta Barluenga - Ozren Bogdanovic - David Buckley - Pau Carazo - Elena Casacuberta - Fernando Casares - Santiago Elena - Borja Figueirido - Francisco Garcia-Gonzalez - Jose A. Godoy - Ivan Gomez-Mestre - Josefa Gonzalez - Alejandro Gonzalez-Voyer - Iker Irisarri - Sin Yeon Kim - Christoph Liedtke - Ignacio Maeso - Inigo Martinez-Solano - Jesus Marugan-Lobon - Dean McKeown - Borja Mila - Juli Pereto - David Posada - Ana Riesgo - Inaki Ruiz-Trillo

The course fee will be 300EUR, 250EUR for members of SESBE, and will include transportation from Seville to the National Park and back, board and lodging.

If you are interested in participating in the course, please send an Expression of Interest (2 pages max.) and an updated CV before November 5th 2026 to igmestre@ebd.csic.es and/or marta.barluenga@mncn.csic.es

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U Autonoma de Madrid Spain New Technologies for Developmental Evolutionary Biology Studies December14-17

Dear all,

We invite you to attend the course New Technologies for Developmental Evolutionary Biology Studies (4th edition), which will take place December 14th-17th 2026 at the Universidad Autonoma de Madrid, Spain. This link - <https://sites.google.com/view/evodevo2026/home> - provides all the information about the course, which is partially sponsored by the Centro de Investigacion en Biodiversidad y Cambio Global (CIBC-UAM - <https://www.uam.es/uam/cibc>), the Sociedad Espanola de Biologia Evolutiva (SESBE - <https://sesbe.org/>) and the Departamento de Biologia (<https://www.uam.es/ciencias/facultad/departamentos/biologia>) de la UAM.

This course, with a strong theoretical foundation and an

intense practical component, aims to update students' knowledge in evolutionary developmental biology and stimulate their creativity, expanding the range of techniques to be used in their research projects.

Topics covered:

comparative transcriptomics single cell transcriptomics bulk transcriptomics spatial transcriptomics ATAC-seq technique phylogenomics comparative genomics gene regulation plastic phenotypes evolutionary novelties

Eligibility and application process:

To apply, please send an email to the following address (ecoevodevo.cibc@gmail.com) indicating your name, position, and home institution. In addition, you should attach a letter of motivation to attend the course. Applicants will be selected based on their motivations and interests. Admitted students will be informed on October 30th. The acceptance email will provide the necessary instructions for the final registration and payment of fees.

Important Program Dates:

application opens: October 1, 2026 application due: October 25th, 2026 decisions sent: October 30th, 2026 early registration: before November 10th, 2026 registration due: November 20th, 2026 program begins: December 14th, 2026

Course Fees: CIBC members: early registration: 200 euros (before November 10th) late registration: 230 euros

non-CIBC members:

early registration: 230 euros (before November 10th) late registration: 260 euros

The Spanish Society for Evolutionary Biology (SESBE) will fund the registration of five participants who are members of the society (become a member here - <https://sesbe.org/asociate/>).

[//sesbe.org/asociate/](https://sesbe.org/asociate/)).

All the information for the course is available at <https://sites.google.com/view/evodevo2026/home> Kind regards,

The organizers: Cristina Grande, Patricia Alvarez-Campos, David Foronda y David Buckley

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UCL UK Morphological Phylogenetics Workshop

WHAT: Morphological Phylogenetics Workshop
WHERE: University College London, UK WHEN: October 9-11 2026 This workshop is joint-run by The Systematics Association, The Palaeontological Association and the Society of Spanish Researchers in the United Kingdom. It is a three day event held at UCL and run by experts in the field of phylogenetics. The workshop will cover a broad range of areas including an introduction to Bayesian inference, discrete character construction and ancestral character estimation, as well as hands on training on how to use tools including MCMCTree and RevBayes. Places are limited and thus priority will be given to attendees that already have the rudiments of phylogenetic analyses and command line use. Student bursaries are also available (see website for details.) DETAILS: <https://systass.org/morphological-phylogenetics-workshop/> REGISTER: <https://forms.gle/yBHR5yDGyFtB2NF49> (to subscribe/unsubscribe the EvolDir send mail to evoldir@evoldir.net) evoldir@evoldir.net)

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to evoldir@evoldir.net. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to evoldir@evoldir.net. In addition, if it originates

from ‘blackballed’ addresses it will be sent to `evoldir@evoldir.net`. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to `evoldir@evoldir.net`. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email `evoldir@evoldir.net`. Do not include encoded attachments and do not send it as Word files, as HTML files, as $\text{\LaTeX}$ files, Excel files, etc. ...plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to `evoldir@evoldir.net` and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by $\text{\LaTeX}$ do not try to embed $\text{\LaTeX}$ or $\text{\TeX}$ in your message (or other formats) since my program will strip these from the message.